

CGTTGAGCCA AATGAAGCTG GAGAAACACG CTTTACCTAT GCCACTTATG GTGAGGGAAA	180
GCTTCCAGAA GGTCTGACCA TTTCCCTCAA GGAGAGTGCA GAAACGAGTG ATTTATTAGG	240
GTCTTACTTG ATGTATCAG GAAGTTTGA TGGAGTGAGC TTACAGACCA CCTTGAAAGA	300
GCTTGGTTAT CAAGGCTTTG TTTTCAATGG AGAAGATCCA TTTTCGATAG TCTTACTATT	360
GACGGCCACC CCTATGGTGC TACTGAGTTT AGCTATTTT CTGCTGACCT TTATGAGTCT	420
GACCCTGATT TATCGGATCA AATCCCTTCG TCAGGCAGGG ATTCGCTTAA TAGCTGGTGA	480
GAGCTTGTTT GGAGTTGCTC TCAGACCAGT GTTAGAAGAT GTGAGACAGC TTATCTGCTC	540
AGTGCTGGTA TCCAGTCTTT TGGGATTGGG GATTCTCTGG TATCAAGGTG CCTTGTTTAT	600
GGCAACGGTG CAACTGGTCA TCATTGCTCT TCTACTTTAT GGATTGACCT TGGCAGGGAT	660
TTCTACCTTA CTAAGTGTG TCTATCTACT TGGTTTACAG GAAAATAGTC TGGTGGATCT	720
ATTGAAAGGG AAACCTCCCTC TCAAACGTAT GATGACATTG ATGATGGTGG GGCAACTCTT	780
AGCTGTATTG GTGGTCGGAT CGAGTGCGAC AGCTCTCCTA CCCCCTACC GTGAAATGCA	840
GGAAATGGAG AGAGCTAGCA ATAAATGGAG CCAGTCTCA GACCGTTACC GTCTATCCTT	900
TGTTTGGTCT AGTGCATTTG CCGATGAAGA AGGAACGCGT AAGGATAATC GTGAGTGGCA	960
GACATTTACT GAAGAACGGT TAGCCAATAC AGACTCTTTT TATATTATGA GCAATGTGA	1020
CAATTTCTCA GATGGAGCAG AAGTGGACCT AGATGGCAAT CGTCTCAGT ACTACACACC	1080
GTCAGGGAAT GTTATCTATG TCTCACCGCG CTATCTGATA GAAGAAAAGA TTACCGTTTC	1140
TTTCAAGTTT ATGGACAAGA TGCAAACTT GTCTGAGGGA GAGTTTGGGC TGATCTTGCC	1200
TGAGAGCTTG CGAGAGCAGT CTGTCTACTA CCAAGGATTG TTTACAGATT ACCTGCAAAA	1260
CTTTTCATCT GAAAGTGTAG AAGTGACGAG TCAGAAACAC TACCTCCCAC AGGTAAGGCT	1320
AGCTTTTACA GAAACAGGAC AGGAACGTTT CCTCTATAAT GATGGGTACA AGACAACACG	1380
CCAGTACCTA AAAGATCCGA TTATTGTAGT TCTAACGCCG CAAGCGACTG GAACAAGACC	1440
TGTTGCAGGG ATGTTGTGGG GAACTACGGC TAATAGTGCC TTGAAACTAG ATCGATATGG	1500
AGACAGCATC ACAGCTCTAA AAGAGAAAGG TCTGTATCAC AAGGTTTCTT ACTTGGTAAA	1560
AAGCCAGCTA TTTTTTGCCA AGGTAATAAA TGACAAACGG GTGGAGTTT ACTCTCTCCT	1620
TATTGGGACG ATTTTGACCC TGTCTACGGC TATCTTGTTA TTTGATTCCA TGAATCTTCT	1680
CTATTTTGAG CAGTTCAGAC GGGAACTTAT GATTAAACGT CTTGCTGGTA TGACAACTA	1740
TGAGCTTCAT GGCAAGTATT TACTGGCGCA AGGAGGAGTT CTCTTGCTTG GCCTAGTCCT	1800
ATCTAGTATT TTGACAAGAG ATGGTTTGAT TAGCGCTCTA GTTGTAGCTT TGTTTACGCT	1860

1000

TAACGCCCTC	TTGATTTTAG	TAAGGCAGGA	CAAAAAAGAA	GAAGCTGGTA	GCATGGCAGT	1920
ATTGAAAGGA	AAATAAGATG	ATTGATATTC	AAGGATTGGA	AAAGAAATTT	AATGACCGCG	1980
CGATTTTCTC	TGGTTTGAAT	CTCAAGCTGG	AGAAGGGCAA	GGTTTATGCC	TTAATCGGAA	2040
AGAGTGGAAG	CGGAAAGACG	ACGCTGCTGA	ATATCTTGGG	AAAGCTAGAA	AAGATAGATG	2100
GTGGAAGGGT	TCTCTATCAG	GGGAAAGATT	TAAAAACCAT	TCCCACTCGT	GAGTATTTTC	2160
GAGACCAGAT	GGGCTATCTC	TTTCAAAAT	TCGGCCTCTT	AGAAAACCAA	TCAATCAAAG	2220
AAAATTTGGA	TTTGGGTTTT	GTTGGTCAGA	AAATCTCAA	AGTAGAACCT	TTGGAAAGGC	2280
AAGTGGGGGC	TTTAGAAAA	GTTAATCTAG	GGTATTTGGA	TTTAGAACAA	AAAATCTATA	2340
CTTTATCTGG	GGGAGAGGCC	CAACGAGTTG	CCCTTGCTAA	GACTATTTTG	AAAAATCCAC	2400
CCTTGATTTT	GGCAGATGAA	CCAACAGCAG	CTCTTGATCC	TGAAAATCA	GAGGAGGTTA	2460
TGAATCTCTT	GGTGGATTTG	AAAGATGAAA	ATCGAATTAT	CATCATTGCG	ACCCATAATC	2520
CCCTAGTCTG	GAATAAGGCT	GATGAAATCA	TTGATATGAG	GAAACTTGCT	CATGTGTGAA	2580
AAAATCCGTA	TTGCGAGGGT	ATCTGATTAT	CCTAGTGCCA	GAGGTGGTTT	AGAAGATATC	2640
CTCATCATGG	AAAATATGAC	CAATCATCTC	CTTTTGTTTC	AAATCCGAGT	GCATGGCTAT	2700
TTGCTTGATT	TTGCTAGTAT	TGAAGGGCAA	AGGCAAAAGC	ATPATCGTTT	GAAAAATTTA	2760
CCTCAGACGG	TTGAACTGAC	ACTGGATGAT	GTGGAGGAGG	ATGTGGATTT	GACCCACCT	2820
GAAAATCGAA	GTTATCAAGA	AGCTGATTTT	TTTGAACGCA	TGTTTCGAGA	GAAGTCTAA	2880
GGCCACTTTT	AAAGATTTC	AAGACTATCT	TTCTTCATGA	GGAAAGATAG	TTTTTTGGTA	2940
TGATTTTCAT	TCCCAAAATA	CAAGGGGAAT	GTGTTACAAT	AGTAGTAACA	GATAATAGAA	3000
AAGAGAATAG	ATGAGAATTG	CAGATTATAG	CGTGACCAAG	GCAGTCTGG	AGCGTCACGG	3060
TTTTACCTTT	AAAAAGTCCT	TTGGGCAAAA	TTTTTTGACG	GATACCAATA	TCCTTCAAAA	3120
AATTGTGGAT	ACGGCTGAAA	TTGATGATCA	GGTCAATGTC	ATCGAAATCG	GGCCAGGTAT	3180
TGGTGCCTTG	ACAGAATTTT	TGGCTGAGCG	TGCAGCCCAA	GTCATGGCTT	TTGAGATTGA	3240
CCACCGTTTG	GTGCCAATTT	TGGCAGATAC	CCTGCGTGAT	TTTGATAATG	TGACCGTAGT	3300
TAACGAAGAT	ATTCTCAAGG	TTGATTTGGC	GCAACATATC	CAGAATTTTA	AAAATCCTGA	3360
CCTGCCAATC	AAGGTAGTGG	CTAATTTGCC	TFACTACATC	ACGACGCCTA	TTCTCATGCA	3420
CTTGATTGAG	AGTGGCATT	CTTTTTGTGA	GTTTGTGGTC	ATGATGCAGA	AAGAAGTAGC	3480
GGACCGCATT	TCAGCCCAGC	CTAACACCAA	GGCTTACGGT	AGCTTGTCTA	TCGCCGTGCA	3540
GTATTACATG	ACAGCCAAGG	TTGCCTTTAT	CGTGCCTCGT	ACGGTCTTTG	TGCCAGCGCC	3600
AAATGTGGAT	TCAGCCATCT	TGAAAATGGT	GCGTCGTCCA	GAGCCAGCCG	TAGCAGTAGA	3660

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AGATGAGAAC	TTTTTCTTTA	AGGTTTCCAA	GGCTAGTTTT	ACCCATCGCC	GCAAGACCTT	3720
GTGGAATAAC	TTGACAGGTT	ACTTTGGTAA	GACTGAAGAG	GTCAAGGACA	AGCTGACCAA	3780
GGCTTTGGAC	CAGGCAGGCT	TGTCACCAAG	TGTGCGTGGG	GAAGCTCTCA	GCTTGGCAGA	3840
ATTTGCCGGT	CTAGCAGACG	CACTTAAAGG	GCAAGGACTC	TAAGATGCAG	GGACAAATCA	3900
TTAAAGCCTT	GGCAGGTTTC	TACTATGTGG	AGAGTGATGG	CCAGGTTTAT	CAAACACGGC	3960
CGCGTGGGAA	TTTCCGTAAA	AAAGCCATA	CCCCTTATGT	TGGGGACTGG	GTAGATTTCT	4020
CTGCCGAGGA	AAATTCAGAA	GGCTATATCC	TCAAAATTC	CGAACGGAAA	AACAGTCTGG	4080
TTGCTCCGCC	TATTTGTCAAT	ATCGATCAAG	CTGTAGTAAT	CATGTCCGTC	AAGGAACCTG	4140
ATTTTAACAG	CAATTTGCTG	GATCGTTTCT	TGGTTCTTTT	GGAGCACAAG	GGCATCCATC	4200
CCATTTGCTA	TATTTCCAAA	ATGGATTTGT	TGGAAGATAG	GGGAGAAGTG	GATTTTACC	4260
AGCAGACCTA	TGGTGACATC	GGCTATGACT	TTGTGACCAG	TAAAGAGGAA	CTCCTGTCTT	4320
TGTTAACAGG	CAAGGTTACG	GTCTTTATGG	GGCAGACAGG	TGTTGGGAAG	TCAACTCTTC	4380
TCATAAAAAT	CGCACCAGAC	CTCAATCTTG	AAACGGGAGA	AATTTAGAC	AGTCTAGGTC	4440
GCGGTCGCCA	TACCACTCGA	GCTGTTAGTT	TTTACAATCT	CAACGGGGGT	AAAATCGCAG	4500
ATACACCAGG	ATTTTCATCC	TTGGACTATG	AAGTATCAAG	GGCTGAAGAC	CTCAATCAGG	4560
CTTTCCCGA	GATTGCTACT	GTAGCCGAG	ATTGTAAGTT	CCGTAAGTT	ACCCATACCC	4620
ATGAGCCGTC	TTGTGCCGTC	AAACCAGCTG	TTGAAGAGGG	TGTTATTGCA	ACCTTCCGTT	4680
TTGACAATTA	CCTGCAATTC	CTTAGTGAAA	TTGAAAATCG	TAGAGAAACC	TATAAAAAAG	4740
TCAGCAAAAA	AATTCAAAA	TAAGGAGAAA	CCTATGTCTC	AATACAAGAT	TGCTCCGTCA	4800
ATTCTGGCAG	CAGATTATGC	CAACTTTGAA	CGTGAAATCA	AACGTCTAGA	AGCAACTGGG	4860
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GCAGGTGTGG	TCGAGAGCCT	TCGTCTCAT	AGTAAGATGG	TTTTCGATTG	CCACTTGATG	4980
GTGTCAAACC	CTGAGCATCA	TCTGGAAGAT	TTTGC CGTG	CAGGTGCAGA	CATCATCAGT	5040
ATCCATGTAG	AAGCAACGCC	TCATATTCAT	GGCGCCCTCC	AAAAAATTCG	TTCACTCGGA	5100
GTTAAGCCTT	CAGTCGTTAT	CAATCCTGGC	ACATCAGTTG	AAGCCATCAA	GCACGTCCTT	5160
CATCTAGTTG	ACCAAGTTTT	AGTCATGACG	GTTAATCCAG	GTTTTGGTGG	GCAAGCCTTT	5220
CTGCCAGAAA	CCATGGATAA	GGTCCGTGAG	TTGGTTGCTC	TTCGTGAGGA	AAAAGGTTTG	5280
AACCTTGAAA	TCGAAGTGGA	TGGTGGGATT	GATGACCAA	CTATTGCTCA	AGCCAAAGAA	5340
GCCGGTGCGA	CTGTTTTTGT	AGCAGGTTC	TATGCTTTA	AGGGAGAAGT	CAATGAGCGA	5400

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GTACAAACTC	TCAGAAAACA	ACTGGACTAG	GGTTGCAGTT	TTTGCAGGCG	GAAACCGCGG	5460
TCATTATCGG	ACAGATTTTG	ATGCTTTTGT	TGGGGTGGAT	CGAGGCTCGC	TCTGGGTCTT	5520
GGAAGAAGAC	TTACCTCTTG	CTCTAGCAGT	CGGAGATTTT	GATTCTGTGA	CGGAAGAAGA	5580
GCGACAGGTG	ATTCAAAAAG	GTGCCCAGTA	TTTTGTCCAA	GCACGACCAG	AAAAGGATGA	5640
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TATTTTCGGT	GCCTTGGGTG	GCCGTATTGA	CCATATGTTG	GCCAATGTCT	TTCTGCCTAG	5760
CAATCCTAAG	TTGGCACCCCT	ATATGCATCA	AATAGAAATT	GAGGATGGGC	AAAACCTTGAT	5820
TACTTATTGT	CCAGAAGGAA	TCAGTCAGCT	AGAACCCTCGT	TCAGACTACG	ACTATCTAGC	5880
CTTTATGCCA	GTTCGGGATA	GCCAGCTGAC	TATTCTTGGA	GCCAAGTATG	AGTTGACAGA	5940
GGAAAATTTT	TTCTTTAAAA	AAGTGTACGC	TTCTAACGAA	TATATAGATA	GGGAAGTGTC	6000
GGTAACTTGC	CCAGATGGTT	ATGTGGTCGT	ACTGCATAGC	AAGGACAGGA	GGTAGGATGG	6060
AAAGTTTACT	TATTCTATTA	TTAATTGCCA	ATCTAGCTGG	TCTCTTTCTG	ATTTGGCAAA	6120
GGCAGGATAG	GCAGGAGAAA	CACTTAAGTA	AGAGCTTGGA	GGATCAGGCA	GATCATTTGT	6180
CAGACCAGTT	GGATTACCGC	TTTGACCAAG	CCAGACAAGC	CAGCCAGTTA	GACCAAAAAG	6240
ATTTGGAAGT	GGTTGTCAGC	GACCGTTTGC	AAGAAGTGC	GATTGAATTG	CACCAAGGTC	6300
TGACCCAAGT	CCGTCAAGAA	ATGACAGATA	ATCTCCTCCA	AACTAGAGAC	AAGACAGACC	6360
AACGTCTCCA	AGCCTTGCAG	GAATCAAATG	AGCAACGTTT	GGAACAAATG	CGCCAGACGG	6420
TCGAGGAAAA	ACTAGAAAAG	ACCTTGCAGA	CACGCTTACA	GGCTTCCTTT	GAGACAGTTT	6480
CTAAACAAC	GGAGTCTGTC	AATCGTGGCC	TTGGAGAAAT	GCAGACAGTT	GCCCCTGATG	6540
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AACTGGGGCA	AATTATTGAA	GACATCATGA	CACCTGCCCA	GTACGAACGA	GAATACGCAA	6660
CGGTGAAAA	CTCTAGTGAA	CGAGTGGAGT	ATGCCATCAA	GTTACCCGGA	CAAGGCGACC	6720
AAGAATACGT	CTATCTGCCA	ATTGACTCTA	AGTTTCCACT	GGCAGATTAT	TACCGCTTGG	6780
AAGAAGCCTA	TGAGACAGGT	GACAAGGATG	AGATTGAACG	CTGTCGTAAG	TCACTCCTAG	6840
CAAGCGTCAA	GCGCTTTGCT	AGGGATATTA	GGAACAAGTA	CATAGCACCA	CCTCGGACGA	6900
CCAATTTTGG	AGTTTGTGTT	GTTCCGACAG	AAGGTCTCTA	CTCAGAAATC	GTCCGCAATC	6960
CGGTCTTCTT	TGATGATTTG	AGACGGGAAG	AACAGATTAT	TGTTGCAGGA	CCAAGTACCC	7020
TATCAGCCCT	TCTTAACTCC	CTATCAGTTG	GTTTCAAGAC	CCTTAATATC	CAAAAGAGTG	7080
CCGACCATAT	CAGCAAGACT	CTTGCCAGTG	TCAAGACCGA	GTTTGGCAAG	TTTGGTGGTA	7140
TTCTGGTCAA	GGCACAAAAA	CATCTCCAAC	ATGCCTCTGG	CAATATTGAT	GAATTATTAA	7200

1003

ACCGTCGTAC	CATAGCTATC	GAGCGGACGC	TCCGTCACAT	TGAGTTGTCA	GAAGGTGAGC	7260
CTGCGCTTGA	TCTACTCCAT	TTTCAAGAAA	ATGAGGAAGA	ATATGAAGAT	TAGTCACATG	7320
AAAAAAGATG	AGTTATTTGA	AGGCTTTTAC	CTAATCAAAT	CAGCTGACCT	GAGGCAAACCT	7380
CGAGCTGGGA	AAAACCTACCT	AGCCTTTACC	TTCCAAGATG	ATAGTGCGCA	GATTGATGGG	7440
AAGCTCTGGG	ATGCCCAACC	TCATAACATT	GAGGCCTTTA	CCGCAGGTAA	GGTGTGCCAC	7500
ATGAAAGGAC	GCCGAGAAGT	TTATAACAAT	ACCCCTCAAG	TCAATCAAAT	TACTCTCCGC	7560
CTGCCTCAAG	CTGGTGAACC	CAATGACCCA	GCTGATTTCA	AGGTCAAGTC	ACCAGTTGAT	7620
GTCAAGGAAA	TTCGTGACTA	CATGTCGCAA	ATGATTTTCA	AAATTGAAAA	TCCTGTCTGG	7680
CAACGGATTG	TCCGAAATCT	CTACACCAAG	TATGATAAGG	AATTCTACTC	CTATCCAGCT	7740
GCCAAGACCA	ACCACCATGC	CTTTGAAACG	GGCTTGGCCT	ATCATACGGC	GACCATGGTG	7800
CGTTTGGCAG	ACGCTATTAG	CGAAGTTTAT	CCTCAGCTCA	ATAAGAGCCT	GCTCTATGCG	7860
GGGATTATGT	TGCATGACTT	AGCTAAGGTC	ATCGAGTTGA	CGGGGCCAGA	CCAGACAGAG	7920
TACACAGTGC	GAGGTAATCT	TCTTGGACAT	ATCGCTCTCA	TTGATAGCGA	AATTACCAAG	7980
ACAGTTATGG	AACTCGGCAT	CGATGATACC	AAGGAAGAAG	TCGTTTTGCT	TCGTCAATGTC	8040
ATCCTCAGTC	ACCACGGCTT	GCTTGAGTAT	GGAAGCCCAG	TCCGTCCACG	CATTATGGAA	8100
GCAGAGATTA	TCCATATGAT	TGACAACTCTG	GATGCAAGCA	TGATGATGAT	GTCAACAGCT	8160
CTTGCTTTGG	TGGATAAAGG	AGAGATGACC	AATAAAATCT	TCGCTATGGA	TAATCGTTCC	8220
TTCTATAAAC	CAGATTTAGA	TTAATAATTT	AAGAAAAATG	AGCATTTTTT	AGGATAAGAA	8280
TGTTTCGTTTT	TTTATGTGAA	TATGGTATAA	TAAGTAAAAG	ACAAAAATGA	ATACTCTTCG	8340
AAAATCTCTT	CAAACCTAGGG	TAGTATCGCC	TTGTCTGATG	TATATATGCA	GGTATATTAC	8400
AGGGTTTGTC	AGTTCTATTG	ACAATCTCAA	AACAGTGTTC	TGAACCACCA	GCGACCAGCT	8460
TTCTAGTTTG	CTTTTTGATT	TTTTGAATAA	AAATGGAATA	GGAAATAGAA	ATGAAATTAA	8520
GAAGAAGTGA	TCGGATGGTT	GTCATTTCCA	ACTATTTGAT	TAATAATCCT	TATAAACTAA	8580
CTAGTCTCAA	TACTTTTGCT	GAAAAGTATG	AGTCTGCTAA	ATCATCCATC	TCAGAAGATA	8640
TCGTCAATAT	CAAACGCGCC	TTTGAGGAAA	TTGAAATCGG	TCATATCCAG	ACAGTGACTG	8700
GGGCTGGCGG	AGGTGTCATC	TTCACACCGT	CTATTTGAG	TCAGGATGCT	AAGGAAATGG	8760
TTGAAGACTT	GCGTACCAAG	TTGTCAGAAA	GTGACCGTAT	CTTGCCAGGT	GGTTATATCT	8820
ATCTGTCTGA	TTTGCTTAGC	ACACCAGCCA	TCTTGAAAAA	TATTGGTCGT	ATTATTGCCA	8880
AAAGCTTTAT	GGACCAAAAA	ATTGACGCGG	TTATGACCGT	AGCAACTAAG	GGTGTGCCAC	8940

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TTGCAAATGC	AGTTGCCAAT	GTCCTCAATG	TCTCTTTTGT	CATTGTGCGC	CGTGACCTGA	9000
AAATTACCGA	AGGTTCAACT	GTTAGCGTCA	ACTATGTTTC	AGGTTCAAGT	GGTGACCGTA	9060
TCGAGAAAAT	GTTCCTTTCA	AAACGTAGTC	TTAAGGCAGG	CAGCCGTGTC	TTGATTGTGG	9120
ATGACTTCTT	GAAAGGTGGC	GGAACGGTCA	ATGGTATGAT	TAGTCTCTTG	CGCGAGTTCCG	9180
ACTCAGAACT	GGCAGGTGTA	GCGGTCTTTG	CGGACAATGC	CCAAGAAGAA	CGTGAAAAGC	9240
AGTTTGACTA	CAAGTCACTC	TTGAAGGTAA	CCAATATTGA	TGTCAAGAAC	CAAGCCATCG	9300
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CGATTGTCCC	AGCCTTTCTT	TGCAAACAGA	ATAGAAGGAA	GCTTATGAAA	ACACCATTTA	9420
TCAATAGAGA	AGAGTTAGAA	GCGATTGTTG	CCGAGTTCCC	GACTCCCTTT	CACTTGTATG	9480
ATGAGAAGGG	GATTCGTGAG	AAGGCAAGAG	CCGTCAACCA	AGCTTTTTCG	TGGAACAAGG	9540
GCTTTAAGGA	ATATTTTGCA	GTTAAGGCTA	CTCCAACCTC	AGCTATTTTG	AAAATTCTCC	9600
AAGAAGAAGG	TTGTGGTGTG	GACTGCTCTA	GTTATGTAGA	GCTTTTGATG	AGCCATAAAC	9660
TGGACTTTCT	GGGTCTGAG	ATTATGTTCT	CTTCCAACAA	CACGCCAGAC	AAGGAATACG	9720
CCTATGCACG	TGAATTGGGT	GCGACCATTA	ACTTGGATGC	CTTTGAAGAT	ATTGAACATC	9780
TGGAGAGAGT	AGCAGGCATT	CCAGAAATCA	TCTCTGTGCG	TTATAATCCT	GGAGGCGTTT	9840
TTGAACTGGG	GACAGACATT	ATGGACAATC	CTGGGGAGGC	TAAGTTTGGC	ATGACCAAGG	9900
ACCAGCTCTT	TGAAGCCTTT	GCTATCTTGA	AGGAAAAAGG	AGCCAAGACT	TTTGGGATTC	9960
ACTCCTTCCT	AGCGTCCAAT	ACCGTGACCC	ATCTCTATTA	TCCAGAGTTG	GCTCGTCAGC	10020
TCTTTGAACT	GGCTGTTGAA	ATCAAGGAAA	AGTTGGGCAT	TTCGCTAGAC	TTTATCAATC	10080
TTTCTGGCCG	TATTGGTGTG	AATTATCATC	CAGACCAGGA	GCCGAACGAT	ATCGCCTTGA	10140
TTGGTGAGGG	AGTTCGTAAG	GTGTATGAAG	AGGTTCTTAC	GTCAGCAGGT	CTTGGTCAGG	10200
TCAAGATTTT	CACCGAATTG	GGTCGTTTFA	TGCTGGCACC	TCACGGTGCT	CTAGTCACAA	10260
GAGTCACTCA	TAAGAAGGAA	ACCTACCGTA	CCTATCTAGG	TGTGGATGCC	TCAGCAGTCA	10320
ACCTCATGCG	TCCAGCTATG	TACGGAGCTT	ACCATCATAT	TAGCAACGTG	ACCCATCCAG	10380
ATGGACCAGC	TGAAGTGTA	GATGTGGTCG	GTTCACTCTG	TGAAAACAAT	GATAAATTTG	10440
CAGTTAATCG	CGAACTGCCT	CATACAGAAA	TCGGTGATTT	GCTGGTCATT	CATGATACAG	10500
GTGCCCACGG	ATTTTCAATG	GGCTACCAAT	ATAATGCCAA	ATTACGTTCT	GCGGAAATCC	10560
TCTATACCGA	AGAAGGTAAA	GCCCCTCAAA	TCCGCCGTGC	AGAGCGCCCT	GAGGACTATT	10620
TTGCAACCTT	ATATGGCTTC	GATTTTGAAG	AATAATCTGA	TAATAGATTG	AAAATGAAAT	10680
TGAAAAACAG	ATFGCTTTCT	AAAAAATAGG	CAAAAATCTT	GTTTTTCCTT	CAAGTCGTGA	10740

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TATAATAAAA	CTATAAAACG	TTTTCAAGGA	AGGTAACGAT	ATGCTCTGAAG	AAACAATTGA	10800
TTATGGACAA	GTGACAGGAA	TGGTGCATTC	GACAGAAAGC	TTTGGGTCAG	TAGATGGGCC	10860
TGGTATTCGC	TTTATTGTCT	TTTTGCAGGG	CTGTCACATG	CGTTGCCAGT	ATGCCCACAA	10920
CCCAGACACT	TGGGCTATGG	AGTCCAATAA	GTCACGTGAA	CGGACGGTAG	ATGATGTCTT	10980
GACAGAGGCC	TTGCGCTACC	GTGGTTTCTG	GGGAAATAAG	GGTGGGATTA	CAGTCAGTGG	11040
AGGAGAAGCT	CTCTTGACAG	TTGATTTCCCT	GATTGCTCTC	TTCACCAAGG	CTAAGGAACA	11100
AGGAATCCAC	TGTACCTTGG	ACACCTGTGC	TCTTCCTTTC	CGTAATAAAC	CACGTTACCT	11160
TGAGAAGTTT	GACAAACTCA	TGGCTGTCAC	TGACTTGGTT	CTTTTGGATA	TCAAGGAAAT	11220
CAACGAAGAA	CAGCACAAGA	TTGTCACTAG	CCAAACCAAT	AAAAATATCT	TGGCTTGTGC	11280
CCAGTATCTA	TCAGATATTG	GAAAACCTGT	CTGGATTCCG	CACGTGCTAG	TTCCAGGATT	11340
GACAGACAGA	GATGATGACT	TGATTGAACT	TGGTAAGTTC	GTCAAGACCC	TCAAAAATGT	11400
TGATAAGTTT	GAAATCTAC	CTTATCACAC	CATGGGTGAG	TTCAAGTGGC	GTGAACTTGG	11460
AATTCATAT	TCCCTCGAAG	GAGTCAAACC	ACCAACAGCA	GATCGCGTCA	AGAACGCTAA	11520
ACAATCATG	GATACCGAAA	GTTATCAAGA	TTATATGAAA	CGTGTACATG	GATAGAAAAG	11580
AAGCCTGATG	GAAACATCGG	GCTTTGACT	TGCAAAAAGA	CTTAGCAAAT	CAGCTAAGCC	11640
TTTTTCTTCT	TATCTCGAAC	GTTGTTTTCC	AGCGTTGCGA	TTTTTGTGTT	TTTTCTTGCT	11700
TGTGATAGCA	GTTGGTTGTT	CAGGGGTAAC	GTCTTTTCGT	CCACTTGGTT	TAGAGAAAAGC	11760
ACTTGCTTTT	GGTGGGTTCT	TGGCTAGTTC	TTCACGGACT	TTTTTGCAG	GTTTGGGACG	11820
AACGATATAG	TTGACGATAA	ACTGTTGGAG	AATCATCATG	AAACCACCGA	CAACCCAGTA	11880
AAGTGTGACA	CTAGCTGGTG	AGAAGAGGGA	GAAGACGACG	ATCATGAGTG	GGCTCATGTA	11940
AATCATTTTC	TTGATTTGTT	CTCTTTGCAT	TTCATCTTCT	ACTCCGTGAA	GTGAAAGGAG	12000
CGATTGAAGA	TAGTAAAGGA	CACCAGCACA	GGCAACCAAA	ATCATACTTG	GAGAACCCTAG	12060
AGGAATGCCT	AGGTAGCTTG	CTTGAGCAAC	CCCTTCAGTA	TGTTGGGCAG	CAAAGTAGAT	12120
AGCAGAGAAG	AAAGGCATTT	GAAGGAGGAT	AGGGAAACAT	CCTACACCGC	CAAACATGCT	12180
GATACCGTGC	TCTTTTGGAG	CAGCAAAGAG	AGCTTGTTGG	GCTTCGAGTT	TTTCTTCTTG	12240
AGTAGTCGCT	TCTTTGAGAC	GCGTTTGGTG	TGGCTCAAGG	ACGTGCTTGA	GGGCGTTCAT	12300
CTTTTCAGAG	TGAAGCGTTG	CCTTCCATGA	TTGGTAGATA	CCAAGTGGTA	AGATAATCAA	12360
GCGTACGATA	ATGGTTACGA	TAATGATAGC	GACACCAAAG	CCTAGACCTT	TATCAGTAGC	12420
GAAGTACTTG	ATGGCTTCAG	CCATAGGCGC	TCCGATCGTA	TTCCAAATAA	ATCCTGTTGG	12480

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CTGACCTGTG GTTTTATCGA CATTGACACA GCCAGTCAAG ACAAGCAACA TAGCCACTCC 12540
 CATAGCCGAG AGTGCAAAAT CGGGGT 12566

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TGACACTCTG TAGGATTGTC GTTAATTGAT TGCTCGTACT CTCTACAATA ACCACCAAAG 60
 TAAAAACGAC ATAGAAAGAT AGCATCAGCT GTAGCCATAG CGCCTTTGAC ACCTTCTGGA 120
 TGATTATGAG TTACCTCTGC AGAAAGACTC GTAAGTCCTC TAGATGATGG CCATATACCA 180
 GTTTTCGCAT AAAAACCCACA GTCCATGATC CAAGCACATG GAGAAATACG CATAGCTGAT 240
 CCATTCCCAA AGCTATTATA AGGCTCACGG TTATCGCTGT TTAGCCATGC ATTAAACCGA 300
 GCACCATAAT CAGCATTCGG ATACATTCTG CCATATTTCT TCATCGCGTC AATGAAGTCA 360
 TCTTTTTGTC CACCATTCAT AATTGCTTCT GCAACAGCAC AGGTCATAAC CGTGTCATCT 420
 GTAAAAAAGC AGTCCTTCCG AAATAAAGGA AAGTCCTTTG TTTTGATATT GTTCCATTTCG 480
 TAAACAGAAC CGACAATATC TCCAATAATT GCTCCAAGCA TCAGATTCCCT CCTTGTTTCAT 540
 TTTGATGCTT TTTATATTGG TTATCTACCA TATTTATTTT AGAAAATAAC ATCCTGTTGG 600
 ATTTTAAAAA TTTTATTTT TTCAAAATAG GGTTTTACCA TTTCTTTCCA CCTAGCTCTA 660
 TGAAAATTGA TTGATTTTAA AGGAGATAGG CCATAATTTT CCAATGCATA ACCATCATTT 720
 ACTTCAACAA CAAGTGTCTT GCCATCGCGA GTAACACCGA TATCTAGTCC ATAAGCTATT 780
 GGCGCATCTT TCCAACATGA TATCGCTTCA TCAATTACAC TTGCATCAA TTGTGCATGA 840
 TAATCACCTG TATAGGTCG AACATCTAAT ACGCGACCAT CTAACACAAA ACAACGCCAT 900
 TCAGCTATGA ATTCTACAAC CTCACTAATC CATATAGGAT AGTCGAAAGG TAGACCAATA 960
 CCTATTAAAT CATGGGTTCC ATTAACAACCT CTTCCAGTAA AGACTTTTGA ACCAGCTTTA 1020
 GGCTTAATAA ATTTTCCCA ATTATCAGGT ATATTCACAA TCTCTCCTAA AATACCAGCA 1080
 TAAATCTTTC GACCATAAAA CTCTTTAAGC TCAATAGGAT AGTCATGAAC CGGAACGTTT 1140
 AAGCCCATCA TTTTATAGTAA TGCTCTAGTC TCCATTATAT AATCTACAAC TATATCTTCA 1200
 CTTGTTAACT CTTTTATTTC AGAAAAAGAT TGATATAAAA TAACTTCTTC TCCTTGTAAG 1260
 TAGGCACCTA CTTGAGCATT GTATTTATTA ATTGAAACCT CACTTGGTAA TTTACTTTGT 1320

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CTAATATAAA	CAACCAT TTC	ATCACTCCTA	TATCACTAGT	GTTACACCAA	TTTGTAAAAA	1380
ATAATAGCAA	TTTTGCTCTT	ATTTTTTTGA	GTAAATAGCC	CCCATAATAT	CATCGAAATA	1440
ATCAACGGTA	TTTAGGAGTA	ATTCAATAAC	CTGGGACTTT	GTTAGTCGCA	TTCCCCTTCT	1500
ATCTCTAGCA	TCTTCTACTA	AATTTTCAAG	TTTCTCTAGA	TTTTTATCAT	CCAAGCTAAT	1560
CATTATTCTA	TTTTTATCGG	TTGCCATTTT	CATCACCTCA	AGTTAATTCT	ATCACAGGTG	1620
TAACACTAGT	GTCAACTGGC	TTTTATAATA	CATTAGTTTA	AAAGTGGAGA	GGATTTTTAA	1680
CACAGTAACT	TTAAATCTTT	GGTATTAAAA	AATTTTCACA	ATATTTATAG	AAATAAAATC	1740
TGTCTCAAAT	CAGTTATCAA	ATCTAGTATA	AATTATGAGC	GGCTACTCTA	ATACTTTCCC	1800
TCTAAACAAG	AAAAAGACTT	ACACTCAAGG	GTTTTCTTCC	CCCCCTTCGT	TATAACGTTT	1860
TGACTCTTTT	ACTAGCAAAG	GTATATACTC	ACAAGGAACT	TTGGTTGACT	ATTGAATCTC	1920
TCCAACTTCT	TCTTTAACAT	ATCCTTCTAC	ATCTTCAATC	TCTACAAACA	TTGGGTCTAA	1980
GTGACACAAG	AAATGCCAAA	CTTCGATCCC	TTTTTTTCTG	TAAAGAATCG	CTTCACCGTC	2040
TTCACTTCCG	AAAAAGCTTC	TGTCGATTTT	ATATCCGCGG	CTTTCTAAGA	AGTCTTTTGC	2100
TTTACGATAG	TTCGTTTCTC	TTGTTTCGAC	ATAGGCTTTA	ACTTCATGGT	TGTTAACGAC	2160
ATATGCATCA	ATTTTTGAAT	ATCCTTCGAT	CACTCTATCA	TTTTTTGAGG	ATAAATTTGA	2220
AATCTCTTTT	CAAATAATGT	TTACATTTTC	CTCAGGATCG	AACATAAATT	TAGATAAAGG	2280
AACAATATTT	CCGTTAAAAA	TAATTTCCAT	ATAATCCGGT	ATGTTTTTAG	GATTAANAATA	2340
CTCCACTTCA	AAACCATCTT	CTGTTTCCAG	AGTGTATCCC	GGGATTTGAG	CTACAAAGGC	2400
TTTCCCATCT	TCTATGGAAT	CAAATGCTAC	TAAATCTTTA	GAATAATCAT	TTTGGTACAA	2460
TTCCAATATA	ACCATCGATA	ATCTCTCCAT	TTTCATTATC	AGGCTAATGT	AAATAAGCAC	2520
GTCACCTGAC	CAATTCAGGC	TCTCTGTATC	ATCTCATCAT	ATTTCCCTACT	TACTTTACGA	2580
GTCTTATACC	CAGAACACAC	CTTATCGACC	TTCCGGTCTCA	CCTCGTCGCA	TTGGCTGAAC	2640
ATCTACTTTT	ACTTTGCTGA	TGCTTCAACT	CGTACAAGCA	GTGATACCGC	CTCAGCGTGA	2700
TGCGTCAGTG	GGACTCAAAA	GGTTCGGGGA	ACCTTTTGAG	GATTAACTAC	GTTTCTCTAA	2760
TAAACTTACA	CATTCAACTT	GTTCATCATT	GTCCAAACCT	ATGTTGAGAT	TTTCTTCTAT	2820
AATTGGTAGC	TTAAAAGTAA	TGGATTTTAG	CCATTGTCCG	TTAGATTGTT	TTTCTTCATA	2880
AACCTGAATT	TCAGAAATCA	AAGCTGAAAT	TAAGTGCCTA	CGCTCTACAT	CATTCATGAC	2940
TTTATAGAGC	TTATCAAAAAT	AGATCAGAAC	CTTATATATG	TTATCTCCTG	TAAGCTTTTC	3000
AGCTTCAATA	GTCTGTTTCT	TTGCTTTTCG	ATCAATTAGT	GATGATTCTA	ATTCATCTAG	3060

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TTTGTACATAC	ATACGATATA	GTCTATCATC	TAAATCCTGT	TTCCCTTCTCT	TATAATGCTT	3120
ATCTTCAACA	TCTAAATTAT	CTATTTCTCT	AATTAGCTTA	AACTTTGTAG	AATGACTCTT	3180
TCTCAATTCC	TTTTGGTAAT	TATCTATTTT	TTTTTCTATT	TCAGAGGTAT	CCACCTTCAT	3240
GTTGATTTTT	TCTTGCATCA	TAGAAGCAAA	TTTCGGATTA	CTTACTATCT	TGACAATCAC	3300
CTCTGCAACA	GCATCATCTA	ACAATTCTTC	TCTAATTTGC	TTACTGAATG	TACACTTATT	3360
ACCTCTTATC	ATCTGCCTAT	GGTTACAACC	ATAGTAATAA	AAATCTTTAT	ACTTTGTGCC	3420
ATCTTTCTTT	TTCTTGATAC	ACTTGTTCCT	AAACATTCCT	ACTCCACATA	TCGGGCATTT	3480
TACAATTCCA	GAAAGCAAGT	GTGTGCGTGT	ATCTTTTCTT	TTATTACAT	GCTCATATTT	3540
CTTTGCTTGA	GATTTTAGCT	TAACCTGAGC	AGCTTGCCAA	ACTTCATCGG	AAACTATAGC	3600
TTTATGTATC	CCTTCAGATA	TTAGATATTC	ATCTTGTTC	ACCTGCTTAT	ATTCATTTCT	3660
TGTACCATGA	ACTTTTCTTA	AAGTTCTTCT	TCCAAATGCT	ATTTTCCCAT	TATATACAGG	3720
ATTTCTTAA	ATCTTTCTTA	TAAGACCTGC	ATCAAACAAA	GGATTCTTAC	CATTCTGTCT	3780
TGGGATTTTT	CTAATTCAT	GATTCTCTAA	GTATTTAGAT	ATCCCATGG	CTCCTATCGT	3840
AGTATTTACA	TACTGGTCGA	AAATCGTTCT	TATTGCAACT	GCCTCTTCT	CATTTATAAA	3900
CAGCTTGCCG	TCTTCAAGTT	TATATCCATA	CGGAGCAAAG	CCACCATTC	ATTTTCTTCT	3960
CCCTGCTTTT	TGAATGCGAC	CTTCCATTGT	TTGAATACTG	ATGTTTCTCT	TTTCTATTTT	4020
AGCCACAGCT	GATAAAACAG	AAATCATTAG	TTTCCCAGCA	TCTTTAGATG	AATCAATGCC	4080
ATCTTCAACG	CAGATAAGAT	TAACCTCCATA	ATCCTGCATT	ATATGAAGTG	TAGAAAGAAC	4140
ATCAGCGGCA	TTTCTTGCAA	ATCTTGATAA	CTTAAACACA	AGAACAAAAG	ATACTCCATC	4200
TTTTCCAGAT	TTTATATCTT	CCATCATTCG	ATTGAACTGT	ATTCTACCTT	CAATAGACTT	4260
GTCAGACTTC	CCGGCATCTT	CATACTCTCC	AACAATTTCA	TAATCGTTGT	AAATAGCAAA	4320
AGCTTTCATT	CGTGATTTTT	GTGCCCTCTAA	CGAATACCCC	TCTATCTGTA	TTGACGTAGA	4380
TACTCGTGTA	TAGAGGTATA	CTTTTATTTT	TTCTTTTGAC	ATAGTATTAA	CCTCAATATA	4440
ATTTTCTAT	ATCATATATA	ATTTTTTAA	TTAAGTTTG	GACTATCATT	TCAAGTATAT	4500
TATAACACTT	TTATTAGTCC	GTCTCAATTT	GTGTTTTTGC	CATGTCAAAA	CTATTTTCA	4560
TCTCTTGATT	TTTTGCTGGC	GTTGGATCGG	GTAGATTATC	TAAATCTAAA	GCACCAGCAT	4620
ATTTTGCAAT	CAGATTTGCT	ATTAATCAG	CCAATCCATT	CCAGTCATTG	TCCAATATAT	4680
ACCTCCTCTA	AAGTTTATA	TCTAATAATT	ATTTGTTTAA	TTAAGTTTTT	TGACATGAC	4740
AAGTGCTTTG	GATTAGCAAC	ATAGGAATCT	CACTTCCGCC	TCTATTCGG	ATGAGCCGGC	4800
TTCAACCTTA	GAAGTATCAT	TACCCTCATT	TTCTTCATAG	CGGATAGGGT	ATCCCTCCCT	4860

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ATATTCAAAC TCTTACTTAT CGCTCACTTT CTTTTTGCTT AGCAGAACTT TTTTTGCCGA 4920
 ATTATTCAGC CGAAAGATCT TGACGGATAG GTTATTACGC TCCAAAAATA ATTAACGTCT 4980
 TGTCTTGGTC TATTCAATTG TTAAGGTTCA AAATTTATCG AGAGTTATTA ATCTTTTAA 5040
 AATTTGACCA TCAGAAAATA TTTATCTTGA TGTAACAAAA TTCTATAAAT TACCCTCTTA 5100
 TACTTAACAG TGAAAAGAAG TCTTTCTTGG TAACCAATTT TGAATAGAA TTTGCTTATA 5160
 TAAAAAGGTC CAATTCCCAC TGCATAAATA GCAGTAAAA TTAGACCCTC TTGGTAACTG 5220
 TCATCTAAAA GTCTTCTA 5238

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GACGATTTAC GAAGAATCGA ACAAGAACCT GCTCCTATCA ATTCCCAACC TCTATCTCTA 60
 AAATCTTGCA GTTCATGCTT ATACTTTTTT AAGAAATCTA GAATCATAGA TACGGTAGAT 120
 GACATCGTCT GGTGACATT GGTCAAAATA GAACAAACCA AAACGACTCG TTCTATACCT 180
 CCAACCTTTC AAATGCATCT CATGTAAATG TTCTTCTTCC TTGTCCAAAT CAACAATGGT 240
 GAAAATCCGA AATTCTACTC TGCTATTCAT TGTCTTACCC CAAAATTAGA AAACATGCCT 300
 GGC GTTATTT ATTAGATAAT TCTTTCCACT TTTGACTCAA TCTCCAAAAA ATATAAGAAA 360
 TCTGAATCGC AAAA ACTATC AATAAAACCC AATCTATTAT GAAAATCAAA AACACTTTCC 420
 AACTGAAAGA ACTACCTCCA GTGACAAACT TTGAGAAAAA CGGTAGTAGA GCTAAAAAGA 480
 GAAATAAAAT AGGAAGCATC CGCATTGTTA AAATCCGTTT GGCATAAAAA AATCTTTATT 540
 TAAACGAAAA TATTATGGCA AAATTTACGC CAGTTTTTGA ACGGCTGATG TAGATATTTT 600
 ATACTTTCAA AATGTTTAAA TGTGATTATT TATTTTTGAA AAATAGATCA CCAGCCCGAC 660
 TGAAAGTGCT TATAGAATGA TAATAAGTCG CCTGCCGAAA ACAGCGAAAA ATAGCGGTGT 720
 TATGCGGAGA TAATCTGACG CGATGCGAAA GTATATTGCA TACTTATTTT CAACAATTTA 780
 GCAGAGTATT TTTATAAGTG TGATATAATA GAAGTATAAT TTGTTCTGAT AGTTTATTTT 840
 ATGGAGAAGT AGATTTTTAG AATGCGGAGG GTTCAATATG GTTGAGTTTA TAAAGCTAA 900
 GAAAGAAATG AGTGAGGAGG ATATTAAAGC AAATTCATC ACTCCTGCTA TTGTATCCAA 960

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AGGATGGAAA	AATGGTGAGC	ATATCGCTTA	CGAAGAATAC	TTCACCTGATG	GTCGAATTGA	1020
AGTTAGAGGA	GATAAGGCTC	GTCGTAAAGA	AGGAAAAAAA	TCAGACTATT	CACTGTATTA	1080
CCAATTTGGA	ACTCGAATTG	CAATTGTTGA	GGCAAAGGAT	AATAAACACA	GCGTTCGAGC	1140
AGGATTACAA	CAAGCTATTG	AATATGGAGA	GATTTTAGAT	GTTCCATTG	TTTATTCTTC	1200
GAATGGTGAT	GGCTTTTATG	AACACGACCG	TATCACGAGA	GAAGAACGTG	AGCTGGAGTT	1260
AGACGAATTC	CCTACTCGTG	AAGAATTATT	TTCTCGTATG	ACGAAGGAAA	AAGGATTGAC	1320
GTACGAAATT	ACAGAAGCTA	TCTCAACTCC	ATACTATACA	GACGCCTTCT	CAATGAAAAAC	1380
GCCACGCTAT	TATCAGCAAA	TAGCTATCAA	CCGTACTATT	GAAACAGTTG	CCAGAGGACA	1440
AAAACGAGTA	ATGTTTGTGA	TGGCAACAGG	AACGGGAAA	ACGTTTCATGG	CTTTTCAAAT	1500
TATTCATCGC	CTTCGAAAAG	CTGGTTTGGC	TAAACGAGTT	TTATTCTTAG	CAGATAGAAA	1560
CATCTTAGTA	GACCAAACGA	TGGCTGAAGA	CTTTAGGCCA	TTCGAAAAGG	TAATGACGAA	1620
AATTACACCA	AAACTTTTGA	CTGCTCCTGA	AAAATTAAT	TCTTTTGAAA	TTTATCTAGG	1680
GCTTTATCAG	CAACTAACTG	GTGAAGATGG	AACTGAAACA	CATTATCAAA	AATTTGACAA	1740
AGACTTCTTT	GATTTAATCG	TAATTGATGA	AGCGCACCGT	GGTTCAGCTA	AGGAAAACAG	1800
TAACTGGCGT	AAGGTAATTG	ATTATTTTCAG	TTCTGCGACA	CAGATTGGGA	TGACCGCTAC	1860
TCTTAAAGAA	ACCAAGAATG	CTTCCAATAC	GGAATACTTT	GGTGAGCCAA	TCTATACTTA	1920
TAGTTTAAAA	CAGGGAATCG	AGGATGGTTT	TTTGGCTCCA	TATCGTGTTA	TGAGGGTTAA	1980
TTTAGATGTG	GATGTGGATG	GTTATCGTCC	AGAAACTGGA	AAAGTTGATG	CTAACGGACA	2040
ATTAATAGAA	GATAGGTAAT	ACGGCAGGAA	AGATTTTGAT	AAAACCATG	TCATTGATGA	2100
TAGAACGCAA	AGAGTTGCCA	AGTTTGTTC	TGATTATATG	AAGCAAAACA	ATGCACGATT	2160
TGATAAAACA	ATTGTTTTTT	GTGTTGATAT	TGACCATGCC	GAGCGAATGC	GTGCTGCACT	2220
TGTAAAAGAG	AATCTAGACT	TAGTCCAAGA	AGACTATCGT	TATGTCAATG	AAGTAAGTGG	2280
TGACAACGCT	GAAGGAAAAG	CTCAACTGGA	TAACCTTATG	GATGTCAATT	CTAATTTTCC	2340
CGCTATTGTA	ACAACGTCTA	AATTATTAAC	GACAGGAGTT	AATGCTAAAA	CATGTCGTTT	2400
GATTGTTTTA	GACTCTAATA	TCCAATCCAT	GACTGAATTT	AAACAAATTA	TTGGTCCGTG	2460
CACACGTCTT	TATCCTCAAA	AGGGGAAAGA	ATTTTTTACG	ATTATTGATT	TTCGAAATGT	2520
TACCAATTTG	TTTGCTGACC	CTGATTTTGA	TGGTGATCCA	GTGAAGGTGC	TAGAAACAGG	2580
TGCGAAAACA	GTCAGTGGTT	CTACGCCCGG	TTTCGTAGAT	GAGGAAGGTG	ACCCAGTAGA	2640
AAAATATATC	GTTACAGACA	AGCAGGTTAC	CATTCTTAAT	TCTACTGTTC	AAGTATTGGA	2700
TGAAAACGGG	AAACTGATTA	CCGAAAGCCT	GACCGACTAC	ACTCGAAAGA	ATATCTTAGG	2760

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TAGCTACGCC	ACTTTGAACG	ATTTTATCAC	AGTTTGGCAT	ACGGCAGATA	AGAAGAAGCT	2820
TATCTTAGAC	GAACCTTATA	AAAAAGGAGT	TTATCTAGAT	GCTATTCGAG	AGTCGGAGGG	2880
AATATCAGAA	CAAGAAATCG	ATGATTTTGA	TTTACTCCTA	AACTTGCCT	ATGGTCAAAA	2940
AGAATTAACC	AAAACGGAAC	GTATCAATAA	ACTCAAACAA	AGCGGATAT	TATATAAATA	3000
TAGTGAGGAA	GCGCGTGCTG	TTTTGGAAAT	TTTACTGAAC	AAATACATGG	ATAAAGGTAT	3060
TGGAGAACTC	GAAAGCATTG	AAACATTAAA	ACTTCCAGAA	TTTCAGATAT	ATGGTGGAAC	3120
CTTCAAAATC	ATCAATACTT	ATTTTGGAGA	TAAAAACGA	TATTTACAAG	CAATTAAGA	3180
ATTGGAGCAA	GAGCTATTTA	CAGTAGCTTA	ATGAAAGGAA	AGTATGTCAA	TTACATCATT	3240
TGTA AAAAGA	ATTCAAGATA	TCACTCGAAA	CGATGCTGGT	GTTAATGGTG	ATGCTCAACG	3300
TATTGAGCAA	ATGTCTTGGT	TATTATTCTT	AAAAATTTAT	GATAGCCGTG	AAATGGTTTG	3360
GGAATTAGAA	GAAGACGAGT	ATGAGTCAAT	TATCCCAGAG	GAATTAAAAA	GGCGAAATTG	3420
GGCTCATGCT	CAAAATGGGG	AACGGGTATT	GACAGGCGAT	GAATTACTTG	ATTTTGTCAA	3480
TAACAAGTTA	TTCAAAGAGT	TGAAAGAGCT	TGAAATAACT	TCAAATATGC	CTATTCGAAA	3540
AACGATTGTT	AAATCAGCTT	TTGAAGATGC	GAACAACTAT	ATGAAAAATG	GCGTCTTGTT	3600
ACGCCAAGTC	ATCAATGTTA	TTGATGAAGT	TGATTTCAAT	AGCCCTGAAG	ATCGTCATTC	3660
GTTTAATGAT	ATTTACGAAA	AAATTCCTAA	AGATATTCAA	AATGCTGGGA	ACTCAGGAGA	3720
ATTTTATACG	CCACGTGCAG	CGACTGATTT	TATTGCCGAA	GTTCTTGACC	CAAAACTTGG	3780
AGAATCAATG	GCAGACCTTG	CTTGCGGAAC	AGGAGGCTTC	TTGACTTCGA	CTCTGAACCG	3840
TTTAAGTAGT	CAACGTAAAA	CTAGTGAAGA	TACCAAAAAA	TATAATACAG	CTGTTTTTGG	3900
TATTGAAAAG	AAAGCATTTC	CTCATCTTTT	AGCAGTTACA	AATCTGTTTC	TTCACGAAAT	3960
TGATGACCC	AAAATGTGTT	ATGGAAATAC	TTTGGAGAAA	AATGTTCCGTG	AATATACGGA	4020
TGATGAAAAA	TTTGACATTA	TTATGATGAA	TCCACCTTTT	GGAGGGTCAG	AATTAGAAAC	4080
AATAAAAAAT	AACTTTCAG	CAGAATTACG	GAGTTC TGAA	ACAGCTGATT	TATTTATGGC	4140
TGTCATTATG	TATCGTTTGA	AAGAAAATGG	TCGTGTTGGA	GTTATTTTAC	CTGATGGTTT	4200
TCTATTTGGT	GAAGGTGTAA	AAACTCGCTT	GAAACAAAAA	CTGGTAGATG	AGTTCAACTT	4260
GCATACGATT	ATTAGGTTGC	CTCATAGTGT	CTTTGCACCG	TATACAGGAA	TCCATACGAA	4320
CATTCCTTTC	TTTGATAAAA	CAAAGAAAAC	AGAAGAAACT	TGGTTTTATC	GTTTAGATAT	4380
GCCAGATGGT	TATAAAAATT	TCTCGAAAAC	TAAGCCGATG	AAGTCAGAAC	ACTTCAATCC	4440
TGTTCTGTAC	TGGTGGGAAA	ATCGTGAAGA	GATTCTGGAA	GGTAAGTTCT	ACAAATCTAA	4500

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ATCATTTACA	CCTAGTGAAT	TGGCTGAGTT	GAATTATAAT	TTAGACCAGT	GTGACTTTC	4560
AAAAGAGGAA	GAGGAAATCT	TAAATCCCTT	TGAGTTGATT	CAGAATTATC	AAGCGGAAAG	4620
AGCAACTTTA	AATCATAAGA	TTGATAATGT	ATTAGCTGAT	ATTTTGCAGT	TGTTGGAGGA	4680
CAAATAATGA	CACCAGAACA	ACTTAAAGCA	AGTATTCTCC	AAAGAGCGAT	GGAAGGGAAA	4740
TTAGTGCCGC	AAAATCCCAA	TGACGAACCT	GCAAGTGAAT	TATTAAAGAG	AATTAAAGCT	4800
GAAAAAGAAA	AACTTATCAG	TGAAGGAAAA	ATCAAACGAG	ATAAAAAGGA	AACTGAGATA	4860
TTTCGTGGTG	ATGATGGGAA	ACATTATGGG	AAGTTTGCTG	ATGGAAGCAC	TCAAGAAATT	4920
GATGTTCCCT	ATGATATTCC	TGATACTTGG	GAGTGGGTGA	GGTTTTCTAC	ATTGGTTGAA	4980
ATTGTCAGAG	GTGGCTCTCC	ACGACCAATC	AAaGATTATC	TTACTTCTGA	AGTAGATGGA	5040
ATAAATTGGA	TAAAAATAGG	TGATACTGAA	AAGGGTGAAA	AGTATATAAA	TAATGTTAAA	5100
GAAAAAATCA	AAAAATCAGG	GCTTAACAAA	ACTAGATTTG	TAAAAAAGG	TACATTTTTG	5160
TTAACTAATT	CTATGAGTTT	TGGTAGACCT	TATATTTTGA	ATGTTGATGG	TGCAATACAC	5220
GATGGATGGT	TGGCTATTTT	GAACATGAA	AACTCATTA	ATAAAGATTA	CCTATCTTAT	5280
ATTCCTTCAT	CAAATGTAGT	TTATCTCAA	TTTCTATCTC	TAATTAGTGG	AGCTGTTGTG	5340
AAAAACTTGA	ATAGTGATAA	AGTTGCTTCT	ATTCTTATCC	CTCTCCCCC	ACTATCCGAA	5400
CAACAACGAA	TAGTAGAAGC	AATCGAATCA	GCTTTAGAAA	AAGTAGATGA	ATATGCTGAA	5460
AGTTATAATA	GACTAGAACA	GCTAGATAAA	GAATTCCAG	ATAAACTAAA	AAAATCTATT	5520
CTTCAATATG	CTATGCAAGG	AAAATTAGTT	GAACAAGACC	CAAATGATGA	ATCAGTCGAA	5580
GTTTTACTTG	AAAAAATACG	AGCAGAAAAA	CAAAAACCTC	TTGAAGAAGG	CAAGATTAAA	5640
AAGAAAGATT	TGGACATTTT	TATTGTTTCC	CAAGGAGATG	ATAACTCTTA	TTATGGGAAT	5700
ATACCTATGA	ATTGGGTTGT	TATAAAAATA	AAAGATATTT	TTTCAATAAA	TACAGGCTTT	5760
TCTTACAAGA	AGGCGGATTT	AAGCATTAAT	AATAAAGGTG	TTAGAATTAT	ACGTGGTGGT	5820
AATATTAAGC	CTTTAGAATT	TTCTCTGTTG	GATAATGATT	ACTACATTGA	TACACAATTC	5880
ATCTCCTCTG	AGCAAGTTTA	TTTAAAACAT	AATCAGCTAA	TAACACCTGT	ATCAACCTCT	5940
TTAGAACATA	TTGAAAGTTT	TGCAAGAATC	GATAAAGACT	ATGATGGTGT	TGTGGCTGGT	6000
GGATTTATTT	TCCAATTAAC	ACCATTCGAA	AGTTCAGAGA	TTATTTCAA	ATTTCTATTA	6060
TTTAACTTGT	CCTCTCCGTT	ATTTTATAAA	CAATTGAAAG	CAATAACTAA	ACTATCAGGT	6120
CAAGCTTTAT	ATAATATTCC	TAAAACCTACA	CTGAGCGAGC	TATTAATTCC	GTTAGCTCCT	6180
TTTGAGGAAC	AGGAACCTAT	TACTCAAAAA	GTTGAGAAAC	TTTTTGAAAA	AGTAAATCAA	6240
CTTTGAAAAT	GATCTTTTTC	ATCTCTTCAT	GATTAGAAAT	AGGGATTAAT	AATTCGGAGA	6300

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TACTGGTACT	ATTTAATGTT	TTCCCTTTGA	TAGCATCTTT	TGAATCACCT	AAAGTAGAGA	6360
TAAGTGGCAA	AAATATCATT	AAGTAATCTC	TGATAATATT	TTCTTTATTA	GCATAGGGGA	6420
ATATCGATAT	AATGGCTTCA	TTATGAGTGG	CAGGAATATC	CAATATGGCA	ACTTTTCCAA	6480
TAGATAATTT	AAAACTCATT	AATAAAGTTC	CTTTAGGTGA	AATGTCTATT	TTCTTTGATT	6540
TTAATGCTAA	TTTAGAAATA	GATTCTCTCG	CATTAGTTAC	ATAACCAGAT	ATAGGCATAT	6600
CTGATATAGA	TACCCAAGGT	ATTTCAGTTC	CCCAAAAAGT	AGCTTCACTG	CGTGGAGGAG	6660
TTTTTCCTAT	TCTGAAGTTA	ACTAGGCTAG	CAAATTTAAT	ATATCTCCAT	GCTTCTGGGA	6720
TTTCATATAT	AGGATAAGAG	GTGTGTTTCGT	CTTGTTCCTC	ATAATAAGAG	CCATAATCAC	6780
AAAAATAGCA	GGTAGTCAGT	TTGACCACCT	GTTATTTTTT	ACCAATTAAC	AATTTTATCT	6840
ACAATATTTT	GTGTTCAGT	AGCTGTTTTT	CTTAGATAAA	TTCGAGTAGT	TTCTATACTT	6900
TCGTGTCCCA	TCAAATCTGC	AAGCAAGGCA	ATATCATTTAT	ACTTCGCTAA	AAAATCTTTA	6960
GCAAATAAAT	GCCTAAAAGA	ATGAGGGTAA	ATTACGTTAG	GATTCATTTT	GTATTTATCA	7020
GCATAATTTT	TTAACTGTTG	AGCAACTCCT	CTTGCTGTAA	TTGGTTCGTT	AAATTTATTC	7080
AAAAATAAAT	AACCACTTCG	GCGATTTTCT	GATTCTAACC	AACTAAGACA	ACTATTTCTT	7140
AATTTTTTTAG	GAATGTACAG	TCTACGAATT	TTACCACCTT	TTGAGTAAAT	GTCAAATAA	7200
CCGATTTCTA	CATGCTCTAC	TTTTAGTTTA	ATAAGTTCAC	TTACACGAGC	CCCAGTTGCA	7260
CCTAAAAACC	AAACGACAAA	ATGCCATTTT	AAAATACCAT	CTTTTTTCAA	ACTACGTTTA	7320
AGAAAAAGGT	AATCAGCATG	GCTAATGACA	TCTTCTAAAA	ACGGTTTTTTG	CTGTACTTTG	7380
ACAAATTTTA	ATTTCAAATC	ATCATGACCA	ATAAAAGCCA	GATATTTATT	TACTCCTTGT	7440
AGTCGCAAAAT	TGACAGTTTT	AGGTTTAAAA	TTGTCTAATA	AATATCCTTT	GTATTCAAAT	7500
AAATCTTCCA	TTTTGAGTTC	GTAATCTCTC	AAGAAAAATC	GAACACCATA	AAGGTACGAA	7560
CGCACAGTAT	TTTCAGCTAA	ACCAGCTTTC	TTCAAATGTA	ATTCAAAATC	TTTCAACGTA	7620
AAACTCCTAT	CTTATGTTTG	ATAGAAATTC	CACCGCACGT	AAAACATTA	TACTAAATTA	7680
GTGCGTCAAT	ATGGGCGAAA	AATTGTTCTGA	TTTTATCAAC	GATTCTGGAT	TGTTCAGGAA	7740
GGGGTGGGAG	GGGGATFAAA	TATTCTTTTA	TAGTTTTTCGT	TAATAATFCT	TTTTGTTTTG	7800
TACTACCCGA	CGCTTTTTCT	TCAATAACTG	ACTGAACAAT	AGGAGAGGAA	AGAAAATTAT	7860
AGATGAAATG	GCAATTAATA	ACCCCGGATA	AGACTCTTAT	AACTGTAACA	TGGCTATCTG	7920
CAACAGCCCA	GCCATAAGGA	TTTTTATTTT	CATGGTAAAT	AGCTAATCGT	CCTAACGTAC	7980
CTAGACCTGT	TGAATTCAC	ATTAAATCAC	CATCTCTTAG	TAATCTTCT	TTCTGGTAAC	8040

1014

TATGAACTGT	TTCGGGATCA	ATAAATCTTG	CTAAGTCAAT	AGAAAAGCCA	GACCATTGAT	8100
TACATTTCTG	AGCAATCACA	GGGTATATAG	GAATATTTGA	ATATTTTGGA	GACTTCCCTC	8160
TTTGAATGTA	GGAGGTTATA	TCGTTTAACC	TCACCCATTC	CCAACTTTCT	GGTATTTTAC	8220
AAGGTACTTC	CTCATAATAA	GAGTTATCAT	CTCCTTGGGA	AACAATAGAA	ATGTCCAAAT	8280
CTTCTTTTTT	AATCTTGCCT	TCTTCAAAGA	GTTTTTGTTF	TTCTGCTCGT	ATTTTTTCAA	8340
GTA AAACTTC	GACTGATTCA	TCATTTGGGT	CTTGTTC AAC	TAATTTTCCT	TGCATAGCAT	8400
ATTGAAGAAT	AGATTTTTTT	AGTTTATCTG	GAAATCTTTT	ATCTAGCTGT	TCTAGTCTAT	8460
TATAACTTTC	AGCATATTCA	TCTACTTTTT	CTAAAGCTGA	TTCGATTGCT	TCTACTATTC	8520
GTTGTTGTTT	GGATAGTGGG	GGGAGAGCAA	TTAATAATAG	ATTAAAATTA	TAATCATTTGA	8580
TTGCAGGATA	ACTTGTTC CA	G TAGATTTAT	TATTAACACG	ATTGATAAAA	TTATCTGATA	8640
ATAAATAATA	TTTCAAATAT	GTTTCGTTAA	G TAAAGTATC	CAAAA CAATA	AATGCTGTAC	8700
TAGCTATCAA	ATACTCTTTA	AGTCTCTTAA	CTACAGCAAT	ATTTTTTAGA	TATGGTCTAA	8760
CTGTTGAAAA	TAAGACACTA	TTCTGCGAAA	CTAATTTTCT	AGCACGGGAA	GGCGCTTGTT	8820
CAGGTGAAAG	ATATTGTAGA	TTTTTGTAGT	TGATTATGTT	CTTTTTTCTA	TCAATACTAG	8880
ACGTATCTAT	ATACCTAAAG	GATTTCTCTG	GCTTATTTTG	CCCAAATTC	CAATAAATTG	8940
ATTTTATCCT	CACCCACTCC	CAAGTATCAG	GAATATCATA	AGGAACATCA	ATTTCTTGAG	9000
TGCTTCCATC	AGCAA ACTTC	CCATAATGTT	TCTTATGTGC	TTCAAGTATA	TAAAAAGGCG	9060
TAAAAATACG	CCTATAGATA	ATGGGGTTGA	AATAGGTTTA	TTGTTGATGA	GATTGTAGAT	9120
AATTCAATTT	TTTACTTCCA	ATCGAATATT	CAAATCCTCC	ACCTTTTCTG	CCTGTAATPG	9180
TTCATCATAA	AATTCAATAT	CTTCAGGATT	TTCCCCTTGG	CAACCTCGGC	AGAAATATTC	9240
TTCCGCTCGA	TCAGGATTCA	AAAATCGACA	AGCACAAACA	AAACAGTCGC	CATCATCATT	9300
TATTGAGATA	ATATAGTAGA	TTGAAATAAG	ATGTAAACAA	ATCGATTAGG	AAAGTTAAAT	9360
TAGTTTCTAG	AAATTTT TAG	CAGATGTAGT	G TACTAT TCT	AGTCTCAATT	TACTATGGCT	9420
TCAAATATAT	CTTTCGAAAA	AATATTTACA	GATGTGTAAT	TTTGAAGCTT	GCAAAAAGTTA	9480
GTAAACTTGT	AGATTTTCGAT	TTGAAGTAAC	TTGTTTTCTT	GCCC GATATT	GTTTTTGAAA	9540
TTGAATTTTT	CCATAGTGAC	TCCTTAATTT	TCTTCTACAC	GTCTGATGAT	AAATCTAATT	9600
CGCAAAAGAG	TCAAGAGGAT	TTTTCGAAAA	ATAAATAGCG	ACCGAAATCG	CTATTTTAAAG	9660
GGTTATAGGT	ATTTGATGGC	TTAGACTGCT	GTGTGACTGT	TTACCCACAG	GCAATCTTTC	9720
TTCTATATTA	GTATTAGTAA	AGGTCTAAAT	AATTATCAAT	TTCCCAT TGT	GAAACGAAGG	9780
TTGCATAACT	TGCCCATTCG	ATTCGTTTGG	CTTCAAGGAA	GCTAGTATAG	ATGTGATCTC	9840

1015

CGAGAGCAGC	TTTAACCACT	TCATCTTCTG	TCAAAGCTTT	CAAAGCGTTG	TGAAGAGTTG	9900
ATGGAAGGTC	TGTAATACCA	GCTTCCTTGC	GCTCTTCTGC	TGTCATGATG	TAGATATTTT	9960
CTTCGATAGG	AGCTGGTGCT	TCGATTTTAT	TTTCAATACC	ATACAAACCA	ACTTCCAAAA	10020
GAACAGCCAT	AGCAACGTAA	GGTTCGCCA	TTGGATCCAC	TGAACGCAAC	TCAAGACGAG	10080
TTCCCATACC	ACGTGAAGCA	GGTACGCGCA	CAAGTGGCGA	ACGGTTACGA	CCAGCCCAAG	10140
CAATGTAAAC	AGGCGCTTCA	TAACCTGGAA	CCAAACGTTT	GTATGAGTTA	ACTGTTGGGT	10200
TCATGATGGC	AGTATAGTTG	TAAGCATGCT	TGATCAAACC	GCCTAGGAAA	TGGTAAGCTG	10260
TTTCTGACAA	CTGCATTCCT	TTTGGATCAT	TTGGATCAAA	GAAGCGTTA	TTTCCTTCTG	10320
CATCAAACAA	GGACATATTA	CAGTGCATAC	CTGATCCAGC	AATACCAAAT	TTTGGCTTCG	10380
CCATAAATGT	TGCGTAAAGT	CCGTGTTTGC	GAGCAATGGT	TTTAAACAACA	AGCTTAAAGA	10440
TTTGAATCTT	ATCACAAGCA	CGGAGAACTT	CATCGTACTT	AAAGTCAATC	TCATGCTGTC	10500
CAACCGCAAC	CTCGTGGTGA	CTCGCTTCTA	CTTCAAATCC	CATTTTGGTC	AAGACATTCA	10560
CAATCTCAG	ACGTGTGTTG	TCCGCAAGGT	CAGTAGGTGC	CAAGTCAAAG	TAGCCACCCCT	10620
TGTCATTCAC	TTCAAGTGTT	GGGTCCCAT	TTTCATCCAA	CTTAAATAGG	AAGAATCTTG	10680
GCTCTGGACC	AAGTTGAAG	GATTTGAATC	CAACTTCTTC	CATGTGACGA	AGAGCTCGTT	10740
TCAAATTACC	ACGAGGGTCA	CCCGCAAATG	GTTCACCTTC	TGTTGTATAG	ACATCACAGA	10800
TCAGACCTGC	AACACTTCCA	TTTTCATCTC	CCCAAGGGAA	GACTGTCCAT	GTATCCAAGT	10860
CCGGGTACAA	GTACATATCC	GACTCATTGA	TACGTACAAA	ACCTTCAATA	GAAGATCCAT	10920
CAAACATAAC	CTTGTTCGAC	AAGACCTTAT	CTAACTGTTC	ATCTGTAGCA	GGAATTTCTGA	10980
CGTTTTTCAT	GGTTCCCAA	ATATCTGAGA	ACATAAGACG	AATAAAGGTA	ACATTTTTTTT	11040
CCFTGACTTC	ACGACGAATA	TCTGCAGCTG	TGATTGGCAT	AAGTTTTCTC	CTTAATCTAT	11100
GACTACTTGC	GGTTGCCTAA	CCGCGACCAA	AAGGTGACTG	TACTGAAGCA	AAACGCCCTT	11160
GTGGAGGAG	TTCATTGTGA	AGTGCACGAC	GTACTTCAGT	CTGACTAACC	GCTTCTTTGG	11220
ATTCGCTTC	ACGTCAGCA	TATTTTTTCT	TAATGGCAGC	GATATTATAA	CCTTCAGAGA	11280
TATAATCTTT	GATTTCAAGC	AGACGATCCA	TGTCATTCAA	GGAATACATG	CGACGATTTT	11340
CTTCGTTTCG	ATCGGGCTTG	ATCAACTCTT	GATCTTCATA	ATAACGAATC	TGACGCGCCG	11400
ATAGATCGGT	CAACTTCATA	ACACTGCCGA	TAGGAAAAAC	AGCCATATTT	CGGCGAAAT	11460
CTTTTTCTTT	CATTTACAAT	TTCTTCTTTT	CTGTCTATTA	TAGTCTAAAA	AAAGACAAAC	11520
GTCAATTGAT	AATGTTATAA	AATGTAAACAT	TATTTTTCTT	TTTTCTCTAA	AAAGAGACGA	11580

1016

ATACGATCAA	TATCGTAATT	TACGATAAAT	GCGACAAAAA	CTCCCATAAA	CGTTTCTAAT	11640
ACACGCACAA	ACACGTACAA	AATTGTCTCA	CCACTTGGAA	TTGATAGGGT	AATGATTAAC	11700
ATAGCTGCTA	CACCACCAAT	AACCCCTGCT	TTGTTATTCA	TGGCTACATT	TGTCATAATG	11760
GTTAACATGG	TGCAGATTGG	AACAAC TACC	AAGGTCACCC	AAAAGGCTTC	GTGGAAAAAG	11820
GTATTTAATA	AGAAGAAGAC	CAAGGCATAG	AGTCCACCGA	TACTATTTCC	TAGAATACGC	11880
GAAGTCCCAA	AATGAACACT	CTCATCAAAA	CTCTCCCTCA	GGCTAAAAAC	GGCTGTCAAA	11940
GCACCAATTT	GAAGACCTTT	CCAGCCAAAA	AAGCCAAAAA	TCAAGAGAAC	TAGAAAAACA	12000
GCAATACCTG	TTTTAAAGGT	TCGCATACCA	AGTTTGAACT	GGGATTTATC	GAATTTATAT	12060
TTTTTAAAT	AACTCATAAT	CTCAACTTTC	TATTTCCATT	TTATCATAAA	TCGGTGATTT	12120
TTATGAGTAA	TAGTTGAGAG	GAAGCGTTTT	TATTTTAAAGC	AAAAGAAAAG	AGGAACTTTC	12180
ATCCCTCTCT	TCTTTGATTT	ATTTATAAAA	TCTTATTTTT	CTGTCAAGGC	TGCAAGTCCT	12240
GGAAGAACCT	TACCTTCAAG	AAGTTCATT	GATGCTCCAC	CACCCGTA CT	AATCCATGAG	12300
AACTTGCTCG	CACGGCCAAG	GTTAATCGCT	GCGGCAGCTG	AGTCACCACC	ACCGATGATT	12360
GATTTAACTC	CTGGTTGTTT	CACGATAGCG	TCCATCACAC	CGATTGTACC	AGCTTGAAAA	12420
TCTGGGTTTT	CAAATACACC	CATAGGTCCG	TTCCATACGA	CTGTTTTGGC	ACCAGTCAAA	12480
GCTTCGTCAA	ATTTGGCGAT	AGATTTTGGG	CCGATGTCAA	GACCAAGGAA	GCCTTCAGAA	12540
ACTGCTTCAC	CTTCAGTGTC	ACGCACTTCA	GTGTAACCAG	CAAATGCGTT	AGCTTCTTTT	12600
GAGTCAACTG	GCAAGATCAA	TTTACCATT	GCTTTTTCAA	GAAGAGCTTT	CGCAACATCC	12660
AATTTGTCTT	CTTCTACAAG	TGAGTTACCG	ATTTGATAC	CTTGTGCTTT	GTAGAATGTG	12720
TAAGTCATCC	CACCACCGAT	AAGGACGTTA	TCAGCTTTTT	CAAGCAAGTT	TTGATAACA	12780
CCGATCTTGT	CTGAACTTT	TGAACCACCA	AGGATAGCCA	CGAATGGACG	TTCTGGAGTT	12840
TCAACTGCTT	CTTGGATGTA	GGCAATTTCG	TTTTCAAGAA	GGAAACCAGC	AACTGCTTTT	12900
TCAACGTTTG	CTGAGATACC	AACGTTAGAT	GCGTGTGCAC	GGTGAGCTGT	ACCGAATGCA	12960
TCGTTTACGA	AGATACCATC	TCCAAGTGAT	GCCCAGTATT	TACCAAGTTC	AGGATCGTTT	13020
TTAGATCTCT	TCTTGCCGTC	AACATCTTCG	TAACGAGTGT	TTTCAACCAA	GAGA ACTTGT	13080
CCATCTTCAA	GAGCGTTGAT	TGCCGCTTCT	AATTCAGCAC	CACGAGTGAC	ACCTGGGAAA	13140
ACAACATCTT	GACCAAGTTT	TGCTGCCAAG	TCAGCTGCTA	CAGGAGCAAG	TGATTTACCA	13200
GCTTTATCAG	CTTCTCTTTT	CACACGTCCA	AGGTGAGAGA	AAAGAATTGC	ACGTCCACCT	13260
TGTTTCGATG	TGACTTAAT	AGTTGGAAGA	GCTGCTGTGA	TACGGTTATC	GTTAGTGATT	13320
ACGCCATCTT	TCAATGGTAC	GTTGAAGTCA	ACACGAACGA	GGACTTTTTT	ACCTTTC AAG	13380

1017

TCAACGTCTT TAACAGTAAG TTTTGCCATG TTACAAAAAC TCCGG 13425

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 905 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GATTTATCCT ACCGnGAAT TTCCGGAGGG GTTCTAGCAG CAATCTTAGG AATCTATGAA	60
CGAATGATTG GCTTTCTGGC CCATCCCTTT AAAGACTTTA AAGAAAATGT TTTGTACTTT	120
ATTCCAGTTG CCATCGGTAT GCTTCTGGGA ATCGGCTTAT TTTCCCTACCC GATTGAATAC	180
CTGCTTGAAA ATTATCAGGT TTTTGTATTA TGGAGCTTTG CGGGAGCTAT TATCGGTACA	240
GTTCCTAGCC TCCTCAAAGA ATCAACTCGA GAATCTGACC GAGACAAGAT TGATTTAGCT	300
TGGTTATGGA CAACCTTTAT CATTTCTGGA TTAGGACTCT ATGCCTTAAA TTTTGTGCGT	360
GGAACCTTAA GCGCCAGCTT TCTTAACCTC GTCCTAGCAG GCGCACTATT GGCCCTTGGC	420
GTCTTGCTC CTGGCCTCAG CCCATCAAAT TTACTTTTGA TTTTGGGACT CTATGCTCCT	480
ATGTTGACTG GTTTTAAAAC TTTTGATTTT TGGGGAACCT TCTTTCCGAT TGGAAATTGGT	540
GCAGGTGCAA CTCTCATCGT TTTTTCAAAA TTGATAGATT ATGCCTTAAA CAACTACCAC	600
TCACGCGTCT ATCATTTCAT CATCGGTATC GTCCTATCAA GTACCCTTTT GATCTTAATT	660
CCAAATGCAG GAAACGCTGA AAGTATCCAA TACACAGGAC TTTCACTTGT CGGTTATGTC	720
ATCATCGCCT TCTTCTTTGC GCTGGGAATC TGGCTTGGTA TTTGGATGAG TCAATTGGAG	780
GATAAATATA AATAATGGCA AAAAAAGTTA AAATCAAAAA AACATTGGTG GAACAAATCC	840
TATCTAAAGC AGCTATCCCT CATCAGGGGA TTCAAATCAA TGCCCTAGAA GGAGAGCTTC	900
CTCAA	905

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

1018

CTTGAATTAA ATAAAAACG TCATGCGACT AAGCATTTTA CTGATAAGCT TGTTGATCCC	60
AAAGATGTGC GTACGGCTAT CGAAATTGCA ACCTTAGCGC CAAGCGCCCA CAACAGCCAG	120
CCTTGGAAT TTGTGGTGGT ACGTGAGAAA AATGCTGAAC TGGCAAAGTT AGCTTATGGT	180
TCCAATTTTG AACAGGTATC ATCAGCGCCT GTAACCATTG CCTTGTTTAC AGATACGGAC	240
TTAGCCAAAC GTGCTCGTAA GATTGCCCGT GTTGGTGGTG CTAATAACTT TTCTGAAGAG	300
CAACTTCAAT ATTTTATGAA AAATCTGCCA GCTGAGTTTG CCCGTTACAG TGAGCAACAA	360
GTCAGCGACT ACCTAGCTCT CAATGCAGGT TTGGTTGCCA TGAAGTTGGT TCTTGCATTG	420
ACAGACCAAG GAATTGGTTC TAACATTATT CTTGGTTTTG ACAAATCAAA AGTTAATGAA	480
GTTTTGGAAA TCGAAGACCG TTTCCGCCA GAACTCTTGA TCACAGTGGG TTATACAGAC	540
GAAAAATTGG AACCAAGCTA CCGCTTGCCA GTAGATGAAA TCATCGAGAA AAGATAGAAA	600
GAAGAAAAA TGACAGCAAT TGATTTTACA GCAGAAGTAG AAAAACGCAA AGAAGACCTC	660
TTGGCTGACT TGTTTAGCCT TTTGAAATC AATTCAGAAC GTGATGACAG CAAGGCTGAT	720
GCCCAGCATC CATTTGGGCC TGGTCCAGTA AAAGCCTTGG AGAAATTCCT TGAAATCGCA	780
GACCGCGATG GCTACCCAAC TAAGAATGTT GATAACTATG CAGGACATTT TGAGTTTGGT	840
GATGGAGAAG AAGTTCTCGG AATCTTTGCC CATATGGATG TGGTGCCTGC TGGTAGCGGT	900
TGGGACACAG ACCCTTACAC ACCAACTATC AAAGATGGTC GCCTTTATGC GCGCGGGGCT	960
TCGGACGATA AGGGTCCCTAC AACAGCTTGT TACTATGGTT TGAAAATCAT CAAAGAATTG	1020
GGTCTTCCAA CTCTAAGAA AGTTCGCTTC ATCGTTGGAA CAGACGAAGA ATCAGGCTGG	1080
GCAGACATGG ACTACTACTT TGAGCACGTA GGAAGTTGCC AACCAGATTT CGGTTTCTCA	1140
CCAGATGCTG AATTTCCAAT CATCAATGGT GAAAAAGGAA ATATCACGGA ATACCTCCAC	1200
TTTGCAGGAG AAAATACAGG TGTGCCCCGT CTTACAGCT TTACAGGTGG TTTACGTGAA	1260
AATATGGTAC CAGAATCAGC AACAGCAGTC GTTTCAGGTG ACTTGGCTGA CTGCAAGCT	1320
AAACTAGATG CCTTTGTGTC AGAACACAAA CTTAGAGGAG AACTCCAAGA AGAAGCTGGC	1380
AAATACAAGG TGACGATCAT TGGTAAATCA GCCCAGGTG CTATGCCTGC TTCAGGTGTC	1440
AATGGCGCAA CTTACCTTGC CCTCTTCTC AGCCAGTTTG GCTTTGCTGG TCCAGCCAAA	1500
GACTACCTG ACATCGCAGG TAAAATTCTC TTGAACGATC ATGAGGGTGA AAATCTTAAG	1560
ATTGCTCATG TGGATGAAAA GATGGGTGCT CTTTCTATGA ATGCCGGCGT CTCCACTTC	1620
GATGAAACAA GTGCTGATAA TACCATTGCC CTCAACATCC GCTATCCAAA AGGAACAAGT	1680
CCAGAACAAA TCAAGTCAAT CCTTGAAAAC TTGCCAGTTG TTTCTGTTAG CCTGTCTGAA	1740
CACGGTCACA CGCCTCACTA TGTGCCAATG GAAGATCCAC TTGTGCAAAC CTTGTTGAAT	1800

1019

ATCTATGAAA AACAACTGG CTTTAAAGGT CATGAACAAG TCATCGGTGG TGGAACCTTT 1860
 GGTGCGCTGC TAGAACGCGG AGTTGCCTAC GGTGCTATGT TCCCAGACTC GATTGATACC 1920
 ATGCACCAAG CCAATGAATT TATCGCCTTG GATGATCTTT TCCGAGCAGC AGCAATTTAT 1980
 GCCGAAGCTA TTTACGAATT GATCAAATAA AACGATAGAA GTCTGAGATC TTATGCTTGG 2040
 ACTTCTTTTT GGAGGGAAAG TAGATGTCTC AAATCGAAAG AATCAAACAG GCTATCATGG 2100
 CGGATTCGCA GAATGCCAGC TATACAGAGC GTGGCATTGA GCCTCTCTTT GCAGCGCCAA 2160
 AAACTGCTCG CATCAATATC ATCGGTCAGG CTCCGGGACT TAAAAC TCAA GAAGCAGGCC 2220
 TTTACTGGAA AGATAAAAAGT GGTGACCGCT TCGGGGACTG GCTAGGTGTG GATGAAGATA 2280
 CCTTTTACAA TTCAGGTAT TTTGCTGTTT TGCCTATGGA TTTCTACTTT CCAGGACATG 2340
 GCAAGTCGGG TGATCTCCG CCTCGTACAG GTTTTGCAGA AAAATGGCAT CCGCAGGTCT 2400
 TACAGGAATT GCCTGATATT CAGTTAACCC TCTTGATGG GCAATATGCC CAAGCCTACT 2460
 ATTTACAGGA GAAAATCAGT GGAAGGTAA CGGAGAGGGT GAAACACTAT AAAGACTATC 2520
 TGCCAGCCTA TTTTCCGCTA GTTACCCAT CACCACGAAA TCAAATCTGG ATGGCCAAAA 2580
 ATCCTTGTT TGAGGCAGAA GTAGTGCCAG ATTTGAAAAA AAGAATTAAA ACCATTTTAT 2640
 AGTCAATGAA AATCAAAGAG CAAACTAGGA AGCTAGTCGT AGGCTGCTCA AAGTACAGCT 2700
 TTGAAGTTGC AGATAAAACT GACGAAGTCG GTAACATACG CACGGTAAGG CGACGCTGAC 2760
 GTGGTTTGAA GAGATTTTCG AAGAGTATTA GAAGAAAAAG AATGAAAGAA ATAGCCTTTG 2820
 ACGCATTTTA CCAGCTTTAC CAAAACGACC AGCTTTCTTT AGTGGATGTG AGAGAAGTGG 2880
 ATGAGTTTGC AGCTCTTCAT TTAGAAGGTG CCCACAACCT ACCGCTTAGT CAATGGCTG 2940
 ATAGTTATGA TTAATTGGAC AAAGATCGCT TGCATTATAT TATTTGCAA TCTGGAATGA 3000
 GATCGGCGCG TGCTTGCCAA TTCCTATTAG AACAAGGTTA TAATGTATC AATGTCCAGG 3060
 GTGGCATGTT AGCCTTTGAA GAACTTTAAA ATTTTGCATT TCTCCTACTT GGTGTGGACT 3120
 GGGTAGGAGA GTTTTATTTT TAGATAATTC TTATTTTAA GAAAATTGAA AACATTTAAT 3180
 ATTTGCCTCG TGATGCTTTT TTCAGACTCC TAATCGTGGT ATACTAGGTC AGTATTTTAT 3240
 AAATATGAAG GAGATTTTAA TGGCTAAAAA AGGTACCCTA ACAGGTTTGC TCCTGTTTGG 3300
 AATATTTTTT GGTGCGGGA ACTTGATTTT TCCGCCTTCT CTAGGTGCTC TATCTGGAGA 3360
 ACATTTTCTT CCTGCCATCG CAGGTTTGT CTTTTCAGGC GTTGGTATCG CCGTCTTGAC 3420
 CCTTATFATT GGAACGCTAA ATCCTAAAGG ATATATCTAC GAGATTTCAA CGAAGATAGC 3480
 GCCTTGTTTT GCGACTCTTT ACCTCTCAGT TCTTTACTTG TCAATCGGTC CATTCTTTGC 3540

1020

TACCCACG	ACTGCTACAA	CAGCTTACGA	AGTAGGGATT	AGCCCCCTTT	TGTCGGATGC	3600
AAATAAAGGA	CTTGGCTTGA	TTGTATTTAC	GGTCTGTAT	TTTGCGGCAG	CCTATTTGAT	3660
TTTCGCTTAAT	CCATCAAAAA	TCTTAGACCG	CATTGGACGT	ATTTTAACGC	CAGTCTTTGC	3720
AATTTTGATT	GTATCTTGG	TCGTCTGGG	AGCTATCAA	TATGGTGAA	CAAGTCTCA	3780
AGCTGCTTCA	CTGCTTATCA	AGCTTCTGCC	TTTGGTACAG	GTTTCCTAGA	AGGTTACAAT	3840
ACCTTGGACG	CCCTTGCCTC	AGTGGCCTTT	AGCGTAATCG	CAGTTCAAAC	CTTGAAACAA	3900
CTTGATTTT	CAAGTAAGAA	AGAATACATT	TCAACTATTT	GGGTGTTGG	TATCGTTGTT	3960
GCCCTTGCCT	TCAGCGCTCT	TTACATCGGT	TTAGGTTTTC	TTGGAAATCA	TTTCCCAGTA	4020
CCAGCTGAAG	CGATGAAGGG	TGGAACACCA	GGTGTTTACA	TCTGTGCACA	AGCCACTCAA	4080
GAAATCTTTG	GCTCAACAGC	TCAACTCTTC	CTTGCAGCTA	TGGTTACCGT	AACCTGCTTC	4140
ACAACGACTG	TTGGTTTGAT	TGTGTCAACA	GCTGAGTTCT	TTAATGAGCG	CTTCCCACAA	4200
ATCAGCTACA	AGGTTTATGC	GACAGCCTTT	ACCTTGATTG	GATTTGCTAT	TGCCAATTTG	4260
GGTCTTGATG	CGATTATC					4278

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

ACCCGATCAA	ATGACAAAAG	CTAACTTTGG	TGTCGTAGGT	ATGGCCGTAA	TGGGTCGTAA	60
CCTTGCCCTT	AATATTGAAT	CTCGTGGTTA	CACAGTTGCT	ATCTACAACC	GTAGTAAAGA	120
AAAAACGGAA	GATGTGATTG	CTTGCCATCC	TGAAAAGAAC	TTTGTACCAA	GCTATGACGT	180
TGAAAGTTT	GTAAACTCAA	TCGAAAACC	TCGTCGTATC	ATGCTGATGG	TTCAAGCTGG	240
ACCTGGTACA	GATGCTACTA	TCCAAGCCCT	TCTTCCACAC	CTTGACAAGG	GTGATATCTT	300
GATTGACGGA	GAAATACTT	TCTACAAAGA	TACCATCCGT	CGTAATGAAG	AATTGGCAAA	360
CTCTGGTATC	AACTTTATCG	GTACTGGGGT	TTCTGGTGGT	GAAAAGGTG	CCCTTGAAGG	420
TCCTTCTATC	ATGCCTGGTG	GACAAAAGA	AGCCTACGAA	TTGGTTGCGG	ATGTTCTTGA	480
AGAAATCTCA	GCTAAAGCAC	CAGAAGATGG	CAAACCATGT	GTGACTTACA	TCGGTCTTGA	540
TGGAGCTGGT	CACTATGTGA	AAATGGTTCA	CAATGGTATT	GAGTACGGTG	ATATGCAATT	600
GATCGCAGAA	AGCTATGACT	TGATGCAACA	CTTGCTAGGC	CTTTCTGCAG	AAGATATGGC	660

1021

TGAAATCTTT ACTGAGTGGG ACAAGGGTGA ATTAGACAGC TACTTGATTG AAATCACAGC 720
 TGATATCTTG AGCCGTAAAG ACGATGAAGG CCAAGATGGA CCAATCGTAG ACTACATCCT 780
 TGATGCTGCA GGTAACAAGG GAACTGGTAA ATGGACTAGC CAATCATCTC TTGACCTTGG 840
 TGTACCATTG TCACTGATTA CTGAGTCAGT GTTTGACAGC TACATTTCAA CTTACAAAGA 900
 AGAAGCTGTA CATGCTAGCA AGGTGCTTCC AAAACCAGCT GCCTTCAACT TTGAAGGAGA 960
 CAAGGCTGAA TTGATGAAA AGATCCGTCA AGCCCTTTAC TTCTCAAAA TCATTTTATA 1020
 CGCACAAGGA TTTGCTCAAT TGCGTGTAGC CTCTAAAGAA AACAACTGGA ACTTGCCATT 1080
 TGCAGATATC GCATCTATCT GGCCTGATGG CTGTATCATC CGTTCTCGTT TCTTGCAAAA 1140
 GATTACAGAT GCTTACAACC GCGATGCAGA TCTTGCCAAC CTTCTTTTGG ACGAGTACTT 1200
 CTTGGATGTT ACTGCTAAGT ACCAAACAAGC AGTACGTGAT ATCGTAGCTC TTGCGGTTCA 1260
 AGCAGGTGTG CCAGTGCCAA CTTTCTCAGC AGCTAFTACT TACTTTGATA GCTACCGTTC 1320
 AGCTGACCTT CCAGCTAACT TGATCCAAGC ACAACGTGAC TACTTTGGTG CTCACACTTA 1380
 CCAACGTAAG GACAAAGAAG GAACCTTCCA CTACTCTTGG TATGACGAAA AATAAGTAGG 1440
 TCAGCCATGG GGAAACGGAT TTTATTACTT GAGAAAGAAC GAAATCTAGC TCATTTTTTA 1500
 AGTTTGGAAC TCCAGAAAGA GCAGTATCGG GTTGATCTGG TAGAGGAGGG GCAAAAAGCC 1560
 CTCTCCATGG CTCTFCAGAC AGACTATGAT TTGATGTTAT TGAACGTTAA TCTGGGAGAT 1620
 ATGATGGCTC AGGATTTTGC AGAAAAATTG AGCCGAAC TA AACCTGCCTC AGTCATCATG 1680
 ATTTTAGATC ATTTGGGAAGA CTTGCAAGAA GAGCTGGAAG TTGTTTCAGCG TTTTTCAGTT 1740
 TCATACATCT ATAAGCCAGT CCTTATCGAA AATCTGGTAG CGCGTATTTT GCGGATCTTC 1800
 CGAGGTCGGG ACTTCATTGA TCAACACTGC AGTCTGATGA AAGTTCCAAG GACCTACCGC 1860
 AATCTTAGGA TAGATGTTGA ACATCACACG GTTTATCGTG GTGAAGAGAT GATTGCTCTG 1920
 ACACGCCGTG AGTATGACCT TTTGGCGACA CGG 1953

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

CCGGCAGTAC ACGAGCTTGG GGAACAGCCA CTGGAACGAT GAGGTGTGAG CTCAAAATAT 60

1022

CCTCCAGTTA TGTTTTTCCT AATAGTATAC CGGAAGAGTG AAAGGATTTT ATAATGGAGC 120
 GGTTACAAAG AACCTACTTT CTATTAAACA GTATACTATG AAAATGTGAA AATTTAACAT 180
 TTTTTGTAC AAATTTTATA AATTATTGCC TTTTAAATAT CAATAGTTAA TCTCTTATCC 240
 AGATCCCCCT TGTGTAAACT TTATCTTTAT AAGCTTCAAG GCCCCTATCC CATCTATTTG 300
 CAACAATTAG ATCACTTTGT TTTGTAAATA GTTCAAAAT CTTTCAATA ATTACGTTAT 360
 CTATACTAAC GTTAAATTT GGTTCATATA CTAAAATTTT TATACCGACA ATCAATAGTT 420
 CATTAATTAT ACTTAAAATA GCTGACTCTT TGTAATTATC TGAATTATAT TTCATCCCCA 480
 ATTTATATAT TCCTACTATC TTTGGCTTTC GTTCCAATAT TTGTTAACT ATGAACTGTT 540
 TTCTATTTGT GTTGTAAATA TCAATCGCTT CTATCACTGG GGCATTTATT TCTATAAATT 600
 CTTTTTTTAA TTGTTTAGTA TCTTTGGGAA GACAAATATCC TCCAAATCCA AAAGAAGGAT 660
 TATTATAAAA ATTTCCAATT CTTGGATCTA AACAAACACC TTTTATTACA ACTTCAGCAT 720
 TTAAGCTTCT CCTCTCAGCA AAAGAATCTA GTTCATTTAA AAAGCAACAC GGAGAGCTAA 780
 GAATGTGTTA GAAAAAAGCT TAATTGCTTC TGCTTCAGTA GGAGAACTA ACATAACATT 840
 TTTAATATTG GCAGTACTAT GAGTACTAAT CGAAAGGAAC AACTCTGCAA TTTTCTTCC 900
 TTCAACTGTC TCATCTCCAA CAACTATGCG ACTTGGATAT AAATTATCAT ATATAGAACA 960
 ACCTTCTCTC AAAAATTCAG GGACAAAAAT GATATTTTTT GTATCAAACA GCCTTTTTTAA 1020
 TTTGTTTGAA AAGCCGATCG GAACTGTTGA CTTTAAAATA ATCTTTCCAT TAGGTTTTTAC 1080
 CCTCAGAATC TTCGATACCG TTTGTTGAT TTCAATATGTA TTAAACTAC CAATTTTCTC 1140
 ATCATAATCT GTCGGAAGCG CAATAATATA ATAATCAATA TTATTTTTTAA TTTCAGAAAA 1200
 TGTATCAAAA AAAGTAATAT TTAAGTTATT CTCGCAAAAA AACTTCATAA GCTCTTCATT 1260
 TTTAGATGGA AGAATGCCCT TTTTAAATTT ATTTATTTTT ACAGAATCTA TATCATATGC 1320
 AACAACTTTA TATTTAGATG CAAATAGTAA CGCGTAGGCC AGCCCAACAT GCCCCAAACC 1380
 AATTACTGCT ATATTCATAA AACTACTTCC TTATTTCTTA ATCCAAAATC TAATAGAAAT 1440
 AGCTGCCCA TTCCTTAAAT ACAACTCTTT AATATTGTTT AAAAGTTTTT CAACTGATTT 1500
 CCAGATTATC AAAATCTGAG ATTTATAGCA CAATATTGAT GATATTCTAT CAATATAATT 1560
 TTTTTCATCA AGTTCCTCTT GATACATTTT TAATCTTTA GTTTTCCCA TATAACTAAC 1620
 CATACTACTA TCACTTACAT ATGGGAAGTC CTCATAATAT ATTACTTTAT AACGCATAAA 1680
 TTCAAGCGCC CTTCCAATAC TATTACAAA AACATGAGCA ACATGGTCAC CAAGTGAAAG 1740
 CGGACAATAT ACGACACATT TGTCGTCTAA ATGCATTAAC AGCTCTTTTA TGATATCATT 1800
 CTTAATGTG TCCTCATTTT TTAATTCACT ATAGATATGA CGGTATAGAA AATTGCCATT 1860

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TCTATCTTTC	CTATAGAGAC	ATTCATAGTA	CGATAAGTGT	CTAAAATCAC	ATTGTAGACG	1920
TTCACAAGCT	AACCTGTCTT	CTTTCTCCTT	TTCTTCAATC	GGATATTTCC	CAAGGTTACA	1980
CAACTTATGA	AATTGCTTAG	CAGAGGGCTG	TAGCTGTTGG	CTCAAAGGGT	AACCAGAAAA	2040
TATAGTAATA	ACAAGTACAA	TTTCTCCTTC	TGAAGTTAAT	TTTGAAATAT	AATCACCACA	2100
GGAAAAAATT	CGCTCATCTA	AATGTGGAGA	TAAAAAGATA	TACTTAGTAT	TGTTACTCAT	2160
AACCATTCCC	TCTACAATTT	ATCTAAAAAC	TCACTAAGTG	TCTGATTAAA	TTCCACATCA	2220
TCAAAAAAAT	TCACCTTATT	CTTAATAATG	AATATTTTCGT	TAAATAAACA	TATATATAAA	2280
TATTTCAATA	TCCTTTCAAT	ATCATCCTCT	AAATTCCTCT	CAATATTTTG	TATCAGCCCA	2340
TTTACAATCT	TATTAATAAA	GATAAGCTCT	TTATCTCTAA	AATTAAATAT	TTTCATACAA	2400
CTGTTGTATC	GAAAAATATA	TAAAAAATTT	TTTACTAATG	TTTGAATATT	TAAACAACCTA	2460
AATAAATGAG	TTGTACCCCG	GACACTATTT	ATGTTATCAA	GAACACTATC	TTGAAACCTC	2520
AACTCACAGT	TCTTTTGTG	AAATTCCTTT	TTATCGTTTA	GATCTGATAT	TTTTTTAGAC	2580
ATTTCAACAA	TCTCAGACAT	TTTATATGGA	TATCTAGGAT	GAATGCCAAA	ACTATGCAAA	2640
ATGAACTGCA	CCCCAAAAGT	TAGACAGAAT	AAATCTAACT	TTTGGGGTGC	AGTTCATAAG	2700
ATTGGGATAT	TTTTTTTGTAG	CTAGAACTAG	TAGAAATATA	TAGTCAAATA	ACAGATACCT	2760
TAAGGGTTTC	TCATCTACAT	AAAAAATGA	TACTTTTTC	TCTTCAGTAA	TTACCTCATA	2820
AGCTTCACAA	TAGAATCTCA	TGTTTCCCTC	CCCTATATTC	TTAAATAAAA	TCCTTTGGAA	2880
ATTGATATAT	CTTAGTAAAA	TATTGTTTAA	GTTCCGGATG	CGGAGCATGG	GTAACAATAA	2940
TGACAGTCAA	ATCCTCTCTA	TCTAATATCT	TACGTTCAAT	CGCTAACGAA	GTTCTCCTAT	3000
CGATAGCAGA	AGTTCCCTCG	TCAATTAATA	CTATTTCTCT	ATTTCTAATT	AGCCCTCTAG	3060
CTAAAGTAAT	TTTTTGTTTC	TGCCCTCCTG	ACAGTAATCT	CCCATCATCA	CCAACATAAT	3120
AATCTAAAAT	GTTATTAGGA	AAATCTTTTA	CACTCAAACC	AACTTGCTCT	AAAGACTGTA	3180
GTATTTCTTC	ATCAGTATAA	TTTTCTTCCA	ATAAAATATT	ATCTCTAATC	GTACCTTCAA	3240
ACAAATAAGC	TTTTTGATCT	ACATATAGAA	CATTCGAAAC	CATATTTAAA	TAGGAGGTTT	3300
TTTTTATATC	ATCCCCGCAG	AATCGCAATT	CTCCACTATA	ATCTCTCAAA	AAGCCATTCA	3360
ATAATTTTAA	TAATGTAGAT	TTCCCGCTTC	CACTTTCACC	TAAAATTAAA	TACTTTTCAT	3420
TACGTTGAAA	ACAAAAATTT	AAGTTTTTTA	ATATTTCTTT	ATCTCCATAC	TTATAGCAAA	3480
TATTTTTTGC	TTCAATAAAC	GGAAAATCTC	TATTCACCTC	ATTTGGTTCG	ATATCATTCA	3540
TTTTTATTGA	CTCAATGGA	TTAATTGAAT	ACAATTTTAA	AAAAATAGGC	TTCGTACCAA	3600

1024

TAATAGAGGA	TAATFGACCT	CCTAATTCAC	CTAGCGCTGT	AAAAATAACA	CCTGTTAGTG	3660
CTCCTATTGC	TTCAATAGTA	CCAATTTTCA	CTATTCCTTT	TATTGCAAGA	TAGCCTGTTA	3720
AAAAACGAG	AGATATCTGA	AAAAAATAT	TGAGAAAGAA	GCTAATAGCG	CCTGCTAACG	3780
TTTCTACAGT	TGTCTTTCTT	TGTATAACCA	TCTTTAATAA	AATTCCTGCT	TCTTTAATTT	3840
TCTTAGGCAA	TACATATAAA	AGATTCAAGG	ACGCTAACAC	ATCAAATCCA	TTCAATATAG	3900
TCTCACTAGA	TTTTAAAAAA	GCTTCATTTT	GGTTAGTTAA	ATTTAGACTA	ACTTCTCGCA	3960
TTTTCGATGC	AAAGATTTT	GGTACAAGTA	GCATAATCAT	TAATGAAAAC	AAGGTGGCTA	4020
CAGTCAATGA	CCAATGATAG	TGATTAAGAG	TCACAACCTGC	AAATATAGTA	CCAGAAATTC	4080
CTTTTATTAC	TAAAAAAGT	TGTTTAAACG	CCTGATCATT	TAAAGTCTGA	ACATCATTAT	4140
TTAGCCACGA	AAGATATGTT	CCTGATGATT	TACTATGAAA	TTCTTGATAG	GTAGAGTTAG	4200
AGATGTCTGT	GGCAACTCTA	TTTCGAATCT	CTAGATTAAA	CTCTTGGATC	ACTTCAACCT	4260
GATAATTTTT	CACTACCCAG	TCAAGGAATA	TTATCCCACA	CCAGACAATC	ATTTGGTAGA	4320
TTGACAAATTT	CAAAAACCGC	TCTAAATTCA	TCGCAATTAA	TTCAATCAAC	ACCAGAGCAT	4380
TAATAGTTGC	TGCATAAATT	AGCAATAATT	GACCAGCAAC	AATAAATATC	GTTAATAAAC	4440
TAAATTTTTT	TATATTTGAT	TTTATAATAG	TATACACAAT	AGTTTCTCAC	TTTCTAAATT	4500
TTAATTGAAC	ATAGTTTTCA	TATATACAAT	AGAAAAAACC	AAAATGATAT	AATAACATAT	4560
ATTTCAAAA	AGAATTCGT	TAAAAATTTT	TTCTTCTCTT	GCCTTCTTGA	TTACTTTTAA	4620
AGCCTTG CAT	TTGTCTCCTA	TTAATAGTAA	CCGCTTTATG	TTTAAAGAAT	AATATTTCTT	4680
TGTAACCAAT	ATTCCTCTCGT	TGAAACTCAA	TAAATTAATA	TATTCCTTAC	AGTAATTATA	4740
ATATTCTTCA	TCTGCATTAA	TTGTTTTTTG	TGCTACTCCA	GTGATACCGT	TTTCTTTACT	4800
GTGAGCGTAG	TAATTCACCA	AGAATTCTCG	CACTATATCA	ATTTGGTATC	CTTGAACAAG	4860
TAGTTTTAAT	AAAACAACAC	CGTCCTGATG	TGAATCTAFT	TTCTCAAAAC	CATTAATTAA	4920
TTCTAGCACC	TCTTTTTTAC	ACAACCAAAA	TGACGTACCT	GCTATATTGT	GAACCATTTG	4980
AACAAACAAG	GGATTTCCAA	CAAAATCGGT	CTTCTCCTCT	TCTCGTGTAC	CATTTGGATA	5040
AATTATTATT	CCATACTAC	AACTAAAGC	TAAATTCTTC	ATTCTACTCT	TTTTAAAACA	5100
AGCCATCAAC	TTTAAAATTC	GATCTGGCAT	ATATTCATCA	TCATCGTCTA	AAAATGATAT	5160
ATACTTACCT	CTAGAATTTT	TGATACCTAT	GTTTCTGGCA	TTAGTTGCAC	CTAAATCTTC	5220
ATTACTTAAA	ATTAACCTAA	TTCTATGATT	GGTATAGCCA	AATTGATGGA	TAATTTTTATT	5280
TCTTAAATTT	ACATTACTAT	AATTATCATC	AATAATTATA	ACTTCGATAT	TTTTATAACT	5340
TTGATGTAAA	CAACTTTTCA	CAGCTCTAAT	CAGAGATTCA	TACCTATTAT	GTGTTGGTAT	5400

1025

TATAATACTT ACTAATTCTT GATCTATATT CCTATCCATG ACTACTCTTC TCTAATAAATT 5460
 CATCATATAC TCTCATGGTT TCTACAAACA TTTTTTGCAC AGAAAAATGT TTTCTTATTT 5520
 TTGATTTACT ATTCTCACCT ATATATTTCA AATACTCAGA ATCATTGAGT AAAAAATTAG 5580
 CACAAGCACA CACTCCCTCA ACATCTTCCT TCTCAAATAA AAATCCATCA ACCCTATGTT 5640
 CAATAATTC ACTTAACCCG CCAACATTAC TAGCTAAAAC CGGAGTTCCT TGTGACATTG 5700
 ACTCTAAAAC ACACATAGGT ATTCCTTCTG TATCAGAAGG AATATACAAT AAATCCGATA 5760
 TTTGGTAAAC TATAGTAGCT GGATAGATTT CACCAAGTAA CCTGAAATTA TCTCTACATT 5820
 TCAAATGGCA AATTTTTTCT TCAAAGCAG CCCACATACT ACCATTTCCA GCCATAATAA 5880
 AAATCACATC TTCTCTGACT AAAAATAATT TTTCTGCAA TCAAGGAAT CTATCCGGCC 5940
 TTTTTTCTGG ATCCAACCTT CCAACATAAC AAATGATTTT TTGTTATTTG GAATACAAAA 6000
 TTCTTTTTTA AAGCTTGAA CACCTACTAC ATCTAAATCG CTATTTGATA CATTAATTCC 6060
 GTTATTTATT GCAACTATCT TCTTATTTT TATTATACTC TCCAATCTTT TTTTTCATAG 6120
 TTTTCAGATAC ACAAATAAAA GCATCTCCA TAGAATATGT CCAAAAATCA AAATAAGTCA 6180
 AGAATTTCTT TTTTAAGTTA TATTCAACCC ATCCATGGCA TGTATCACT GTCTTAACCT 6240
 TTCCAAATCC ATCTTGTCA AGTTTTTTTA ACATATATAA AAAATAATTA GTTGAGTAGC 6300
 CATGACAGTG TATAAGTTGG ATTTTTAATA ATTTTAAAT ATTTTAAAG TGTAAGGCAG 6360
 TTTCAAATTT ATTTGAACAT TGAGTACAAT CAACATAGGC AATATCTAAA TTTTATAAAT 6420
 CATCAATAAC CTTTGAATCT CTAGATACAA TTATCAAAAT AGGGAATAGA GACA 6474

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

TATTTAACGA TTTTTTTCAT GTCATTTCCCT CAAAATAGA ATACCTTATA ATCTTAACAG 60
 AAAAAGAGCA TTTACGCCAT TATATGATAT CTATCTCTGT GATAAGTTT TTTTATGGGT 120
 AATTTAAAAG ACCAAACGCA AGATGGCAAT CAAGACCACT CCAAGAGAA CTGTTCCGAC 180
 TAGATTGCGG TAGCGAAAG CTACCCAAGC TGTTGGAAAG ACGGCTAAGA AGTCCAGTCA 240
 TTTGATTTGA GGAAGACTGC CAACCTTACC TGCTACTACG CTGAAAGAA TCAGGGCAAA 300

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GATAATGGAA	ACAGGCAAAA	ACTTCAAAAA	ACGCTCAACA	ATCGCAGGCA	GGCCCTTATA	360
CTTGACCAAG	ATGAAGGGAA	TCATACGGGG	AATCCAAGTC	ACCAAGCCAG	AGAAAATAAC	420
TGCTAATAAA	AGATACTTAC	TGACCATCTA	AAACCACCCC	CATGCTACAA	CCAAGTAGCG	480
TCGCAAAACAG	AACAGCTAGT	GACTGAGACA	TCACTGTCAA	GAGCAAAAAG	AAGGACACCG	540
CAACAACCTGC	TAGGATAATG	AGCAGATTGC	GGACAGGAAT	CCGTCTTTGC	ATAATCTGAA	600
ATTGCGAAGC	AAAATACCAA	TAAACATCCC	AACCAGGGCA	AAATCCAAGC	CAAAGATTTC	660
TGGATTTGGT	AGCAGGCCAC	CCAGAGCCGT	TCCGACTACT	GTCCCCACAA	ACCAAGCCAC	720
ATAGCTGTTA	AGATTGTTTC	CGTGCATCCA	CATAGGATTT	ACCTTGTCTG	TATGGGCCAA	780
TTCACCCATC	AAAACGCCAT	AGGTCTCATC	TGTC AAGATA	CTAGACATAC	CGATATTGTA	840
CCAAAGACTG	GTATGACGGA	AATAAGTCGA	TGCGTGTAAA	CTCAACAAAA	AGAGACGCAA	900
GTTGATTAGA	AAAACCGTCA	TAGCAATAGC	TGCCACAGGA	GCTTGAACCA	CAATCAGTGC	960
CAACATGGCA	AACTGGGCAC	TCCCAGCATA	AACAAAGAGA	CTCATCAAGC	CCATCTCAAC	1020
AGGTGTCACA	TAGGGCGCAC	CGATAATTCC	ACAGGCCAGG	CCGATACTGA	CATAGCCAAG	1080
AGCCGTGGC	ATGGCTGCCT	GCGCCCCCTC	CTAAAATCCT	TTTTCTTTCA	TCTTCTCTCT	1140
CATATTGTCT	TAATAATACT	CAATGAAAA	CAAAGAGCAA	ACTAGGAAAC	TAGCCGCAGG	1200
TTGCTCAAAA	CACTGTTTTG	AGGTTGCAGA	TAGA ACTGAT	GAAGTCAGCT	CAAAACTG	1260
TTTTGAGGTT	GTTGATAGAA	CTGACGAAGT	CAGCTCAAAA	CACCGTTTTG	AGGTTGTGGA	1320
TAGA ACTGAC	GAAGTCAGTA	ACCATACCCTA	CGGCAAAGTG	AAGCTGACGT	GGTTTGAAGA	1380
GAGTTTCGAA	GAGTACAAGT	AGGCTGAAAA	GAATCCAACC	ACAGCATGGA	CTATTATATA	1440
GCAGATTGAA	ATAAGATGAG	AACAAATCGA	TTGGGAAAGT	AAAATTAATT	TCTATAAATG	1500
TTTTAGCAAT	TGTTTCGTAC	TATTTTAGAT	TCAGTCTATT	ATAACACATT	CAGAAAAGAG	1560
AAAAAAGTCT	GTTGATTTTG	ACCATCATAA	AAAGACTGGC	AATCCAGTCT	CAAACATATA	1620
TTATAGAAAT	TCTCCACTAA	ATACTTTCAC	GAATATTCAG	AAGCATAACA	AAGGCAACTA	1680
GAAGAAATAG	CAATAAAAACA	AAGCTAACTG	CCAGAGTTCC	AAAGCTAGTA	GCAATGGTTA	1740
CCAAAGCTAT	TGTAATAAAG	CTAGGTAAAA	CAACCGTAAT	GGCACCGATA	GAGGATTGAA	1800
CTGCTCCCAT	TGACTCCTCA	GGTATTTGTT	TAAAAACGAG	TTCTTGCAAT	CTAGGAGAGA	1860
GAACACCTGC	GAAAAAGGCA	TCCAAGGTAC	TAAAGATGAG	AATCCAGTCA	AAACGAACTG	1920
TGGCAAATCC	TACTAGAAGA	AGCAACTGGA	TGACAAGTGA	GGCATAGAGA	GCTGTTTTTA	1980
TGGAAATGGT	ATGTTGCAGA	TAGCCACTTA	CAAGGCTTCC	GACAATCAGG	GCTGATAATT	2040
CTAGTGTGGC	TAACAAGGCA	AGAGATTGAC	CAGTTTGTA	ATTCAAAAAG	GGCTGGTTCC	2100

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TTAAAAATAG	AGTGGAATA	GGAACCGTAA	CATTTATCAC	TGCTTGACTA	GTAGAGATAA	2160
TAAACAAAAC	CAAGAGCACC	TTATTCATAT	TCCATATCAA	TTTCGATGAT	TGGAGCAAAT	2220
GCTGGCAAAA	GGATTTTACA	GAGAGTCCTT	CTTGATAGCT	AATCGTTTTT	TCTACTTTCA	2280
AGAGGTCAGT	TTTTATGAAG	AGGATACCTA	AAAATGCGAT	TAAAAAGGTA	AGAGCGTTCA	2340
GTAAGGAAAT	AAACTGGATG	GATAGAATGC	CTAGTAAGAC	TCCTCCTAGG	ATATTACTGA	2400
TTGTTTTTAC	TAAACTAACA	GTTGACTGTT	TAAAGCCAAT	AGCTTCTGCC	AGATGGTCTT	2460
GCCCAATAAT	TCTAATGAAA	ATCGGAGTGA	GCATGGCGCC	TGAAAAATAA	CTCAATGTGT	2520
CAGACAAGAG	GTTAATCAGA	CAAATAAATG	CTACTAGCAA	CAAGGAGAAA	GACTGCCCTG	2580
AAAGTGATAA	AGACACTATA	GAGTAAAGCA	AAAATTTTGC	AAAATAATG	ACTGTGTATT	2640
TCAAGACACG	ATGATGTTGA	AAATCCGCCA	AAACTCCCAG	AAAGATTTGT	AGAACTTGGG	2700
GCAGGGTTC	TGAAATCGTG	ATGAGTAAAA	TCGCCAAAGG	GGCAAAGAT	GCATCTGCCA	2760
CATAATTCAG	GAAGGCCAGA	TAAAAAATCG	TATCCCCAAG	CGTTGAAATC	CACTGGTTGA	2820
TAGTTAATTG	CCTAAAATCT	CTATTTTGAA	GAAATACTTT	CATCACAAC	CCTTCTTAAG	2880
TTCAAATGGG	AATCTTTCCC	CAAGGATAGA	CCGCGATACT	ACTAACAACC	AAAATTACAG	2940
TAACATCAA	AGCTGACCAA	TGCCATTGTA	GACTATATGC	AGTCCAATAG	GCCAATAAAT	3000
TGACTTTGTC	ATTCTAAATA	AGACTGCAAA	TATAAGACCT	CCACCCATAT	AGAAGACAAA	3060
GTCTGTCAAG	ACCCAACCGT	GATTACTAAT	GTGCGAGACC	CCAAATAAAA	CAGCGGAACC	3120
AAGTACATCT	AGCCCCATT	TCTTTCCTTT	TTCAGAGCA	GTCATCACTA	ATCCACGATA	3180
AATCATGTCT	TCAAAAATGG	GACCTGCAAT	CACAGGATAA	AAAAAATACA	TCAAAAATGC	3240
TGTAGCCCT	GTAAAAGTCG	GAGCAGCATG	TGATAAGAA	ATTTCAATTC	GAGTAGGTGG	3300
GAAAAGAAAA	AAGGTAACGA	AATTCCAAAC	AACAAAAGCA	AGCAGAGCTA	GGAAGGAATA	3360
GAAAAGATAG	GATCCTTTAA	ACTTCTACT	ATTGATTTTC	TGCCATTTCC	CCGACCAAAT	3420
CATAGCAATA	AGAGCAAATA	AAACCACAAG	AAAATTC AAC	ATCATATCCG	ACAGATAATA	3480
GGCAAAGTCA	GATAGCCAG	TAACAAGGTC	GCTGCGTAAA	ACTAGAACAC	TGAACTTCTG	3540
GTCAGCAATA	ACTAGTAGAA	AAACTATAAT	AAAGTAGCGG	TGTGAGATTA	TCTTTTTCAT	3600
ATATCACCTT	TCTAATATCC	AAATACCAAT	AAAGTAACAA	TGAGTAAGAA	ACTATTCCAT	3660
GAAGCATGCA	GAGCTATAGC	CCAATAGATG	GATCGGGTGT	AGCGAACAT	CATACAAAAT	3720
ATCAAGCCCA	TTCCAAAATA	CTTTATGAAA	TCTGTCTGTTA	TCCAACCATA	CTGCAAAACA	3780
TGCATAGCGC	CAAATATGGC	AGCGGAAACA	AGAACATCAA	GATAGTATCT	CTTAACTTTA	3840

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GATAAACTTG TCATCAAAAAG ACCACGACAA ACAACCTCTT CTGATACAGG TGCATAATA 3900
 CTAGTATAAA GTATTGCGGT AACAAAATAG CTAATTCCTG TTAAATTGGT GGCTACTTCT 3960
 ACGACTGTAC TTCCATTCTG GGTACGAGGA AAGATATAGG TTGTTAGATT TGCCACACCG 4020
 AACAAATAAGA AAAAAGAAAG AAGGAAAACA CCCAGGTAAG ACCAACGAAA CTGGAAACGA 4080
 CCACACTCTT TCCAATGTTC ACTTTTGACA AAAGCAATTG TAGCTATAGT TCCCAGAATA 4140
 AGTACCAATA AAACCTGGAA CACATAGTAC ATATTATCAG ACAAAGCAAC CATAAAATCT 4200
 AAGTCTGATG TGACATTAAG AATGAGGTAA TAAGTCAAAA TCAACAAGCC AGTTGCTAGG 4260
 TGAATTTCA CTTCTTTCAT TTTCTTCATC CTATTATCTC CTATAAGAGC CTATCTTCTA 4320
 CGGCGGCCAA ACAATCCATC TGCTAAATCT ATAGTCCAAT CAAAAGCTCC ACGATTAGGA 4380
 CTCATCCCTT GATGCCCCA ACCAGGGTAA ATTCTGGGA CGCCCCAACC AGATATACCA 4440
 CTTCTCCAC CACCTCCCAT AGAATTTACG AGGTTGCCTC CTCTAACATC TTGCAACTCA 4500
 GCTTCTGTCA ATTCCATTGT TTCTGCAAAT TGTAATTTA ACATCTTTA CACTCCTTCA 4560
 ATATCTTCA TTTGTAAACC ACTTCTGCGA CCTAGGATTT GCTTCAAGTG CTTTACAAGT 4620
 ACAGTATAAC ACGAACATG GCTTATTTA GAAAATCGCA TATTTGATAT TTTTCTTAT 4680
 AGAAATTTCA GATTTGCGAT TTTGGTGAAT TTGATTACTT CTCTGGTATA ATAAAGTTAC 4740
 TACTAATGAG GAGTGGAGAA ATATGAAGAA ACAAATTTA ACATTATGA AA 4792

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CCGTTCCTCGG CGACGGCCAT CTGATGAAGC TATTTATGAG GGAAACTGGC AAGCTGGAGA 60
 GTCAGAGTAT CTAGTCTTTC ACCGATTGCT GTGGCAGCAG ATGTGCAGGG AAAAGGAGTT 120
 GCTCAAACCT TCTTAGAGGG CTGATTGAA GTTTTGATT ATCTTGATTT TCGCTCAGAT 180
 ACGCATGCTG AAAACAAGGT TATGCAACAT ATTTTTGAAA AACTTGTTT TAAACAAGTC 240
 GGTAAGATGC CAGTAGATGG CGAACGCTTG GCCTATCAAG AATTAAGAA ATAATGCAA 300
 AGAAGTATGT AAAAATCCTC TACTCCTCAC CAATTGGTAT TCTATCACTT GTAGCTGATG 360
 ACCATTATTT GTATGGAATT TGGGTCAGG AGCAGAAGCA TTTTGAGAGG GGACTIONGAG 420
 ATGAAACGAT AGAAGAAGTT GTTAGTCATC CTATTTTAGA CCCAGTTATT GCTTGCTTAG 480

ATGATTACTT TAAAGGCAAG CCTCAGGATT TATCCAACCTT GCTCTTGGCG CCAATCGGAA 540
 CGAATTTTGA AAAGAGAGTT TGGGACTATT TACAGGGCAT TCCTTATGGT CAGACAGTGA 600
 CCTATGGACA AATFGCTCAA GACCTGCAAG TGGCTTCTGC TCAAGCAATT GGTGGAGCAG 660
 TGGGACGCAA TCCTTGGTCT ATCCTAGTAC CTTGTTCATCG TGTGTTGGGA GCAGGCAAGC 720
 GTCTGACAGG TTATGCTGCA GGAGTGGAAA AGAAAGCTTG GCTCTTGGAG CATGAAGGAG 780
 TAGATTTTAA AGATAGAAGC AATAGAAGGA GAAGCACATG TTAGAATTTA TCGAATACCC 840
 CAAATGTTCA ACTTGTAATA AAGCAAAACA AGAATTAAT CAATTAGGTG TGGACTATAA 900
 AGCCGTCCAT ATCGTGGGAA AACACCTAG CCAAGAAGTC ATTTTGAATT GGCTAGAAAC 960
 CTCAGGATTT GAATTGAAGC AATTTTTCOA CACCAGTGGT ATCAAATACC GTGAATTAGG 1020
 GCTAAAAGAT AAGGTAGGAA GTTTGTCAA CCAAGAAGCG GCTGAGTTC TAGCAAGTGA 1080
 CGGTATGTTG TTTAAACGGC CCATTTTAGT AGAAAATGGA ACTGTTAAGC AAATCGGTTA 1140
 TCGAAAATCT TATGAGGAAC TGGGACTGAA ATAGTTTTTA TCTATCTCTT TGATAGATAA 1200
 AATATATAAC TTCCCTGTTT CAAAGTATGA TAAACTAGTA GGTAGACAAA GTCTGTATCT 1260
 GACCGTAGCA AATAATTTCA TTGACGGCAG AAGCATGGTA GCATGAATCA TTATCAGAAG 1320
 AGGATGTTTT TATGAATGTT ACAACGATTT TAGCATCAGA TTGGTACCAA AACTTGATGC 1380
 AATTGATTC GGATGGCAAG CTGTTTAGCC TACGTTCGGT CTTTGATGGA ATCCCTAGAA 1440
 TTGTCCAACA ACTTCCAACA ACAATTATGT TGACAATGG TGGTGCCCTT TTTGGCTTGG 1500
 TTTTGGCGCT TCTTTTGCC ATTGTGAAGA TCAATCGTGT CAAGATTTTA TATCCCTTGC 1560
 AGGCCTTCTT TGTTAGTTTC TTTAAAGGGA CACcGATTTT GGTGCAACTC ATGTTGACCT 1620
 ACTACGGAAT CCCTTTGGCT TTGAAAGCCC TCAATCAGCA ATGGGGAACCT GGTCTCAATA 1680
 TCAATGCGAT TCCAGCTGCA GCTTTTGCGA TTGTGCGCTT TGCCTTTAAT GAGGCAGCTT 1740
 ATGCTAGTGA AACCATTCGT GCAGCCATTC TCTCAGTTAA TCCTGGTGAG ATTGAGGCGG 1800
 CACGCAGTCT GGGTATGACC CGAGCGCAAG TTATCGACG AGTGATTAT CTAATGCAG 1860
 CGGTGGTAGC TACTCCAACC TTGATTAATT CCCTCATCGG TTTGACCAAG GGAACATCTC 1920
 TAGCTTTTAG TGCGGGTGT GTGGAAGTCT TTGCCCAAGC TCAGATTCTA GGTGGAGCTG 1980
 ATTATCGCTA TTTTGAACGC TTCATCTCCG TTGCCCTTGT TTATTGGGTA GTCAATATCG 2040
 GAATTGAAAG CCTCGGTCGT TTCATCGAGA GAAAAATGGC TATTTCTGCA CCTGATACAG 2100
 TGCAACAGAT GTGAAAGGAG ACCTTCGTTA ATGATTAAGA TTTCGAATTT AAGCAA 2156

(2) INFORMATION FOR SEQ ID NO: 158:

1030

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GTATCTCTAC ACATGTCTTC AATCGATTTT GTTGCTCCTCC AATTTAATTC CTTATATGCT	60
TTGTCTGCAT TTGCATAACA AGTTGCAACG TCTCCTGAAC GTCTTGGAAC TATTTTATAA	120
GGAATAGGGA TCTTATTAAC ACTTTCAAAT GTATTTACAA GTTGTAAATAC ACTAGTGCCT	180
TCTCCCAGGC CTAGGTTATA GATATAAACA TCTGTTTTTT CAGATACTTT TTCTAAAGCT	240
TTTATATGTC CTATTGCTAA ATCTACTACA TGGATATAAT CACGCACACC AGTACCATCA	300
AGCGTATCAT AATCATTTCC GAACACACTT AGCTCTGATA GCTTACCTAC CGCTACTTGT	360
GCAATATAAG GCATCAAGTT GTTAGGAATT CCTGAGGGAT CTTCCCAAT CAAACCAGAC	420
TCATGAGCAC CAATTGGATT GAAATAACGA AGCAACGCAA TACTCCATTC TGAATCTGCC	480
ACATGAACAT CTTTTAAAAT TTGCTCAAGC ATCACTTTCG TATACCCATA AGGATTTGTC	540
GCACTTGTTC GCATCGTCTC AATTAGAGGT GACTGATTGT TAATCCATA TACAGTCGCA	600
CTTGAAGAAA AGACAATCTT TTTAACATTA AATCTGACA TCACTTCAAC AAGTGCCAAT	660
GTACTCATAA TATTATTTTT GTAGTACATC ACAGGCTTTT GCACGGATTC TCCGACAGCT	720
TTATAACCTG CAAAATGAAT TGCAGCATCA ATCGATTCTT GTPCAAATAC CTTTCTCAAT	780
GCTTGTTTAT CACAAACATC TAATTCGTAA AACACGGGAC GTATTCCTGT AATTGCTTCA	840
ATACGGTCTA GCACCAAGAT GCTAGAGTTC GAAAGGTTGT CGACAATGAT AACTTCCTTT	900
CCTAAATTTA GTAATTCTAC TACGGTATGG CTACCAATAT AACCAGCTCC GCCTGTTACC	960
AATATTGCCA TCTGGGTTC CTCCTAATTA ATTCCAACCG ACTTAACAAA TCTCATAAAC	1020
GCTTCATGCC CAGACGGTGT ATTCTTATAA ACTCCTGCAT CTTCCAGAAC TCTCGCAAAC	1080
ACTTGTCCCTG CTTCTGTGTTG AACTACGCTA TTAACCTCTT CTTTATTAAT GCGAGGATAT	1140
TTTTCTTTCA ATTTGGTCGGC CCATTCTAAA TGATAATCCG CAATTGCATT ATCCTCTCCT	1200
AAAAGATATT TTCCAACCTC TTCTAACTCT GGTTTCAAAC GAGGTGGTAA TATCGCAAGT	1260
CCCATCACTT CGATTAACCC GATATTTTCC TTTTAAATAT GTTGTACATC TTGATGAGGA	1320
TGGAAAACAC CATCTGGGTA TTGTTTCAGTA GTATGATTAT CTCTTAGAAC AATATCTAAT	1380
TCGTATCTCC CGTCCACTTT ACGAGCAATA GGAGTCACCG TATGGTGTGG GACATCTTCA	1440
GCATAGCAA TGATGTCTAC TTCTAAATCT GAATATTCTC TCCAATTATT TAGAATTTTA	1500

GTAGCTAAAT CTAACAAGCG ATTTTATTTT TCACTTTGTA ACCTAATTAC TGACATTGGC 1560
 CTTTTTACAA TACCAGCATT AACATCCTCA AAGTCTTTAA AACAAAATTC ACTCTCAAAT 1620
 TTTGCTTTTT CCATTGGGAA AATATGTTTC CCTCCCTGGT AGTGGTTATG ACTAAGAATG 1680
 GAGCCTCCTG AGATAGGAAG ATCAGAATTT GAACCAGCAA AATATCCTGG CAAAATATCA 1740
 ACAATCTCCA ATAATGTGTC AAATGTTTTA GAGGTAATAG CCATTGGTAC ATGTTGACTA 1800
 TTCAAAAATA TCGCATGCTC ATTAAGTAT GAGTAGGGAG AATACTGGAA TCCCCATACT 1860
 TCGTCACCAA GTTTC AACCG AATAATCTA TGATTGGAAC GTGCTGGATA ATTTATTCGC 1920
 CCCTGATATC CTTCAATTTT CATAATAGT AAACATTTGG GATAATTAGT TGCTTTTACT 1980
 AATTTTTTCAG CAGCAATTGT TTTTGGATCT TTTTCGGGTT TTGACAAAT TATCGTAATC 2040
 TCTAGCTCTC CGTATTTAGT TGATGCTCGA AACTCAATAT TCTTAGCAAT AGCAGAAGTT 2100
 TTAATATAAT CACTATCTTT ACTTAACTTA TAAACTCTT CAACTGCTTC TTGAGGTGAT 2160
 ATATCATATG AACTCCAAAA AATATCATTT AATCGACTAG GTAAAGGAAC TATGAAATTC 2220
 ATTAACTCTG CTCCTAAACA TTCCTTTTCC TCGATFAAAT CTTTAATTTT ACCGTTTTTT 2280
 AAGGCGATTT CCACTAAGTA ATCTTTTATT TGTTTCAGGT CATTTCATC GGAAATGCGA 2340
 TCAATFCCCT CCTCACCTAT TAACGCTAGT ACTCTATTTT TCACATATAT TTTGTCAATT 2400
 TCATTATACA TTCCGTATTC AATTACTCTA TCAACAAAAAT TATCAATAAT TGTTTTCATA 2460
 TATTTTTCTT TCTAATTTAT GTTCCCATAT TTTCTATACA TTATCCATTT ATAAATGCT 2520
 TGCCTAGTAT GAGCAATTTT ATCAAGGTGA TGAATAATAT CTAAAGCACT AATTACTTCA 2580
 GAAACGTTCC CATCATCTTC AAATATGTAA TTCATATTTT TCTTTTCCAT ATTTATACTA 2640
 AGCTCTTCTA TCTCATCTG TTTTGTATA ACAACCATAT CTAAACATCC AGATTGTTCC 2700
 TCTCTATAAC AAGATATAGC CCTATTCATA TGCAGTCCGA TAACTTCATG AAGTATTTTT 2760
 ATTTTGTAAA TAATTTTCTT CAAAATTTCA TTATTTTGAA GAATCTGTAG ATTTTTTAAA 2820
 ATTTCAACAA TTCTATCCCC AATACGTTCA ATGTCAGTTG ATATTTTAT TACACTAATA 2880
 ATTCTTCTTA AGTCATATGA AACAGGATGT TGTAACAAA TTAATCATA TCCTTTTTTA 2940
 TCAATATTTA GAACTGACTC ATTTATGATT AAATCTTCTT TAATCAATTC TACTCGTTCT 3000
 TCATTGATA AATATCAAA TAACTTCTCA TATTTATCAA GCACAGATAC CCAAATGGTC 3060
 TCTAAATTAT TTGATAATTC TATAATTTCA TTTTCTAAAT ATAACCTTAA CATTAGGTA 3120
 CCTCTTCTTA ACAAAGTTCC 3140

(2) INFORMATION FOR SEQ ID NO: 159:

1032

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9048 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CCGGATGATT TCCTGGTCAG ATAGGGGGAA AGTGACTTCC TCAGCAATCG CGCGTAGAGT	60
AGGATCCCTT TCACGGATAA TATCGTTCAT ATCAATTAAG TGAGCAGCTT TTGTAATACG	120
TTCTATTGCA GACATTTTCT CTCCTTATAT TATGTTTAGT GCAGTTAGCT ACTGCCAAAG	180
CCCAAGTGGT ATRACTTGAA TAAGCCACTG TGGATTAGTT CATTTTCTTT CATTACCTCT	240
ACATGATATC ACAAAAATGAC AAGAATTGAA AGCATTATGG CATTTAGGAT TTATAGAAAA	300
TAGATAGGAA GTTCAATTCA ATTGTGAAAAG AAATACTTAT CTGTGATATA ATAAAAAGAA	360
AAGGCTTGCA TAAGAAAGTA GGGAGAACGA AGATACAAAG AAGACAAAAT CGAAATCAGG	420
GTGGTTTAGC TTTTCGTTTT ATGAAGGGCT TGGTAACTT TTTAGGAGTT ATCGCAAGTG	480
GAGCAATAAG GGATTTGTGG CGATACTCTT GCTAGCAGTT GGTTTATCAA TGGGCTTGGT	540
CTTGTGTTTT GAAAGCTTCC AAGGAATCCC TTGACTAGTC AAAAACGAGA TACTATTTCT	600
CAAGAGGGGA CTAAGCAAAA GTCTCAGGAG TAGGAAGAGG AAAAACTGC CAGAATTATG	660
GCCCACGGGG ATTTGCTCTA CCACGATGGA CTTTCTTTT CAGCTAAAAA AGAAGACGGT	720
ACCTATGACT TTCATGAAAA TTTTGAGTAT GTGACTCCTT GGCTCAAGCA AGGGGACTAA	780
GCAGCAGATT TAGCTATTGG TGATTTTGAA GGAACCATTA ATAAGGATCA TTATTTAGCG	840
GGTTATCTTC TCTTTAATGC TCCTGTTGAA GTTATGGATG CTATTAAGGA GGCAGGTAT	900
CATGTGCTGG ATTTAGCTCA TAATCATATT TTGGATTTCG AAATTGAGGG AGTTATTTCA	960
ACGGCCGATA TTATTGAGAA AGCTGGAATC ACTCCAATCG GAGTTTATAC GCACGAACCA	1020
CGTGATCAGG CTCCGCTGGT CATTAAAGGAA GTGAATGGTA TCAAGGTGTC ATTGTTAGCC	1080
TATTCCATATG GTTTC AATGAGCAG TATATTTCTC AGGAAGACTA TAATCGTTAT	1140
CTTTCAGATT TAAACGAAGA TAAGATGAAG GTTGA AATG AACGGGCAGA GAAGGAAGCA	1200
GATATCACCA TTATCATGCT TCAGATGGGT GTTGAGTATC GATTGGAACC AACTGAAGAA	1260
CAAAAAGCTC TTTATCACAA GATGATCGAT TTGGGAGCGG ATATTATCTT TGGAGGCAT	1320
CCTCACGTTG TTGAACCATC TGAAACGGTT GAAAAAGATG GAGATAAGAA ACTCATATC	1380
TATTAATGG GGAAC TTCAT TTCCAATCAA CGAATTGAAT CTATGGGAGA TGAAGAGAAT	1440
GCTAAGTGGA CTGAACGTGG TGTTCATG GATGTCACCA TCAAGAAGAA GGATGGAAAA	1500

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ACAACATATCG GAACAGCTAA AGCTCATCCT ACTTGGGTCA ATCGAACACC AAAGGGAACC	1560
TTTTCCACCAG AAGGATATCC CTTGTATCAT TACCAAACCT ATATTTTGGG AGATTTTATA	1620
GAGGATGGCA GTCATCGTGA CCAGTTAGAT GAAGCGACTA AGGAACGAAT TGATACAGCC	1680
TATAAAGAAA TGAATGAACA TGTGGGATTG AAGTGGTATT AGCTTGAATC CAGAGGAAAAG	1740
TAAATGATGA TTAAGGTAAT TGCACAGAT ATGGATGGGA CCTTGCTGGA TGCTAGAGGT	1800
CAGCTTGATC TCCCACGATT GGAAAAGATT TTAGATCAGT TGGATCAAAG GGGCATTCGT	1860
TTTGTTCATG CGACGGGCAA TGAATTCAC CGCATGAGAC AACTACTGAG TCCCTTGGTG	1920
GATCGAGTGG TTTCTGGTGT TGCTAATGGC GCTCGTATTT TTGAAAACAA TGAATTGATT	1980
CAGGCTCAGA CATGGGATGA CGCCATTGTC AACAAGGCTT TGAATCATT CAAGGGTCGA	2040
GCGTGTCCAG ACCAGTTTGT TGTAACGGGG ATGAAGGGTG ATTTTGTCAA GGAAGGTACG	2100
ATTTTACAG ATCTTGAAG TTTTATGACT CCAGAAATGA TTGAAAATTT CTACCAACGG	2160
ATGCAATTTG TGGATGAATT AACATCTGAC CTCTTGGTG GTGTGCTCAA GATGAGCATG	2220
GTTGTTGGTG AGGAACGTTT GAGTTCGGTT TTGGAAGAAA TCAATGCTCT CTTTGATGGC	2280
CGTGTCCGAG CTGTATCCAG TGGCTATGGT TGCATTGATA TCCTCCAAGC TGGGATTCAT	2340
AAAGCATGGG GCTTGGAGGA ATTACTCAAG CGCTGGGACT TGAATCCCA AGAATCATG	2400
GCTTTTGGTG ATAGTGAAAA TGATGTTGAA ATGCTTGAAA TGCTGGAAT TGCTATGCG	2460
ATGGAAAATG CTGATGAGAA AGCCAAAGCT GTGGCGACTG CTCTAGCACC AGCCAACAGC	2520
CAAGGAGGAG TTTATCAAGT CTTGGAAAAC TGTTAGAAA AAGGAGAATG AAGTGGCAGT	2580
ACAGTTATTA GAAAATTGGC TCCTAAAGGA ACAAGAAAA ATTCAAACTA AGTATCGTCA	2640
CCTAAATCAC ATTTCTGTTG TAGAACC AAA CATCTTTT ATTTGGGGATT CCATTGTGCA	2700
GTATTATCCT CTACAGGAGC TATTTGGGAC TTCAAAGACG ATTTGTCAATC GAGGAATTCG	2760
TGGCTATCAG ACAGGACTGT TACTAGAGAA CCTTGATGCT CATCTATATG GTGGAGCAGT	2820
AGATAAAATT TTTCTTCTGA TTGGGACAAA TGATATCGGA AAGGATGTTT CTGTGAATGA	2880
GGCTCTCAAT AATCTCGAAG CTATCATTCA ATCCGTTGCT CGCGATTATC CATTGACAGA	2940
GATTAATTTG CTTTCCATTT TGCCTGTCAA TGAGAGAGAG GAGTACCAGC AGGCAGTCTA	3000
TATCCGCTCG AATGAAAAA TTCAGAATG GAATCAAGCC TATCAAGAGC TTGCATCTGC	3060
CTATATGCAG GTGGAATTTG TGCCAGTATT TGATTGTTT ACAGACCAAG CAGGCCAACT	3120
CAAAAAAGAA TATACAACTG ATGGACTGCA CCTCAGTATT GCTGGTTATC AGGCTTTGTC	3180
AAAATCCTTG AAAGACTATC TTTACTAAAT AGCTAAATAA TGTTAAATTT GAGCATAATA	3240

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TCTTGTA	AAAA	AATTC	AAAA	TCCTT	AAAA	TAAAA	AAGTGA	CGGAG	GAATT	TATGA	ATGTA	3300
AATCAG	ATTG	TACGG	ATTAT	TCCTA	CTTTA	AAAGC	TAATA	ATAGA	AAAATT	AAATG	AAACA	3360
TTTTAT	ATTG	AAACC	CTTGG	AATGA	AGGCC	TTGTT	TAGAAG	AATCG	GCCTT	TCTGT	CACTA	3420
GGTGAC	CAAA	CGGGT	CCTGA	AAAGC	TGGTT	TTAGA	AAGAAG	CTCCC	AGTAT	GCGTA	CTCGT	3480
AAGGT	AGAG	GAAG	AAAAA	ACTAG	CTAGA	TTGAT	TGTCA	AGGTG	GAAAA	TCCCT	TAGAA	3540
ATTGA	AGGA	TCTTA	TCTAA	AACAG	ATTCG	ATTCAT	CGAT	TATAT	AAAGG	TCAA	AATGGC	3600
TACGC	TTTTG	AAATTT	TCTC	ACCAG	AAGAT	GATTT	TGATTT	TGATTC	ATGC	GGAAG	ATGAC	3660
ATAGC	AAGTC	TAGTA	GAAGT	AGGAG	AAAAG	CCTGA	ATTC	AAAC	AAGATT	GGCAT	CAATT	3720
TCTTT	AAGTA	AATTT	GAGAT	TTCT	TATGG	TTACAT	CTCC	CAACT	GATAT	CGAA	AGTTTC	3780
TTGGA	ATCAT	CTGAA	ATTGG	GGCAT	CCCTT	GATTT	TATTC	CAGCT	CAGGG	GCAGG	ATTTG	3840
ACTGT	GGACA	ATACG	GTAC	CTGGG	ACTTA	TCTAT	GCTCA	AGTT	CCTGGT	CAATG	AATTA	3900
GACAT	AGCAA	GTCTT	CGCCA	GAAGT	TTGAG	TCTACT	GAAAT	ATTTT	ATTC	TAAGT	CTGAA	3960
AAATT	CTTCC	TTGGT	AAGA	TAGAA	ATAAT	GTTGA	ATTGT	GGTT	TGAAGA	AGTAT	GAAGT	4020
GGACCA	AAGAT	TATTA	AAAAA	ATAGA	AGAAC	AAATC	GAGGC	AGGG	ATTTAT	CCCGG	AGCCT	4080
CTTTT	GC GTA	TTTTA	AGGAC	AATCA	ATGGA	CAGAG	TTCTA	TTTAG	GCCAG	AGTG	ACCCAG	4140
AGCAT	GGCTT	GCAG	ACTGAG	GCAGG	ACTAG	TTTAT	GACCT	AGCT	AGTGC	AGCA	AGGTTG	4200
TTGGG	TTGG	CACAG	TTTGT	ACCTT	CTTGT	GGGAA	AATAG	TCAAT	TAGAT	ATTG	ATAGAC	4260
TGGTA	ATAGA	TTTTT	TACCT	GAGAG	TGATT	ATCC	AGACAT	CACT	ATTCGC	CAGCT	CTTGA	4320
CTCAT	GCAAC	AGACC	TTGAT	CCTTT	TATTC	CTAAT	CGTGA	TCTTT	TAACA	GCCC	CTGAAT	4380
TAAAG	GAAGC	GATGT	TTTCAT	CTCA	ACAGAC	GAAGT	CAGCC	AGCCT	TTTCTT	TATTC	GGATG	4440
TCCAT	TTTTT	GCTGT	TGGGC	TTTAT	TTTGG	AAAGA	ATTTT	TAAT	CAAGAT	TTGG	ATGTA	4500
TTTTA	AAGGA	TCAAG	TCTGG	AAAC	CTGGG	GAATG	ACCGA	AACT	AAGTTT	GGG	CCAGTTG	4560
AGCTT	GCTGT	TCCA	ACAGTT	AGAG	GTTAG	AGGC	AGGCAT	AGT	GCATGAT	CCCA	AGGCTC	4620
GTCTC	CTGGG	TAGAC	ATGCT	GGG	AGTGCTG	GTTT	ATTTTC	GA	CTATAAAG	GATTT	TACAAA	4680
TCTTT	TTTGA	ACACT	ATTTA	GCAG	ATGATT	TTG	CAAGAGA	CTT	AAATCAA	AATTT	TTCTC	4740
CTTTG	ATGA	CAAG	GAACGT	TCTTT	TAGCAT	GGA	ATTTGGA	AGG	AGATTGG	CTAG	ACCATA	4800
CGGG	CTATAC	AGGT	ACCTTT	ATCAT	GTGGA	ATCGT	CAGAA	GCA	AGAAGCC	ACT	ATTTTCC	4860
TATCG	AATCG	TACCT	ATGAA	AAGG	ACGAGA	GAGCT	CAATG	GAT	ATTAGAC	CGCA	ATCAAG	4920
TGATG	AACTT	GATTC	GCAAA	GAAG	AGTAAG	GAG	AGACATG	TCA	AATAGTT	TAAA	AGGGAC	4980
TTTACT	AAACA	GTGTG	GGCTG	GTATT	GCTTG	GGG	TTGTCA	GGA	ACGAGTG	GCCA	ATACCT	5040

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AATGGCACAC GGAATTTCCG CTCTGGTCTT GACTAACTTG CGTCTTTTAA TCGCTGGTGG 5100
 AATFCTCATG CTCTTGGCTT ATGCTACTGC AAAGGATAAA ATACTGGTCT TTTTAAAGGA 5160
 TAGAAAGAGT TTGCTGTCTC TTCTTATTTT TGCTCTGATT GGTCTTTTTT TCAACCAATT 5220
 CGCCTATCTG TCTGCTATTC AGGAGACCAA TGCGGGAACA GCGACGGTGC TTCAGTATGT 5280
 TTGTCCTGTC GGAATTTTAA TTTATAGCTG TATCAAGGAT AGGGTGGCAC CGACACTGGG 5340
 AGAGATAGTT TCCATCATAT TCGCCATCGG AGGAACCTTC CTGATCGCAA CACATGGGCA 5400
 GTTGGACCAG TTATCCATGA CACCTGCTGG TCTGTCTTGG GGTCTCTTTT CTGCCTTGAC 5460
 TTATGCTCTG TATATCATTT TACCCATAGC CTTGATTAAG AAGTGGGGGA GCAGCTTGGT 5520
 CATTGGTGTG GGAATGGTCA TAGCAGGTTT GGTGCGCCCT CCTTTTACAG GGGTTCTACA 5580
 GGCCGATATC CCGACTAGTC TTGATTTTCT CCTGCGTTT GCAGGCATTA TCCTTATCGG 5640
 GACTGTCTTT GCCTATACAG CTTTCCTTAA AGGAGCCAGT CTGATAGGAC CGGTCAAGTC 5700
 AAGCTTGTTG GCTTCAATG AGCCAATATC GCGGATTTTC TTTGCCTTCT TAATAATGAA 5760
 TGAACAATTT TATCCCATG ATTTTCTTGG TATGGCAATG ATATTGTTTG CTGTAACCTT 5820
 GATTTCTTTG AAAGATTTAT TCTTAGAAAA ATAAAAAGA CTCTTTGTCC GTGACAGAGA 5880
 GTTTTTGCGT GGTAACTTAA TTATTTTCAA GATAAAATTC AAAGCGTTCG CCTACATATT 5940
 GACTTTTTAC GTATTCAAAA GCAGTACCAT CTCTAGGTA GGAAACCTGG GTCAATCCAA 6000
 GAATAGCATG TCCTTTTCA ACTTCCAAAT AGTGGGCAAT CTTTTCTTTA GCAAGGCGAG 6060
 CATAGATGGT CTGTTGAGAT TTGCCGATAC GATAGCCATG TTTTGTGCAAG GTTTGGAAGA 6120
 AATGACTGGT GATTTCTTCT TTTTAAAGT CCTTAATGAA TTTTTCAGGA ATAGAAGCAA 6180
 CTTCATAAAC TAGGGGAAC TGGTCGGCAT AGCGGACCCG CTCCATTTCGG ATAATATTGT 6240
 CCGTTGGAAA AATTCCTAGC TTGGCAACTT CTGCTCATT GGAATGGTT TTTTGTAGG 6300
 AAATGAGCTG GCTAGAGGGA ACTTTACCTT GGGATTTGAC AATTTAGTA AACTGGTTG 6360
 TCCCTCGCAT CTTTTCTTGT ACTCGAGTAC TGGAAACAAA GGTGCCGCTT CCTACACGGC 6420
 GCTCTAAGAC GCCTTCTTCG ACTAATAGAG ATACGGCTTG GCGGAGGGTC ATGCGACTGA 6480
 CCGCAAACCTG CTCAGCTAAA TCTCTTTCAC TGGGAAGCCT CTCACCAATA GCCCAACGGT 6540
 ACTCGTCAAT ATCCTTTTTT ATCTGATCAT GGATTTTAT ATAAGCAGGT AGCATATTTT 6600
 TCACTTCATT TCTATCTTTT CTCTATTGTA CCCCAATAAA CTAGAAAAAG TCAAACCTCG 6660
 CCTTGTTAG TTGGTAATTC GCCCTTATTT GTGATAGAAT ATGAGAAAA GATATTTCTT 6720
 TTGAGAAAGG AAAAAGATGA GCAACATTC AACTGATTTG CAAGATGTAG AAAAAATCAT 6780

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CGTATTGGAC	TATGGTAGCC	AGTACAACCA	GCTGATTTCA	CGCCGTATCC	GTGAGATTGG	6840
TGTTTTTTTCA	GAACATAAAA	GCCATAAAAT	TTCAGCTGCT	GAAGTTCGTG	AAGTCAATCC	6900
TGTAGGAATT	ATTCTATCAG	GTGGTCCAAA	TTCTGTATAT	GAAGATGGTT	CATTTGATAT	6960
TGACCCAGAA	ATCTTCGAAC	TCGGAATTC	AATTTTGGGA	ATCTGTTATG	GTATGCAGTT	7020
ATTGACCCAT	AAACTTGGAG	GAAAAGTTGT	TCCTGCAGGT	GATGCTGGAA	ATCGTGAATA	7080
CGGTCAATCA	ACCCTAACTC	ACACACCATC	AGCGCTTTTT	GAATCAACAC	CTGATGAACA	7140
GACTGTTTTG	ATGAGCCATG	GTGATGCGGT	TACTGAGATT	CCTGCTGACT	TTGTTTCGTAC	7200
AGGTACATCA	GCTGACTGCC	CATACGCAGC	CATCGAAAAC	CCAGATAAAC	ACATTTACGG	7260
TATCCAATTC	CACCCAGAAG	TTCGTCAATC	TGTATACGGA	AATGATATCC	TTCGTAACCTT	7320
TGCCCTTAAC	ATTTGTAAGG	CTAAAGGTGA	CTGGTCAATG	GATAATTTCA	TTGACATGCA	7380
GATCAAAAAA	ATTCGTGAAA	CCGTCGGTGA	TAAACGTGTC	CTTCTTGGTC	TATCAGGTGG	7440
TGTTGACTCA	TCTGTCGTTG	GGGTTCTTCT	CCAAAAAGCG	ATTGGCGATC	AATTGATCTG	7500
TATCTTCGTA	GACCACGGTC	TTCTTCGTAA	AGGCGAAGCT	GATCAAGTTA	TGGACATGCT	7560
CGGTGGTAAG	TTTGGTTTGA	ATATCGTCAA	AGCAGACGCT	GCTAAACGTT	TCCTTGACAA	7620
ACTTGCTGGC	GTTTCTGACC	CTGAACAAAA	ACGTAAAATC	ATCGGTAACG	AGTTTGTCTA	7680
TGTATTCGAT	GACGAAGCAA	GCAAGCTCAA	AGATGTGAAA	TTCTTGCTC	AAGGTACTTT	7740
ATATACAGAT	GTTATCGAGT	CTGGTACGGA	TACAGCTCAA	ACTATCAAGT	CACACCACAA	7800
CGTGGTGGTC	TTCAGAAGA	TATGCAGTTT	GAATTGATTG	AACCACTCAA	TACTCTTTAC	7860
AAGGATGAAG	TTCGTGCTCT	TGGTACAGAG	CTTGGTATGC	CAGACCATAT	CGTATGGCGC	7920
CAACCATTCC	CAGGACCAGG	ACTTGCTATC	CGTGTCAATG	GTGAAATCAC	TGAAGAGAAA	7980
CTTGAACCG	TTCGTGAATC	AGACGCTATT	CTTCGTGAAG	AAATCGCTAA	AGCTGGACTT	8040
GACCCGATA	TTTGGCAATA	CTTCACTGTT	AACACAGGCG	TTCGTTCACT	CGGTGTTATG	8100
GGTGACGGTC	GTACGTATGA	CTACACGATT	GCAATCCGTG	CTATCACTTC	TATCGATGGT	8160
ATGACTGCTG	ATTTTGCCAA	AATTCCATGG	GAAGTACTTC	AAAAAATCTC	AGTACGTATC	8220
GTAATGAAG	TGGATCATGT	TAACCGTATC	GTCTACGATA	TTACAAGTAA	ACCACCTGCA	8280
ACAGTTGAGT	GGGAATAATC	GCAAAAAAAT	TAAAAGCTTT	GTAAAAATCAA	CGGTTACAGA	8340
GGATTAAAAA	CTGTAACCTG	GATTAACACG	GGAACATTTG	CTAAAAAGAA	TAAATTGAAT	8400
AATAGTTCCA	AGTGGTTTAC	ATTTGGACAA	AAAATTAGAC	CGTAGTTTTT	AAGCTGCGGT	8460
CTTTTGATAT	ATATAATGAG	AATTAATGGC	TCTTTGTCAA	CTGTAGTGGG	TTGAAGTCAG	8520
CTAAGCTCGA	GAAAGACAA	ATTTTGTCTT	TTCTTTTTTT	ATATTCAGAG	CGATAAAAAAT	8580

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CCGTTTTTTG AAGTTTTCAA AGTCCGAAA ACCAAAGGCA TTGCGCTTGA TAAGTTTGAT 8640
 GAGATTATFG GTCGCTTCCA ATTTGGCGTT AGAATAGTGT AGTTGAAGGG CGTTGACGAT 8700
 TTTCTCTTTG TCCTTTAGAA AGGTTTTAAA GACAGTCTGA AAAAGAGGAT GAACCTGCTT 8760
 TAGATTGTCC TCAATGAGTC CGAAAAATTT CTCCGGTTCC TTATTCTGAA AGTGAAACAG 8820
 CAAGAGTTGA TAGAGCTGAT AGTGATGTTT CAAGTCTTGT GAATAGCTCA AAAGCTTGTT 8880
 TAAAATCTCT TTATTGGTTA AATGCATACG AAAAGTAGGG CGATAAAAAT GTTTATCGCT 8940
 GAGTTTACGA CTATCCTGTT GTATGAGCTT CCAGTAGCGC TTGATAGCCT TGTATTCATG 9000
 AGACTTTCGA TCCAATTGAT TCATGATTTG AACACGCACA GACTCGG 9048

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

GTACCTTTAT TGATGAATGG ACTGTTTAAA TCAGTAGCAC GCCAACCAGA TATGCTTTCT 60
 GAGTTTCGTA GTTTGATGTT TTTAGGTGTT GCCTTTATTG AAGGAACTTT CTTTGTA ACT 120
 CTGTGCTTCT CATTTATFAT CAAATAAATA CATGGAACGA GAAGAAAAGG GAGGATTTTA 180
 GATGGAAGAA AGTATTAATC CAATCATCTC TATTGGTCCT GTTATCTTCA ATCTGACTAT 240
 GTTAGCCATG ACTTTGTTGA TTGTGGGAGT TATTTTGTG TTTATTTATT GGGCAAGCCG 300
 CAATATGACC TTGAAACCCA AAGGAAAGCA AAATGTACTT GAGTATGTCT ATGACTTTGT 360
 TATTGGATTT ACAGAACCTA ACATTGGTTC GCGCTACATG AAAGATTACT CACTCTTTTT 420
 CCTTTGTTA TTCCTTTTCA TGGTGATTGC CAATAACCTT GGCTTAATGA CAAAGCTTCA 480
 AACGATCGAT GGGACTAACT GGTGGAGTTC GCCAACCCTT AATTTACAGT ATGACTTAAC 540
 CTTATCTTTT CTGTGCATTT TGTGACACA TATAGAAAGC GTTCGTCGTC GTGGATTTAA 600
 AAAAAGTATA AAATCTTTTA TGAGTCCTGT TTTTGTGATA CCGATGAATA TCTTGGAAGA 660
 ATTTACAAAC TTCTTATCTT TGGCTTTGCG GATTTTGGG AATATCTTTG CAGGAGAGGT 720
 CATGACGAGT TTGTTACTTC TTCTTTCCCA CCAAGCTATT TATTGGTATC CAGTAGCCTT 780
 TGGAGCTAAT TTGGCTTGA CTGCATTTTC TGTCTTTATT TCCTGCATCC AAGCTTATGT 840
 TTTTACTCTT TTGACATCTG TGTATTTAGG GAATAAGATT AATATTGAAG AGGAATAGAA 900

1038

AGGAGTAACT GATGCACGTA ACAGTAGGTG AATTAATTGG TAATTTTATT TTAATCACTG 960
 GCTCTTTTAT TCTTTTGCTA GTCTTGATTA AAAAATTTGC ATGGTCTAAT ATTACAGGCA 1020
 TTTTCGAAGA AAGAGCTGAA AAAATTGCTT CAGATATTGA CAGAGCTGAA GAAGCCCGTC 1080
 AAAAAGCAGA AGTATTGGCT CAAAAACGCG AAGATGAATT GGCTGGTAGC CGTAAAGAAG 1140
 CTAAGACAAT CATTGAAAAT GCAAAGGAAA CAGCTGAGCA AAGTAAGGCT AATATCTTAG 1200
 CAGATGCTAA ACTAGAAGCA GGACACTTAA AAGAAAAAGC CAATCAAGAA ATTGCTCAAA 1260
 ATAAAGTAGA AGCTTTACAG AGTGTAAAGG GTGAGGTCGC AGATTTGACC ATCAGCTTAG 1320
 CTGGTAAAAAT CATCTCACAA AACCTTGACA GTCATGCCCA TAAAGCACTC ATTGATCAGT 1380
 ATATCGATCA GCTAGGAGAA GCTTAATGGA CAAGAAAACA GTAAAGGTAA TTGAAAAATA 1440
 CAGCATGCCT TTTGTCCAAT TGGTACTTGA AAAAGGAGAA GAAGACCGTA TCTTTTCAGA 1500
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 GGCAGTAGAC GAGTCGGATA AGGAAAAAAC AATTGCTTTT TTCCAAGATT CTGTGTCGCC 1620
 TTTATTACAA AACTTTATCC AGGTCTGGC CTACAATCAC AGAGCAAATC TTTTTTATGA 1680
 TGTGCTTGTG GATTGCTTGA ACCGACTTGA AAAAGAAACA AATCGATTTG AAGTGACGAT 1740
 TACGTCTGCT CATCCTCTAA CTGATGAACA GAAGACTCGT TTGCTCCCTT TGATGAGAA 1800
 AAAAATGTCT CTGAAAGTAA GGAGTGTAAG AGAACAAATC GATGAAAGTC TCATTTGGTGG 1860
 TTTTGTCAAT TTTGCCAATC ACAAGACAAT TGATGTGAGT ATTAACAAC AACTTAAAGT 1920
 TGTAAAGAA AATTTGAAAT AGAAAGTGGT GTTCTTTTGG CAATTAACGC ACAAGAAATC 1980
 AGCGCTTTAA TTAAGCAACA AATGAAAAAT TTCAAACCCA ATTTTGATGT GACTGAAACA 2040
 GGTGTTGTAA CCTATATCGG GGACGGTATC GCGCGTGCTC ACGGCCTTGA AAATGTCATG 2100
 AGTGGAGAGT TGTGAATTT TGAAAACGGC TCTTATGGTA TGGCTCAAAA CTTGGAGTCA 2160
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 CGCCGTACAG GAAAAATCAT GGAAGTCCCT GTAGGTGAAA GTCTGATTGG TCGTGTGTG 2280
 GATCCGCTTG GTCGTCCAGT TGACGGTCTT GGAGAAATCC AACTGATAA AACTCGTCCA 2340
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 GGTGACCGTC AGACAGGGAA AACAACCATT GCGATTGATA CAATCTTGAA CCAAAAAGAT 2520
 CAAGATATGA TCTGTATCTA CGTCGCGATT GGACAAAAAG AATCAACAGT TCGTACGCAA 2580
 GTAGAAACAC TTCGTCAGTA CGGTGCCTTG GACTACACAA TCGTTGTGAC AGCCTCTGCT 2640
 TCACAACCAT CTCATTGCT CTTCCTAGCT CCTTATGCTG GGGTTGCTAT GCGGAAGAA 2700

1039

TTTATGTATC	AAGGTAAGCA	TGTTTTGATT	GTATACGATG	ATCTATCAAA	ACAAGCGGTA	2760
GCTTATCGTG	AACTGTCGCT	CTTGCTTCGT	CGTCCTCCAG	GTCGTGAAGC	CTTCCCAGGG	2820
GATGTTTTCT	ATCTCCACAG	CCGTTTGCTT	GAGCGCTCAG	CTAAAGTTTC	TGATGAACTT	2880
GGTGGTGGAT	CAATTACAGC	CCTACCATTT	ATCGAGACAC	AAGCAGGAGA	TATCTCAGCC	2940
TATATCGCAA	CCAACGTGAT	TTCTATCACT	GATGGACAAA	TCTTCCTTGG	CGATGGCCTC	3000
TTCAATGCAG	GTATTCGTCC	AGCCATCGAT	GCGGGTTCAT	CTGTATCTCG	TGTAGGTGGT	3060
TCTGCACAAA	TCAAAGCCAT	GAAGAAGGTT	GCTGGTACAC	TTCGTATCGA	CCTTGCTTCA	3120
TACCGTGAGT	TGGAAGCCTT	TACTAAGTTT	GGTTCTGACT	TGGACGCAGC	AACACAGGCT	3180
AAGTTGAACC	GTGGACGTCG	TACCGTTGAG	GTCTTGAAAC	AACCTGTTCA	CAAACCATTA	3240
CCTGTTGAGA	AACAAGTAAC	CATTCTTTAT	GCTTTGACAC	ATGGTTTCTT	GGATACTGTT	3300
CCAGTAGATG	ATATTGTTTC	TTTCGAGGAA	GAGTTCATG	CCTTCTTTGA	TGCTCAACAT	3360
CCAGAGATTT	TGGAACCAT	TCGTGATACA	AAAGACTTGC	CAGAAGAAGC	AGTCTTGGAT	3420
GCTGCGATTA	CAGAGTTTCT	CAATCAATCT	AGCTTCCAAT	AAGAATAGAG	GTGTCAGATG	3480
GCAGTATCTC	TAAATGATAT	TAAAACAAAA	ATCGCCTCAA	CAAAAATAC	GAGTCAAATC	3540
ACTAATGCCA	TGCAAATGGT	ATCGGCTGCT	AAGTAGGTC	GTTCTGAAGA	AGCTGCTCGC	3600
AACTTCCAAG	TTTACGCTCA	GAAAGTGCCT	AACTTTTGA	CAGATATCCT	TCATGGTAAT	3660
GGAGCTGGTG	CTTCAACTAA	TCCGATGTTG	ATTAGCCGTT	CTGTGAAGAA	GACAGGCTAT	3720
ATCGTTATCA	CTTCAGACCG	CGGTTTGGTT	GGAGTTATA	ATTCCTCTAT	TTTCAAAGCT	3780
GTTATGGAGT	TGAAAGAAGA	ATACCACCCA	GACGGTAAAG	GTTTTGAAAT	GATCTGTATC	3840
GGTGGGATGG	GAGCTGATTT	CTTTAAGGCT	CGCGGTATTC	AACCACTTTA	TGAATTACGT	3900
GGCTTGTCAG	ACCAACCTAG	CTTTGATCAA	GTTCGTAAGA	TTATTTCAAA	AACTGTTGAA	3960
ATGTACCAAA	ATGAACTCTT	TGATGAGCTT	TATGTTTGCT	ACAACCACCA	TGTCAATACG	4020
CTAACCAGTC	AAATGCGTGT	GGAACAAATG	CTTCCGATTG	TTGACTTGGA	TCCAAATGAA	4080
GCGGATGAAG	AGTACAGCTT	GACTTTTGAA	TTGGAAACCA	GCCGAGAAGA	AATCTGGAG	4140
CAGTTGTTGC	CTCAGTTTGC	AGAAAATATG	ATTTACGGTG	CCATTATCGA	TGCCAAGACA	4200
GCTGAGAATG	CTGCGGGCAT	GACAGCCATG	CAACAGCGA	CAGATAATGC	TAAGAAAGTC	4260
ATCAATGATT	TGACAATTCA	GTATAACCGT	GCCAGACAGG	CGGCGATTAC	ACAAGAAATT	4320
ACAGAAATCG	TAGCAGGTGC	TAGTGCCTTA	GAATAGGCTC	TAGTCCAGCT	CGTATGAAAA	4380
TGAACTTAGG	ACCTAGTTGA	GCTAGGAACC	GACAGTATCT	TATATAGAAT	AGGAGAAGGA	4440

1040

GATGAGTTCA	GGTAAAATTG	CTCAGGTTAT	CGGTCCCGTT	GTAGACGFTT	TGTTTGACAG	4500
AGGGGAAAAA	CTTCCTGAGA	TAAACAATGC	ACTTGTCTGC	TACAAAAATG	ACGAAAGAAA	4560
AACAAAAATC	GTCCTTGAAG	TAGCCTTGGA	GTTAGGAGAT	GGTATGGTTC	GTACTIONCGC	4620
CATGGAATCA	ACAGATGGGT	TGACTCGTGG	AATGGAAGTA	TTGGACACAG	GTCGTCCAAT	4680
CTCTGTACCA	GTAGGTAAAG	AAACTTTGGG	ACGTGTCTTC	AACGTTTGG	GAGATACCAT	4740
TGACTTGGA	GTCCTTTTA	CAGAAGACGC	AGAGCGTCAG	CCAATTCATA	AAAAAGCTCC	4800
AACTTTTGAT	GAGTGTCTA	CCTCTCTGA	AATCCTTGAA	ACAGGGATCA	AGGTTATTGA	4860
CCTTCTTGCC	CCTTACCTTA	AAGGTGGTAA	AGTTGGACTT	TTCGGTGGTG	CCGGAGTTGG	4920
TAAAAGTGC	TTAATCCAAG	AATTGATTCA	CAACATGACC	CAAGAGCACG	GTGGTATTTT	4980
AGTATTTGCT	GGTGTGGGG	AACGTACTCG	TGAGGGGAAT	GACCTTFACT	GGGAAATGAA	5040
AGAATCAGGC	GTTATCGAGA	AAACAGCCAT	GGTCTTTGGT	CAGATGAATG	AGCCACCAGG	5100
AGCACGTATG	CGTGTGCCC	TTACTGGTTT	GACAATCGCT	GAATACTTCC	GTGATGTGGA	5160
AGGCCAAGAC	GTGCTTCTCT	TTATCGATAA	TATCTTCCGT	TTCACTCAGG	CTGGTTCAGA	5220
AGTATCTGCC	CTTTGGGGTC	GTATGCCATC	AGCCGTTGGT	TACCAACCAA	CACTTGCTAC	5280
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CCAGGCTATC	TATGTGCCAG	CGGATGACTA	TACTGACCCA	GCGCCAGCAA	CAGCCTTCGC	5400
TCACTTGAT	TCAACAACAA	ACTTGAACG	TAAGTTGGTA	CAATGGGTA	TCTACCCAGC	5460
CGTTGACCCA	CTTGCTTCAA	GCTCACGTGC	CTTGGCACCT	GAAATCGTTG	GAGAAGAGCA	5520
CTATGCAGTT	GCTGCTGAAG	TAAAACGTGT	CCTTCAACGT	TACCATGAAT	TGCAAGATAT	5580
CATTGCTATC	CTTGGTATGG	ATGAGCTTTC	TGATGAAGAA	AAGACCTTGG	TTGCTCGCGC	5640
CCGTCTGATC	CAGTCTTCT	TGTCACAAAA	CTTCAACGTT	GCGGAACAAT	TTACTGGTCA	5700
GCCAGGTTCT	TATGTTCCAG	TTGCTGAAAC	TGTACGTGGC	TTTAAGGAAA	TCCTTGATGG	5760
TAAATACGAC	CACTTGCCAG	AAGATGCCTT	CCGTGGTGTA	GGTCTATCG	AAGATGTGAT	5820
TGCAAAAGCT	GAAAAAATGG	GATTTTAAGA	GGTGATCTAT	GGCTCAGTTA	ACTGTCCAGA	5880
TCGTGACACC	AGATGGTCTC	GTCTATGATC	ACCATGCCAG	CTATGTATCG	GTTCGAACTC	5940
TGGATGGTGA	GATGGGGATC	TTGCCACGAC	ATGAAAATAT	GATTGCGGTT	TTAGCAGTTG	6000
ATGAAGTAAA	GGTAAAACGT	ATCGATGATA	AAGATCACGT	GAACCTGGATT	GCAGTAAACG	6060
GTGGCGTTAT	TGAAATGACC	AATGATATGA	TCACAATCGT	CGCTGACTCT	GCAGAACGTG	6120
CTCGTGATAT	CGATATCAGT	CGTGCAGAAC	GTGCCAAACT	TCGTGCAGAA	CGTGCAATTG	6180
AAGAAGCACA	AGACAAACAT	TTGATTGACC	AAGAACGTCG	TGCTAAGATT	GCTTTGCAAC	6240

1041

GTGCTATTAA	CCGTATTAAAT	GTCGGAAATA	GACTATAAGA	AAAAATGAAC	TTGAAAATAC	6300
CAAGTTCATT	TTTTATGGTG	TTTTAAGGAG	CAAACGGAT	GCAGACTGCT	TCGGGAACAT	6360
GGAAAGTCGT	GGAGAGTTCT	GCTAGACGAC	CATTGTCCACA	ATTACGTTTA	AAGACAGTTG	6420
CATTGTCAGA	GTCTTGATGG	ACAACAATGA	GAAATTTTGG	GTCGGGTGTC	AAATCAAAAT	6480
CACGTGGAGT	CTGACCATGC	GTTGGAACGA	TTTCTAATAA	CTCTAAGCTA	CCGTCCGCAA	6540
GGATGGTATA	TACTGCGATA	GAATCATGGC	CACGGTTAGA	AGCGTAGAGG	TATTTACCGT	6600
CTTTAGAGAG	ATGAATAGCA	GCGGTTCCAT	TAAAGCCTTC	GTAAGCTTCC	GGTAAAGTTG	6660
AAATGACCTG	CATACGTTC	AATTCGCCAA	CGCCATCGTA	GATTAAAACT	TCGATAGTAC	6720
TATTGAGTTC	ACAAATGAGA	TAAGCGATTT	TATAGTGGTT	ATGGAAAATG	ATATGGCGTG	6780
AGCCTGCTCC	TGGCTTGCTG	TGATAGGTAT	AGAGCTTAGA	TAATTTTCCT	TCTTGATCGA	6840
GGTCATAGGT	GATGACTTGG	TCAGTTCCCA	AGTCGCAGGT	CACTAGATAG	TGGTCAGGTG	6900
TTAAATCTGT	ATAGTGAACA	TGGGGGGAAG	CTTGATTTTC	ATGTGGACCT	TGGCCACTGT	6960
GTTGATCCAT	ATCACTAAGT	AGAAGACTAC	CATCTTCTCG	GCGTTTATAA	ACAAGGACTT	7020
GTCCCTTGTTG	ATAGTTAGCT	GCGTAAACCA	AATCACGCTT	TTCATCGACA	GCAACATAAC	7080
AGTGGGGAGC	TCCTTCTTCA	ACAACATGAT	TTAACACAGT	CCCGTCAGTT	TGATAGGCTG	7140
CAATTCCCCC	CTTATCGTCT	TGGCTACCAA	CAGTGTATAA	ATGTTGGTGC	TGGTCAAAGG	7200
CAAGGTAGGT	TGGACTTGGC	TCAGCTGCAA	AAAGTTCTAG	ATTTGAAAGC	TGACCAGTTT	7260
CTGTATCAA	GTCTGCCTTG	TAAATCCCTT	GAGAAGTACG	ACGTGTATAA	GTTCCAAAAT	7320
AAACAGTTTC	TTTCATTACT	ATACCTCTGT	GTAAGATAA	GACTATTATA	TCACAAAAC	7380
AAGTAAATTA	AAGATATCCA	ATTAGATGTA	AGCACTTTAA	AAAAGAGTTA	TTTTGTTTCA	7440
AAAATGGTAT	AATGAGAGAA	CAATAGAAAAG	GAAGTATTTA	TGGAGCAAAA	AGAGAAACAT	7500
TTTAGCCTAT	CTTGGTTTTT	CAAGTGGTTT	TTAGATAACA	AGGCAATTAC	GGTATTTTTA	7560
GTAACCTTAT	TATTGGGACT	GAATCTTTTT	ATTTTAAGTA	AGATTAGTTT	TCTATTTTCA	7620
CCTGTTTTAG	ACTTTTTTAGC	AGTTGTGATG	TGCCCAGTCA	TTTTGTCTGG	TTGTTTATAT	7680
TATTTGTTGA	ATCCTATTGT	TGATTGGATG	GAGAAGCATA	AGGTTAATCG	TGTTATAGCT	7740
ATCACTATTG	TCTTTGTTAT	CATCGCTCTC	TTTATCATT	GGGGCTTGGC	AGTCGCCATT	7800
CCAAATCTGC	AACGTCAGGT	TTTGACCTTT	GCAAGAAACG	TTCTGTTTA	CTTAGAAGAT	7860
ATAGATAGGA	TTGTTAATGG	ATTGGTAGCC	CAGCACCTGC	CAGATGATTT	CAGACCTCAA	7920
TTAGAGCAAG	TTTTGACCAA	TTTTTCTAGC	CAGGCTACAG	TTTTGGCAAG	TAAGTTTCA	7980

1042

TCTCAGGCAG TCAACTGGGT GAGTGCCTTT ATTAGCGGGG CTTCTCAAGT GATTGTTGCC 8040
 TTGATTATCG TTCCTTTTCAT GCTCTTTTAT CTCTTGCGTG ATGGGAAAGG CTTGCGTAAC 8100
 TATTTGACCC AATTCATTCC AAGAAAATTG AAGGAACCTG TTGGACAAGT TTTATCAGAT 8160
 GTGAATCAAC AGTTGTCCAA CTATGTTCCGA GGGCAAGTGA CAGTGGCTAT TATTGTAGCA 8220
 GTAATGTTFA TCATCTTCTT CAAGATTATT GGTCTACGCT ATGCGGTTAC GCTGGGGGTT 8280
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 CTAGTATTGG GTTTGATTGC TGGTCCAGTC ATGCTTTTGA AAGTAGTGAT TGTCTTTATC 8400
 GTAGAACAAA CTATTGAAGG CCGTTTTGTC TCTCCATTGA TTTTGGGAAG TCAATTAAC 8460
 ATCCACCCTA TTAATGTTCT CTTTGTTTTG TTAAGTTCAG GATCTATGTT TGGTATCTGG 8520
 GGAGTTTAC TTGGTATTCC GGTATTGCC TCTGCTAAGG TTGTCATTTC AGCCATTTTC 8580
 GAATGGTATA AGGTAGTCAG TGGTCTATAT GAATTAGAGG GTGAGGAAGT CAAGAGTGAA 8640
 CAATAGTCAA CAGATGTTAC AGGCTTTGGA GGAGCAAGAT TTAAGTAAGG CTGAGCATT 8700
 TTTCGCCAAA GCTTTAGAAA ATGATTCAAG TGATCTCTG TATGAATTGG CAACTTATCT 8760
 TGAAGGGATT GGTTCCTATC CTCAGGCCAA GGAATTTTAC CTGAAAATG TAGAGGATTT 8820
 TCCAGAGGTT CATCTTAATC TAGCTGCAAT TGCTAGCGAG GATGGTCAA TAGAAGAAGC 8880
 CTTTACCTAT CTTGAGGAAA TCCAAGCTGA CAGTGACTGG TATGTCTCGT CTTTGGCTCT 8940
 GAAGGCAGAC CTTTACCAGC TGGAAGGTTT GACAGATGTG GCACGTGAGA AATTATTGGA 9000
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 TGAGCAAACG GGCATTTCCA CCTATCAACG AATTGGCTTT GCCTATGCTC AGTTAGGGAA 9180
 ATTTGAAACG GCTACTGAGT TTTTAGAAAA AGCCCTGGAG TTAGAATACG ATGACTTAAC 9240
 AGCTTTTGAG TTGGCCAGTC TTTATTTTGA TCAAGAAGAA TATCAAAAAG CCACCCTCTA 9300
 CTTTAAGCAG CTTGATACCA TTTCTCCTGA CTTTGAAGGC TATGAGTATG GGTACAGTCA 9360
 GGCTTTACAT AAGGAACATC AAGTTCAAGA AGCCCTGCGT ATCGCTAAGC AAGGATTAGA 9420
 GAAAAATCCC TTTGAAACTC GCCTCTTGCT AGCTGCTTCA CAATTTTCTT ATGAATTGCA 9480
 TGATGCTAGT GGTGCAGAAA ATTATCTCCT TACTGCAAAA GAAGACGCTG AGGATACAGA 9540
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 AGAATTGCAG AGTGAGGAGC CAGAAAATCT TTTGACCAAG TGGATGATG CTCGTTCTTA 9660
 TCAAGAAATG GACGATTTGG ATACTGCTTA TGAGTATTAT CAAGAGTTGA CAGGAGATTT 9720
 GAAGGACAAT CCAGAATTTT TGGAACACTA TATCTATCTC TTGCGTGAAT TGGGACATTT 9780

1043

TGAAGAAGCA AAAGTCCATG CTCACACTTA CTTAAAACCTG GTTCCAGATG ATGTGCAAAT 9840
 GCAAGAAGCTG TTTGAGAGAT TGTAAGAATG TTTAACCCAA ATCATTCATA CCTCTCTCAA 9900
 CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT TTCTTCCTCC TCATGAGGTC 9960
 AGTTTTACTT TCTGCTGTTC CAGTATCGTT TTTCTCGCT AGATTCCTC AAAAGGGCAG 10020
 ACTCCTCCCT TGGTGCCTCA CACGATTTTT TCATCTCGAC TGTTCCTTAA TGCATCATTA 10080
 ACGACGCTTT TCTTCTAGGT GGTCATAAG GAACAGGAAG ATTCAGGTTG ACTTTTCTAA 10140
 TCCTAGAATA AAGTGCTGAA AACAATTCGG AATAGGCATA GAGACTAGAC AATTTGAGGA 10200
 GCTGCTTGCG TCCTGTTTCA ACACATTTTC CCACCACGTG AAGAAAAAGA TGGCGGAAGC 10260
 GTTTGATTGT TAAAGTTTGG AAGTCACCTC CAGCTAGATG TTTGAGAAAA AGATAGAGAT 10320
 TGTAGGCGAT ACAGCTCATC ATCATACGAA TTCGTTTTTG ATTAAGGTTG AACTATCCGT 10380
 TTTATCGCCA AAAAATCGG 10399

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GATAAGATTA AGTTAGAAAA GAAAGAATA GGACATATCT ACCAGATTCA GGTTTTTAAT 60
 AGCTATGGGC AGGAAGAAAT CTATCGTGTG ATTTTGATGG AGACCAATAT TAGTTCGGTT 120
 TCAACCAATA TCAAGTATGC TGCTGTCTTG ATTAATACCA GTCAGTTGGA ACAGGCTAGT 180
 CAAAAGCATG AGCAATTGAT TGTGGTCGTG ATGGCTAGTT TCTGGATTTT GTCTTTACTT 240
 GCCAGTCTCT ATCTAGCTAG GGTCAGTGTT AGGCCCTGC TTGAGAGTAT GCAGAAGCAA 300
 CAGTCTTTTG TGGAAAATGC CAGTCATGAG TTACGAACTC CACTCGCAGT TTTGCAAAAT 360
 CGCTTAGAGA CCCTTTTTCG TAAGCCAGAA GCTACCATTA TGGATGTGAG CGAAAGCATT 420
 GCATCGAGTT TGGGAAGAAGT CCGAAATATG CGTTTTTTAA CGACAAGCTT GCTGAACTTA 480
 GCTCGGAGAG ATGATGGGAT TAAGCCGGAG CTTGCAGAAG TTCCAACCTAG CTTTTTTAAT 540
 ACAACTTTCA CAACTACGA GATGATTGCT TCGGAAAATA ATCGTGTCTT CCGTTTTGAA 600
 AATCGTATCC ATCGAACAAT TGTCACAGAT CAGCTTCTTC TGAACAACCT GATGACCATT 660
 CTTTTCGATA ATGCCGTCAA GTATACTGAG GAGGATGGTG AAATTGATTT TCTTATCTCG 720

1044

GCGACCGATC	GCAATCTTTA	TTTACTTGT	TCTGATAATG	GAATCGGTAT	TTCGACAGAA	780
GATAAAAAGA	AAATTTTGA	CCGTTTTTAT	CGAGTAGACA	AGGCTAGAAC	CCGGCAAAAA	840
GGTGGTTTTG	GTTTAGGATT	ATCCCTAGCC	AAGCAAATG	TAGATGCTCT	AAAAGGAACT	900
GTTACTGTCA	AAGATAATA	ACCCAAGGGA	ACAATCTTTG	AAGTGAAGAT	TGCCATTCAG	960
ACACCATCTA	AAAAGAAAA	ATAAAAATAT	CGTCCAATT	GGGGCGATAT	TTTGGATTTA	1020
TCTTCTACGT	TTTCGTTGA	TAATAGACCG	TTGAACTTTT	AAAACAAGTA	AGCTGAATCC	1080
GATTGCTGCG	GCAAAGGCAA	GAGCAGTTGA	TAATTTTAA	GCTAAAAAGA	TAAAACATAA	1140
GATAGCAATA	CAGATACAAA	AAACAGCGAT	ATTAATAAAA	AATAGGATTT	CCTTGAGATT	1200
GGCATCAGAT	TGCGCTTCAG	GTGTATAAGC	TTGGTAATGA	GGAAGCTGCT	GGTTTAATTC	1260
TTCTTGATAG	TCTACCTCAT	AGGATTGTAA	TTTCTTACG	GGCATGATTC	TCTCCTTAAC	1320
AGTACATACC	TATTTTATCA	TTTTTTCGGC	AGAGAATTAT	TACAGAAAAG	TTACAAAAAG	1380
AATAAAGTCC	CTTTTCATTT	TCAAAGCATG	GCTGATTTTG	GAGAAATGTG	GTATAATTTT	1440
TCTTATGGAA	AAGATTGTCA	TTACAGCAAC	TGCTGAAAGT	ATTGAACAAG	TTGAACAAC	1500
ACTCGAAGCT	GGCGTAGACC	GTATCTATGT	CGTGAGAAA	GATTTTGGTC	TTCGTCTGCC	1560
AACGACCTTT	AGTTATGACC	AATTACGTGA	AATCGCTAAG	TTGGTTCATG	ATGCTGGTAA	1620
GGAATTGATC	GTTGCGGTCA	ATGCTCTCAT	GCACCAAGAT	ATGATGGACC	GTATCAAGCC	1680
TTTCTTAAAC	TTCTTGAAG	AAATCAAGAC	AGACTATATT	ACGATTGGGG	ATGCAGGCGT	1740
CTTTTACGTA	GTTAACCGCG	ATGGTTATTC	ATTTAAGACC	ATCTACGATG	CTTCAACCAT	1800
GGTAACTAGC	AGTCGTCAGA	TTAACTTCTG	GGGACAAAAG	GCTGGCGCAT	CTGAGGCTGT	1860
TTTGGCGCGT	GAAATTCAT	CAGCTGAACT	TTTCAAAATG	CCAGAGATTT	TGGAAATTCC	1920
TGCTGAAGTT	TTGGTTTACG	GTGCTAGCGT	CATCCATCAT	TCTAAACGTC	CACTCTTGCA	1980
AAACTACTAT	AACTTTACAC	ATATCGATGA	TGAAAAGACG	CATAAACGTC	ACCTCTTCTT	2040
GGCTGAGCCA	AGTGATCCAG	AGAGCCACTA	TTCCATTTT	GAAGATAATC	ATGGGACCCA	2100
TATCTTTGCC	AACAATGACC	TTGATTTGAT	GATCAAATTA	ACAGAATTGG	TGGAGCATGG	2160
CTTTACTCGC	TGGAACTAG	AAGGGCTCTA	CACTCCTGGT	CAGAACTTTG	TTGAGATTGC	2220
AAAACCTTTT	ATCCAAGCGC	GTAGCTTGAT	TCAAGAGGGC	AACTTTAGTC	ATGCTCAAGC	2280
CTTCTTGCTG	GATGAAGAAG	TTCGTAAACT	TCACCCATAA	AACCGTTTCC	TTGATACAGG	2340
ATTTTATGAC	TACGATCCTG	ACATGGTTAG	ATAAAAATACA	TGATTCGTTG	AGAGAAGGAA	2400
GATGCAAACA	TTTCTTCTCT	CAATTTTTCG	TATTTCTTCA	CTATTTTACA	AAAATCAGCA	2460
GGCTAGAATG	CTCTATTCGA	TGGGATTTTT	AAGAAAAGTA	GTGTTCTTGA	GTTTGAAAAT	2520

1045

TATCCTATGT	TTGCAGGTGC	CAAATGGCCC	TTTTTTTGGT	ATAATTTTTT	ATAATGAAAA	2580
CGATTGGTAA	TCGCTATGTT	GTGGTGGATT	TAGAGGCAAC	TAGCACAGGT	AGTAAGGCTA	2640
AAATTATCCA	AGTGGGAATT	GTCGTGATTG	AGGACGGAGA	AATCGTCGAT	CACTATACGA	2700
CGGATGTCAA	TCCACATGAA	CCCTTGGATG	CTCATATCAA	AGAACTGACA	GGATTGACAG	2760
ACCAACGTCT	GGCGAAGCA	CCTGATTTTT	CGCAAGTTGC	CAGAAAAATA	TTTGACTTGG	2820
TGGAGGATGG	GATTTTTGTA	GCCCATAATG	TTCAGTTTGA	TGCTAATCTC	TTGGCGGAAA	2880
ATTTATTTTT	TGAAGGCTAT	GAGCTAAGAA	ACCCTCGTGT	TGATACGGTC	GAATTGGCCC	2940
AGGTCTTTTT	CCCTGAACTG	GAAAAATATA	GCTTGCCGAT	TTTGTGTCGA	GAATTAGGAA	3000
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CTATCCTGAG	TTCTCCAGAC	TTGGTCCAAG	TTCAAGGTCT	ATATTTTAAG	AAAACGGAAG	3240
CTTCTCTGGA	GCCACGAAAA	CTATCTCAAG	ACTTTTCTAA	AAATATTTCT	CTGTTGAACC	3300
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AACCTGTCTC	TCTGATFCAA	GCGCCGACAG	GGATTGGGAA	AACCTATGGC	TATCTCTTAC	3420
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AAAATCAAAT	CATGGAAGAA	GAAGGTAAAC	GCCTCAAGGA	AGTGTCCCAT	ACAGATATTC	3540
ATAGCTTAAA	GGGACCACAA	AATTATCTGA	AGTTGGATGC	CTTTTATCAT	TCCTTGCAGG	3600
AAAATGATGA	AAATCGCTTA	TTTAGACGCT	TTAAAATGCA	AGTCTTGGTC	TGGCTTACTG	3660
AGACAGAGAC	AGGAGATTTG	GATGAAATCG	GGCAACTCTA	CCGTTACCAA	CATTTTCTAG	3720
CAGACCTTCG	TCATGATGGG	AATTTATCAT	CCCAGAGCTT	ATTTGTGACG	GAAGATTTTT	3780
GGAAACGTAG	TCAAGAAAGG	GCAGAGACTT	GCAAGCTTTT	AGTGACTAAT	CATGCCCTATC	3840
TCGTAACCAG	ACTTGAAGAT	AATCCTGAAT	TTGTCACTGA	CCGTTTACTG	ATTATTGATG	3900
AAGTCCAAAA	GATTTTGTTA	GCTCTAGAAA	ATCTGCTTCA	AGAGACCTAC	GATATACAAT	3960
CTATTATCGA	TTTAATTGAT	AAGGCTTTAG	TAGGAGAAGA	AAACAGGGTT	CAACAACGGA	4020
TACTAGAAAAG	TATTCGCTTT	GAGTGTCTCT	ACTTGATAGA	ACAATTCAG	TCTGGCAAAT	4080
CTAGGAAAAA	TATCTTAGAT	TCTCTGGACA	ATCTCCATCA	GTATTTTCA	GAATTGGAAG	4140
TAGAAGACTT	TGATGAGCTG	GTTTCGTATT	TTACAGCTGA	AGGTGATTAC	TGGCTTGAAG	4200
TAACTGAAAC	GAGTCAAAAG	AAAATTCAGA	TTTCTTCTAC	AAAATCAGGC	CGTACTCTTC	4260

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TGTCCTCTTT	ACTTCCTGAG	AGTTGCCAAG	TCTTGGGAGT	ATCGGCTACT	CTTGAGATTA	4320
GTCAGAGGGT	TTCTTTGGCA	GACCTTTTAG	GCTATCCTGA	AGCTAAATTT	GTCAAGATTG	4380
AATCTCGGGG	AAAACAGGAA	CAAGAAGTGG	TCATGGTCAA	AGATTTCCCT	CTGGTAACAG	4440
AAACCTCCTT	AGAAGTCTAT	GCCAGAGAGG	TAGCTGCTTT	ACTAGTGGAA	ATTCAAGCTT	4500
TCCAGCAACC	GATTTTGGTT	CTCTTTACCG	CTAAAGACAT	GCTTCTAGCA	GTATCGGATT	4560
TACTTACAGT	TAGCCACTTG	GCCCAGTATA	AAAATGGGGA	TGTTTCATCAG	CTAAAGAAAC	4620
GCTTTGAAAA	AGGTGAACAA	CAAATCTTGC	TTGGTGCAGC	AAGTTTCTGG	GAGGGAGTTG	4680
ATTTTCAAG	CCATCCTTCT	GTGATTCAAG	TTGTACCGAG	GCTTCCTTTC	CAAAATCCTC	4740
AAGAACCCTT	GACGAAAAG	ATTAATCAAG	AACTGAATCA	AGAAGGGAAA	AATGCCTTTT	4800
ATGATTATCA	ATTGCCAATG	GCCATTATTC	GTTTAAAACA	GGCTTTGGGA	AGAAGTATGA	4860
GACGTGAATA	CCAACGTFCC	TTAACTCTTA	TTTTGGATAG	GAGAATCGTC	GGAAAACGAT	4920
ACGGCAAACA	AATAGTAGCA	TCTCTAGCAG	AAGAAGCGAC	TGTTAAAACC	ATCTCTCGAT	4980
CCGAAGTTGA	CGAGGCTATT	GATAGATTTT	TTAATGAGCT	TTGATAAATA	GTATTGTATG	5040
AAAGTATAAG	GTTAGTATAT	ATGAAACGTT	CTCTCGACTC	AAGAGTCGAT	TACAGTTTGC	5100
TCTTGCCAGT	ATTTTTTCTA	CTGGTCATCG	GTGTGGTGGC	TATCTATATA	GCCGTTAGTC	5160
ATGATTATCC	CAATAATATT	CTGCCCATTT	TAGGGCAGCA	GGTCGCCTGG	ATTGCCTTGG	5220
GGCTTGATG	TGGTTTTGTG	GTCATGCTCT	TTAATACAGA	ATTTCTTTGG	AAGGTGACCC	5280
CCTTTCTATA	TATTTTAGGC	TTGGGACTTA	TGATCTTGCC	GATTGTATTT	TATAATCCAA	5340
GCTTAGTTGC	ATCAACGGGT	GCCAAAAACT	GGGTATCAAT	AAATGGAATT	ACCCTATFCC	5400
AACCGTCAGA	ATTTATGAAG	ATATCCTATA	TCCTCATGTT	GGCTCGTGTC	ATTGTCCAAT	5460
TTACAAAGAA	ACATAAGGAA	TGGAGACGCA	CGGTCCGCT	GGACTTTTTG	TTAATTTTCT	5520
GGATGATFCT	CTTTACCATT	CCAGTCTTAG	TTCTTTTAGC	ACTTCAAAGT	GACTTGGGGA	5580
CGGCTTGGT	TTTTGTAGCC	ATTTTCTCAG	GAATCGTTTT	ATTATCAGGG	GTTTCTTGGA	5640
AAATTATTAT	CCCAGTATTT	GTGACTGCTG	TAACAGGAGT	TGCTGGTTTC	TTAGCTATCT	5700
TTATTAGCAA	GGACGGACGA	GCTTTTCTTC	ACCAGATTGG	AATGCCGACC	TACCAAATTA	5760
ATCGGATTTT	GGCTTGCTC	AATCCCTTTG	AGTTTGCCCA	AACAACGACT	TACCAGCAGG	5820
CTCAAGGGCA	GATTGCCATT	GGGAGTGGTG	GCTTATTTGG	TCAGGGATTT	AATGCTTCGA	5880
ATCTGCTTAT	CCCAGTTCGA	GAGTCAGATA	TGATTTTTAC	GGTTATTGCA	GAAGATTTTG	5940
GCTTTATTGG	CTCTGTCCCTG	GTTATTGCCC	TCTATCTCAT	GTTGATTTAC	CGTATGTTGA	6000
AGATTACTCT	TAAATCAAAT	AACCAGTTCT	ACACTTATAT	TTCCACAGGT	TTGATTATGA	6060

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TGTTGCTCTT	CCACATCTTT	GAGAATATCG	GTGCTGTGAC	TGGACTACTT	CCTTTGACGG	6120
GGATTCCCTT	GCCTTTCATT	TCGCAAGGGG	GATCAGCTAT	TATCAGTAAT	CTGATTGGTG	6180
TTGGTTTGCT	TTTATCGATG	AGTTACCAGA	CTAATCTAGC	TGAAGAAAAG	AGCGGAAAAG	6240
TCCCATTCAA	ACGGAAAAAG	GTTGTATTAA	AACAAATTAA	ATAAGGAGAA	AATCATGGTA	6300
AAAGTAGCAG	TTATATTAGC	TCAGGGCTTT	GAAGAAATTG	AAGCCTTGAC	AGTTGTAGAT	6360
GTCTTGCGTC	GAGCCAATAT	CACATGTGAT	ATGGTTGGTT	TTGAAGAGCA	AGTAACGGGT	6420
TCGCATGCAA	TCCAAGTAAG	AGCAGATCAT	GTCTTTGATG	GAGATTTATC	AGACTATGAT	6480
ATGATTGTTT	TTCCCTGGAG	TATGCCTGGT	TCTGCACATT	TACGTGATAA	TCAGACCTTG	6540
ATTCAAGAAT	TGCAAAGCTT	CGAGCAAGAA	GGGAAGAAAC	TAGCAGCCAT	TTGTGCGGCA	6600
CCAATTGCC	TCAATCAAGC	AGAGATATTG	AAAAATAAGC	GATACACTTG	TTATGACGGC	6660
GTTCAAGAGC	AAATCCTTGA	TGGTCACTAC	GTCAAGGAAA	CAGTAGTGGT	AGATGGTCAG	6720
TFGACAACCA	GTCGGGGTCC	TTCAACAGCC	CTTGCCTTTG	CCTACGAGTT	GGTGGAGCAA	6780
CTAGGAGGGG	ACGCAGAGAG	TTTACGAACA	GGAATGCTCT	ATCGAGATGT	CTTTGGTAAA	6840
AATCAGTAAA	ACGGGAGTTA	TTCTCTCGTT	TTTTATGTGG	AAAACTCAGG	GAAATCATCG	6900
CTTTTTTCAT	AAAAAATGC	TATAATGAAG	GGTATGAAAT	ATCACGATTA	CATCTGGGAT	6960
TTAGGTGGAA	CTTTACTGGA	TAATTATGAA	ACTTCAACAG	CTGCATTTGT	TGAAACATTG	7020
GCACTGTATG	GTATCACACA	AGACCATGAC	AGTGTCTATC	AAGCTTTAAA	GGTTTCTACT	7080
CCTTTTGCGA	TTGAGACATT	CGCTCCCAAT	TTAGAGAATT	TTTTAGAAAA	GTACAAGGAA	7140
AATGAAGCCA	GAGAGCTTGA	ACACCCGATT	TTATTTGAAG	GAGTTTCTGA	CCTATTGGAA	7200
GACATTTCAA	ATCAAGGTGG	CCGTCATTTT	TTGGTCTCTC	ATCGAAATGA	TCAGGTTTGG	7260
GAAATTTTAG	AAAAAACCTC	TATAGCAGCT	TATTTTACAG	AAGTGGTGAC	TTCTAGCTCA	7320
GGCTTTAAGA	GAAAGCCAAA	TCCCGAATCC	ATGCTTTTATT	TAAGAGAAAA	GTATCAGATT	7380
AGCTCTGGTC	TTGTCAITGG	TGATCGGCCG	ATTGATATCG	AAGCAGGTCA	AGCTGCAGGA	7440
CTTGATACCC	ACTTGTTTAC	CAGTATCGTG	AATTTAAGAC	AAGTATTAGA	CATATAAGAA	7500
AAAGGAATAA	GATGACAGAA	GAAATCAAAA	ATCTGCAGGC	ACAGGATTAT	GATGCCAGTC	7560
AAATTCAAGT	TTTAGAGGGC	TTAGAGGCTG	TTCGTATGCG	TCCAGGGATG	TACATTGGAT	7620
CAACCTCAA	AGAAGGTCTT	CACCATCTAG	TCTGGGAAAT	TGTTGATAAC	TCAATTGACG	7680
AGGCCTTGCC	AGGATTTGCC	AGCCATATTC	AAGTTTTTAT	TGAGCCAGAT	GATTCGATTA	7740
CTGTTGTGGA	TGATGGGCGT	GGTATCCCAG	TCGATATTCA	GGAAAAACA	GGCCGTCTCG	7800

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CTGTTGAGAC CGTCTTTACA GTCCTTCACG CTGGAGGAAA GTTCGGCGGT GGTGGATACA	7860
AGGTTTCAGG TGGTCTTCAC GGGGTGGGGT CGTCAGTAGT TAATGCCCTT TCCACTCAAT	7920
TAGACGTTCA TGTTACACAA AATGGTAAGA TTCATTACCA AGAATACCGT CGTGGTCATG	7980
TTGTGCGAGA TCTTGAAATA GTTGAGATA CGGATAAAAC AGGAACAAC TTTCACTTCA	8040
CACCGGACCC AAAAATCTTC ACTGAAACAA CAATCTTTGA TTTTGATAAA TTAATAAAC	8100
GGATTCAAGA GTTGGCCTTT CTAATCGCG GTCTTCAAAT TTCAATTACA GATAAGCGCC	8160
AAGGTTTGA ACAACCAAG CATTATCATT ATGAAGGTGG GATTGCTAGT TACGTTGAAT	8220
ATATCAACGA GAACAAGGAT GTAATCTTTG ATACACCAAT CTATACAGAC GGTGAGATGG	8280
ATGATATCAC AGTTGAGGTA GCCATGCAGT ACACAAC TGG TTACCATGAA AATGTCATGA	8340
GTTTCGCCAA TAATATTCAT ACCCATGAAG GTGGAACACA TGAACAAGGT TTCCGTACAG	8400
CCTTGACACG TGTTATCAAC GATTATGCTC GTAAAAATAA GTTACTGAAA GACAATGAAG	8460
ATAATTTAAC AGGGGAAGAT GTTCGCGAAG GCTTAACTGC AGTTATCTCA GTTAAACACC	8520
CAAATCCACA GTTTGAAGGA CAAACCAAGA CCAAATTGGG AAATAGCGAA GTGGTCAAGA	8580
TTACCAATCG CCTCTTCAGT GAAGCTTTCT CCGATTTCCCT CATGGAAAAT CCACAGATTG	8640
CCAAACGTAT CGTAGAAAAA GGAATTTTGG CTGCCAAGGC TCGTGTGGCT GCCAAGCGTG	8700
CGCGTGAAGT CACACGTAAA AAATCTGGTT TGGAAATTTT CAACCTTCCA GGGAACTAG	8760
CAGACTGFTC TTCTAATAAC CCTGCTGAAA CAGAACTCTT CATCGTCGAA GGAGACTCAG	8820
CTGGTGGATC AGCCAAATCT GGTGCTAACC GTGAGTTTCA GGCTATCCTT CCAATTCGCG	8880
GTAAGATTTT GAACGTTGAA AAAGCAAGTA TGGATAAGAT TCTAGCCAAC GAAGAAATTC	8940
GTAGTCTTTT CACAGCCATG GGAACAGGAT TTGGCGCAGA ATTTGATGTT TCGAAAGCCC	9000
GTACCAAAA ACTCGTTTTG ATGACCGATG CCGATGTCGA TGGAGCCCAC ATTCGTACCC	9060
TTCTTTTAACT CTGATTATAT CGTTATATGA AACCAATCCT AGAAGCTGGT TATGTTTATA	9120
TTGCCCAACC ACCAATCTAT GGTGTCAAGG TTGGAAGCGA GATTAAAGAA TATATCCAGC	9180
CGGGTGCAGA TCAAGAAATC AACTCCAAG AAGCTTTAGC CCGTTATAGT GAAGGTCGTA	9240
CCAAACCGAC TATTCAGCGT TATAAGGGC TAGGTGAAAT GGACGATCAT CAGCTGTGGG	9300
AAACAACCAT GGATCCCGAA CATCGCTTGA TGGCTAGAGT TTCTGTAGAT GATGTGCAGA	9360
AGCAGATAAA ATCTTTGATA TGTGATGGG GATCGAGTTG TCCTCGTCG	9409

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6415 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CCTGGGAAAG TCTTGAAAAT TATGATAGAA TGGTGGAAAGG AAAAAATTCAG GAGAGTAGTA	60
GTGACTCAAA ATGTTGAAAAG TCTTCTCGTA TCCATTGTAA TCAGTGCATA CAATGAAGAA	120
AAATATCTGC CTGGTCTAAT TGAAGACTTA AAAAAATCAA CCTATCCTAA AGAGGATATT	180
GAAATCTCTAT TTATAAATGC TATGTCCACA GATGGGACCA CAGCTATCAT TCAGCAATTT	240
ATAAAGGAAG ATACAGAGTT TAACTCAATT AGATTGTATA ACAATCCTAA GAAAAATCAA	300
GCTAGTGGTT TTAACCTGGG AGTTAAACAT TCTGTAGGGG ACCTTATTTT AAAAAATGAT	360
GCTCATTCAA AAGTTACTGA GACTTTTGTA ATGAACAATG TGGCTATTAT TCAACAAGGT	420
GAATTTGTCT GTGGGGGGCC TAGACCGACG ATTGTGGAAG GAAAAGGAAA ATGGGCAGAG	480
ACCTTGCATC TTGTTGAGGA AAATATGTTT GGCAGTAGCA TTGCCAATTA TCGAAATAGT	540
TCTGAGGATA GATATGTTTC TTCTATTTTT CATGGAATGT ATAAACGAGA GGTTTTCCAG	600
AAGGTTGGTT TAGTAAATGA GCAACTTGGC CGAACTGAAG ATAATGATAT TCATTATAGA	660
ATTCGAGAAT ATGGTTATAA AATCCGCTAT AGCCCAAGTA TTCTATCTTA TCAGTATATT	720
CGACCAACAT TCAAGAAAAT GCTGCATCAA AAGTATTCAA ATGGTTGTG GATTGGCTTG	780
ACAAGTCATG TTCAGTTTAA GTGTTTATCA TTATTTCACT ATGTTCCCTG TTTATTTGTT	840
TTGAGTCTTG TGTTTAGTCT AGCATTGTTA CCGATCACAT TCGTATTCAT AACTTTACTA	900
TTAGGTGCCT ATTTTCTACT TTTGTCAATTA CTCACTTTCG TGACTTTATT AAAACATAAA	960
AATGGATTTT TAATTGTGAT GCCCTTTATT TTATTTTCCA TTCACTTTCG TTATGGCCTT	1020
GGGACGATTG TAGGTTTAAAT TAGAGGATTT AAATGGAAGA AGGAGTACAA GAGAACAATA	1080
ATTTATTTGG ATAAAATAAG CCAAATAAAT CAAAATATGC TATAATAACA ATATAGTAAA	1140
ACTCTTTTAA GGAGGAGTAG ATTTCTATGA ATAAAAAAT AACAGATTAT GTGATTGATC	1200
TGGTGGAAAT TTAAATAAAA CAACAAAAGC AGGTTTCTG GGGAATATTT GATATTTTCA	1260
GTATGGTGGT TTCCATCATT GTATCTTATA TTTTATTTTA TGGGCTGATT AATCCAGCAC	1320
CTGTTGACTA CATTATCTAT ACGAGTTTGG CCTTCCTGTT CTATCAATTG ATGATTGGTT	1380
TTTGGGGGTT GAACGCGAGC ATTAGTCGTT ACAGCAAGAT TACGGATTTT ATGAAAATCT	1440
TTTTTGGTGT GACTGCTAGC AGTGTCTTGT CATATAGTAT CTGTTATGCC TTCTTGCCAC	1500
TCTTCTCCAT CCGTTTCATC ATTCTCTTTA TCTTGTGAG TACCTTCTTG ATTTTATTCG	1560

1050

CACGGATTAC	TGGCAGTTA	ATCTACTCCA	GACGCAAAAA	AGGTAGTGGT	GATGGAGAAC	1620
ACCGTCGGAC	CTTCTTGATT	GGTGCCGGTG	ATGGTGGGGC	TCTTTTATG	GATAGTTACC	1680
AACATCCAAC	CAGTGAATTA	GAAGTGGTCG	GTATTTTGA	TAAGGATTCT	AAGAAAAAGG	1740
GTCAAAAACT	TGGTGGTATT	CCTGTTTTGG	GCTCTTATGA	CAATCTGCCT	GAATTAGCCA	1800
AACGCCATCA	AATCGAGCGT	GTCATCGTTG	CGATTCCGTC	GCTGGATCCG	TCAGAATATG	1860
AGCGTATCTT	GCAGATGTGT	AATAAGCTGG	GTGTCAAATG	TTACAAGATG	CCTAAGGTTG	1920
AAACTGTGTG	TCAGGGCCTT	CACCAAGCAG	GFACTGGCCT	CCAAAAAATT	GATATTACGG	1980
ACCTTTTGGG	TCGTCAGGAA	ATCCGTCTTG	ACGAATCGCG	TCTGGGTGCA	GAAGTACAG	2040
GTAAGACCAT	CTTAGTCACA	GGAGCTGGAG	GTTCAATCGG	TTCTGAAATC	TGTCGTCAAG	2100
TTAGTCGCTT	CAATCTGAA	CGCATGTCT	TGCTCGGTCA	TGGGGAAAAC	TCAATCTACC	2160
TTGTTTATCA	TGAATTGATT	CGTAAGTTCC	AAGGGATGGA	TTATGTACCT	GTGATTGCGG	2220
ACATTCAAGA	CTATGATCGT	TTGTTGCAAG	TCTTTGAGCA	GTACAAACCT	GCTATTGTTT	2280
ATCATGCGGC	AGCCCAACAAG	CATGTTCCCTA	TGATGGAGCG	CAATCCAAAA	GAAGCCTTCA	2340
AAAACAATAT	CCGTGGAAC	TACAATGTTG	CTAAGGCTGT	TGATGAAGCT	AAAGTGTCTA	2400
AGATGGTTAT	GATTTGACA	GATAAGGCAG	TCAATCCACC	AAATGTTATG	GGAGCAACCA	2460
AGCGCGTGGC	GGAGTTGATT	GTCACTGGCT	TTAACCAACG	TAGCCAATCA	ACCTACTGTG	2520
CAGTTCGTTT	TGGGAATGTT	CTTGGTAGCC	GTGGTAGTGT	CATTCCAGTC	TTTGAACGTC	2580
AGATTGCTGA	AGGTGGCCT	GTAACGGTGA	CAGACTCCG	TATGACCCGT	TACTTTATGA	2640
CCATTCCAGA	AGCTAGCCGT	CTGGTTATCC	ATGCTGGTGC	TTATGCCAAA	GATGGGGAAG	2700
TCTTTATCCT	TGATATGGGC	AAACCAGTCA	AGATTTATGA	CTTGGCCAAG	AAGATGGTGC	2760
TTCTAAGTGG	CCACACTGAA	AGTGAATTC	CAATCGTTGA	AGTTGGAATC	CGCCCAGGTG	2820
AAAAACTCTA	CGAAGAACTC	TTGGTATCAA	CCGAACCTCGT	TGATAATCAA	GTTATGGATA	2880
AGATTTTCGT	TGGTAAGGTT	AATGTCATGC	CTTTAGAATC	CATCAATCAA	AAGATTGGAG	2940
AGTTCGCAC	TCTCAGTGA	GATGAGTTGA	AGCAAGCTAT	TATCGCCTTT	GCTAATCAAA	3000
CAACCCACAT	TGAATAAAAA	AGAAAAACGC	ATAGTATCAA	GTTACACAAC	CTTGGTAATA	3060
TGCGTTTTAT	TATGTAGAGA	CTTATACTCT	TCGAAAATCT	CTTCAAACCA	CGTCAACGTC	3120
GCCTTGCCGT	ATATGGTTAC	TGACTTCGTC	AGTTCATCC	ACAACCTCAA	AACAGTGTTT	3180
TGAGyTGACT	TCGTCAGTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGc	TGAcTCGTC	3240
AGTTCATCC	ACAACCTCAA	AACAGTGTTT	TGAGCTGAcT	TCGTCAGTTC	CATCCACAAC	3300
CTTAAAACAG	TGTTTTGAGy	TGAcnTTCGT	CAGTTCATC	TACAACCTTA	AAACAGTGT	3360

TTGAGCTGCC CGCAGCTAGT TTCCTAGTTT GCTCTTTGAT TTTCATTGAG TATTACTTCA 3420
TTTTCTTCTG AAATGGAATT GTTACCCAGT CTATGCTATT GAAAATACGC CAAAACCTTCT 3480
AAGGGTTTGT GAGCGATATA ATCAGGTTGA TAGTTTAGTA GATCTGCTTG CTCTCCAAAT 3540
CCCCAAGTGA TGGCCAATTT CTGAATACCT GTTTCTCGAG CTCCCAGCAT ATCAAACCTTG 3600
GTATCTCCGA TGATGATGGC TTGTTCTGGT GCTAGTTGAT GTGTCTGCAA GGCTTGGTGA 3660
ATGACATCTG CCTTATGGGG TGCTTCAGGG CTAGAACCAT AAATGCCATC AAAGAAATGA 3720
TGGATTTCCA AGTTTTTTGC CATGTCTTGA GCAGTAGATG TATCCTTTGT CGTGGTGATG 3780
TAGAGTGGAT AACTGCTCGA TAACTCCTCA AGCAAGTCTA TAATCTGAGG AAAGAGTTGA 3840
GCTTCATAGA TGCCTTTTGC CTTATAGTAA GAACGATATA TCTGCACGGC TTCAGAAATT 3900
TGGTCTTTGG ACAGGCAGGT CGCAAACTA CTTTCGAGAG GTGGTCCCAT AAAACCACGA 3960
ATAGTTTTGG CATCAGGGCT AGGCACCCCC AGCTCTTTAA AGGTATAGGT AAAGGCATTG 4020
TGAATCCCGA TAGAACTATC AACGAGGGTT CCATCCAAAT CGAAAAAAT CGCTGTGATA 4080
GAGGTATG GGGTGGTAGC GAGTCCACCT TCAGCTGTTT CACGAAAGGC AGTTGGCATG 4200
CTTGCTCCTA CTTGGTACAT GGCATCGATC ACTTCATCCA CAGGGATTTT AGATTGATA 4260
CCTGCCAAGG CCATGTCTGC TGCGATGAAA GCAAAGCTAG CTCCCATGGC ATTACGTTTG 4320
ACACAGGGAA CTTTCGACCAA ACCTGCAACA GGGTCACAGA TGAGGCCTAG CATATTTTTA 4380
ATGACAAAGG CAATAGCTTG ACTGGCCTGA TAAGGTGTTT CACCTGCAGC CAGAGTCAAG 4440
GCGGCAGCAC TCATAGCAGA GGCTGAACCA ACTTCAGCTT GACACCCACC CTCAGCACCT 4500
GAGATGGAGG CATTGTTTGC GATGACTAGT CCAAAGGCAC CAGCAGCAA GAGGAAATCC 4560
AATTGTTGCT CGTGGCTGAG GTCTAATTTT TCAATAGCAG CAGTGAGAAC GGATGGCAGA 4620
CAGCCAGCAC TTCCAGCGGT TGGAGTGGCA CAGACCAAGC CCATTTTGGC ATTGTGTTCA 4680
TTGACTGCGA TGGCAFTTCG GGCAGCCGAG AGAATCGTAT AATCTGACAG AGTTTTTCCG 4740
TTTTCGATGT AGTGATCCAA TTTGGCAGCA TCTCCACCTG TCAGGCCACT ACGAGATTTA 4800
TTTTCATTTGA GGCCAAGTTG GACAGAGGCT TTCATAACTT CCAGATTGCG TTCCATGAGA 4860
AGGAAGACTT CTTACGTTT CCGACCGGTC AATTCAAACCT CTGTTGTAAT CATGAGTTCT 4920
GCGACATTTT CTTGAAAGTC CAGATCTGCT TGCTCGACCA ATTCTTTGAT AGAATAAAAC 4980
ATGCTTCCTC CTATTTAAAG AAATGACAT TGTGGAGATG AGGGATTTTT CGAATTTCTT 5040
CGATAGCCTC ATCACAGTTG CGACTGTCAA CTTGATAAT CATAATGGCT TTTTCACCAG 5100

1052

CTTTTTCACG AGTGACATTC ATCTGGGCGA TATTGATACC ATAGCGGGAA AGCGCCTCTG 5160
 TAACAAGGGC AATCATACTT GGAATATCTT GATGAACGAT GATGATAGTC GGTGTATTCA 5220
 TATTGAGAGA GACGGCAAAA CCATTGAGTT CGGTTACCTG AATATTTCCCT CCACCGATAG 5280
 AAATACCAGT CACGCTGATG GTCTTGTGGG CATTTTTAAC AGTAATTTTA GTGGTGTTAG 5340
 GGTGAGGGGC ATTGCTGTCT TTCTGAATGG TCCAGACAAT CTTGATACCA CGCTTGTGGG 5400
 CAATTTCCAG ACTATTTGGA ATPTCAGGAT CATCTGTATC CATTCCTAAA ATACCTGCAA 5460
 CAAGGGCTAG GTCTGTTCG TGACCACGAT AGGTCTTGGC AAATGAGTTA AAAAGTTGGA 5520
 ATTCAACTTC TGTCGGAGTA TCATCAAAAA TGGAAGAGAC AATCTTCCCA ATACGAACAG 5580
 CACCAGCGGT ATGGCTACTA GATGGGCCAA TCATAACTGG TCCGATGATA TCAAAGACAG 5640
 ATTGAAAACG AAGTGATTTT ATCAGTTTCC CCTTATAAAA ATPTCTTATCT CTATTATATC 5700
 AAAGAATGAG GGGCTTGGCT TTAATTGTGG ATGAAAACCT TTCTAATACC TCAAATAGCA 5760
 TAAAAATAGT ATCTTTTATG ACAAAAAACA CCTTATTTAG GGAAATAAAA AATAATTTTG 5820
 TAATATTTCT ACATAAAAGT GTCAAGAAAC GGTAATATTT AAAGGGTATG ATAGAACTAT 5880
 AGAAAGAAGG AGAATTTTCG AATATGAAAT CAATAACTAA AAAGATTAAA GCAACTCTTG 5940
 CAGGAGTAGC TGCCTTGTTT GCAGTATTTG CTCATCATT TGTATCTGCT CAAGAATCAT 6000
 CAACTTACAC TGTTAAAGAA GGTGATACAC TTTCAGAAAT CGCTGAAACT CACAACACAA 6060
 CAGTTGAAAA ATTGCCAGAA AACAACCACA TTGATAACAT TCATTTGATT TATGTTGATC 6120
 AAGAGTTGGT TATCGATGGC CCTGTAGCGC CTGTTGCAAC ACCAGCGCCA GCTACTTATG 6180
 CGGCACCAGC CGCTCAAGAT GAAACTGTTT CAGCTCCAGT AGCAGAACT CCAGTAGTAA 6240
 GTGAAACAGT TGTTTCAACT GTAAGCGGAT CTGAAGCAGA AGCCAAAGAA TGGATCGCTC 6300
 AAAAAGAATC AGGTGGTAGT ATACAGCTAC AAATGGACGT TATATCGGAC GTTACCAATT 6360
 AACAGATPCA TACCTGAACG GTGACTACTC AGCTGAAAAC CAAGAACGGG TACCG 6415

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TACCCCTTTC GAATTTTGGC AAAAATTCGG TAAGGCTTTG ATGGTAGTTA TCGCGGTTAT 60
 GCCGGCTGCT GGTTTGATGA TTTCAATCGG TAAGTCTATC GTGATGATTA ACCCAACCTT 120

1053

TGCACCACTT	GTCATCACAG	GTGGAATTCT	TGAGCAAATC	GGTTGGGGGG	TTATCGGTAA	180
CCTTCACATT	TTGTTTGCCC	TAGCCATTGG	AGGAAGCTGG	GCTAAAGAAC	GTGCTGGTGG	240
TGCTTTCGCC	GCTGGTCTTG	CCTTCATCTT	GATTAACCGT	ATCACTGGTA	CAATCTTTGG	300
TGTATCAGGC	GATATGTTGA	AAAATCCAGA	TGCTATGGTA	ACTACTTTCT	TTGGTGGTTC	360
AATCAAAGTT	GCTGATTACT	TTATCAGTGT	TCTTGAAGCT	CCAGCCTTGA	ACATGGGGGT	420
ATTTCGTAGG	ATTATCTCAG	GTTTTGTAGG	GGCAACTGCT	TACAACAAAT	ACTACAACCT	480
CCGTAACACT	CCTGATGCAC	TTTCATTCTT	CAACGGGAAA	CGTTTCGTAC	CATTTGTAGT	540
TATTCCTCGT	TCAGCAATCG	CTGCAATTCT	ACTTGTCTGCT	TTCTGGCCAG	TAGTTCAAAC	600
AGGTATCAAT	AACTTCGGTA	TCTGGATTGC	CAACTCACAA	GAAACTGCTC	CAATCTTTCG	660
ACCATCTCTG	TATGGTACTT	TGGAACGTTT	GCTCTTGCCA	TTTGGTCTTC	ACCACATGTT	720
GACTATCCCA	ATGAACTACA	CAGCTCTTGG	TGGTACTTAT	GACATTTTAA	CTGGTGCAGC	780
TAAAGGTACT	CAAGTATTCG	GTCAAGACCC	ACTATGGCTT	GCATGGGTAA	CAGACCTTGT	840
AAACCTTAAA	GGTACTGATG	CTAGTCAATA	TCAACACTTG	TTAGATACAG	TACATCCAGC	900
TCGTTTCAAA	GTTGGACAAA	TGATCGGTTT	ATTCGGTATC	TTGATGGGTG	TGATTGTTGC	960
TATCTACCGT	AATGTTGATG	CTGACAAGAA	ACATAAATAC	AAAGGTATGA	TGATTGCAAC	1020
AGCTCTTGCA	ACATCTTGA	CAGGGGTTAC	TGAACCAATC	GAATACATGT	TCATGTTTCT	1080
CGCAACACCT	ATGTATCTTG	TTTACTCACT	TGTTCAAGGT	GCTGCCTTCG	CTATGGCTGA	1140
CGTCGTAAAC	CTACGTATGC	ACTCATTCGG	TTCAATCGAG	TTCTTGACTC	GTACACCTAT	1200
TGCAATCAGT	GCTGGTATTG	GTATGGATAT	CGTTAACTTC	GTTTGGGTAA	CTGTTCTCTT	1260
TGCTGTAATC	ATGTACTTTA	TCGCAAACTT	CATGATTCAA	AAATTCAACT	ACGCAACTCC	1320
AGGGCGCAAC	GGAAACTACG	AAACTGCTGA	AGGTTTCAGAA	GAAACCAGCA	GCGAAGTGAA	1380
AGTTGCAGCA	GGCTCTCAAG	CTGTAAACAT	TATCAACCTT	CTTGGTGGAC	GTGTAAACAT	1440
CGTTGATGTT	GATGCATGTA	TGACTCGTCT	TCGTGTAACT	GTTAAAGATG	CAGATAAAGT	1500
AGGAAATGCA	GAGCAATGGA	AAGCAGAAGG	AGCTATGGGT	CTTGTCTATG	AAGGACAAGG	1560
GGTCAAGCT	ATCTACGGTC	CAAAAGCTGA	CATTTTGAAA	TCTGATATCC	AAGATATCCT	1620
TGATTCAGGT	GAAATCATTC	CTGAAACTCT	TCCAAGCCAA	ATGACTGAAG	CACAACAAAA	1680
CACCTGTTCA	TTCAAAGATC	TTACTGAGGA	AGTTTACTCA	GTAGCAGACG	GTCAAGTTGT	1740
TGCTTTGGAA	CAAGTAAAGG	ATCCAGTATT	TGCTCAAAAA	ATGATGGGTG	ATGGATTTGC	1800
AGTAGAACCT	GCAAATGGAA	ACATTTGTATC	TCCAGTTTCA	GGTACTGTGT	CAAGCATCTT	1860

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CCCAACAAAA	CATGCTTTTG	GTATTGTGAC	GGAAGCAGGT	CTTGAAGTAT	TGGTTCACAT	1920
TGGTTTGGAC	ACAGTAAGTC	TTGAAGGTAA	ACCATTTACA	GTTCATGTTG	CTGAAGGACA	1980
AAAAGTTGCA	GCAGGAGATC	TCCTTGTAC	AGCTGACTTG	GATGCTATCC	GTGCAGCAGG	2040
ACGTGAAACT	TCAACAGTAG	TTGTCTTAC	AAATGGTGAT	GCAATTAAAT	CAGTTAAGTT	2100
AGAAAAACA	GGTTCTCTTG	CAGCTAAAAC	AGCAGTTGCT	AAAGTAGAAT	TGTAATATAC	2160
TTGAGGTTGG	AAGCTGTATT	CCAACCTCTT	ATTTTGGGAG	AAAAGAATGA	AATTTTAAAC	2220
ACTCAATACT	CACAGTTGGA	TGGAGAAAAG	AGCAGAGGAA	AAATTCCAGA	TTTGTGCTGA	2280
AGATATCTTT	GAAAAGGACT	ATGATTTGAT	TTGTTTTCAA	GAAATCAATC	AGGAGATGAC	2340
CTCGTCAGAG	GTGGAGGTTA	ATGACCTTTA	TCAAGCTTTG	CCAGCAGCTG	AGCCTATTCA	2400
CCAAGACCAT	TATGTTAGAC	TCTTGGTTGA	AAAGTTGTCT	GAGCAAGGGA	AAAATTACTA	2460
CTGGACCTGG	GCCTATAACC	ATATCGGCTA	TAACCGCTAC	CACGAAGGTG	TGGCTATCTT	2520
GTCTAAAACA	CCTATGAAG	CCAGAGAAAT	TTTGGTTTCA	GATGTGGATG	ATCCAACAGA	2580
CTATCATACT	CGCCGTGTTG	CCCTAGCTGA	AACTGTAGTC	GATGGCAAGG	AGCTAGCAGT	2640
TGCCAGTGTT	CATCTCTCTT	GGTGGGATAA	AGGTTTCCAA	GAAGAATGGG	CACGATTTGA	2700
GGCTGTCTTG	AAAAAATGA	ACAAGCCACT	TTTACTAGCT	GGAGATTTCA	ACAATCCGGC	2760
TGGACAGGAA	GGTTACCAAG	CTATTTTAGC	TAGTCCATTA	GGCTTACAAG	ACGCATTTGA	2820
AGTTGCTCAA	GAGAAAAGTG	GTAGCTATAC	TGTTCCGCCT	GAAATTGATG	GCTGGAAAGG	2880
GAACACTGAA	CCCCTTCGAA	TGGATTATGT	CTTTACTACC	AAAGAGTTAG	CGGTGGAAAA	2940
TTTACATGTC	GTATTTGATG	GTAACAAGAG	TCCACAAGTG	AGTGATCACT	ATGGCTTGAA	3000
TGCTATATTA	AACTGGAAAT	AATAACTGAA	AAGAGGTTGG	AACTATAAAA	TTCCAGCCTT	3060
TTCTTACTAG	AGAAGCTACT	GGAAATAGCC	TAAATAAGTG	AGACTACTGT	AATGGAATAA	3120
AATATGGTAT	AATTGATAAG	GTAGATAGAA	TCGAGGATGT	TATGTCATTT	ACGAAATTTT	3180
AATTTAAAAA	CTATATTAGA	GAAGCCTTGA	AGGAGTTAAA	ATTTACAAC	CCAACAGAGG	3240
TGCAAGACAA	GTTGATTCCT	ATTGTTTGG	CAGGTCGTGA	CCTAGTAGGA	GAATCAAAAA	3300
CAGGTTACAG	TAAGACTCAT	ACTTCTTGT	TACCGATTTT	CCAGCAATTA	GATGAAGCTA	3360
GCGATAGTGT	ACAAGCAGTG	ATTACTGCAC	CGAGTCGTGA	GTTGGCTACT	CAAATTTACC	3420
AAGTAGCCGG	TCAGATTTCA	GCTCACTCAG	ATGTCGAAAT	TCGTGTGGTT	AATTATGTGG	3480
GTGGTACGGA	TAAGGCTCGC	CAGATTGAGA	AATTGGCAAG	CAATCAGCCT	CATATTGTTA	3540
TTGGAACACC	AGGCCGTATC	TACGACTTGG	TTAAATCTGG	TGATTTAGCT	ATTCATAAAG	3600
CCAAGACATT	TGTTGTTGAT	GAAGCAGATA	TGACCTTGG	TATGGGATTC	TTGGAAACTG	3660

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TTGATAAGAT	TGCTGGCAGT	CTTCCAAAAG	ACTTGCAATT	CATGGTCTTC	TCAGCGACTA	3720
TCCCACAAA	ACTGCAACCA	TTCTTGAAAA	AATACTTATC	AAATCCTGTT	ATGGAGAAAA	3780
TTAAGACCA	AACGGTTAT	TCTGACACCA	TTGATAATTG	GTTGATTCG	ACCAAGGGAC	3840
ATGATAAGAA	TGCTCAAAT	TACCAGTTGA	CTCAGTTGAT	GCAGCCGTAT	TTGGCAATGA	3900
TTTTTGTAA	CACTAAAACG	CGTGCTGATG	AATTGCATTC	ATATCTGACT	GCTCAAGGCT	3960
TGAAGGTTGC	AAAAATCCAT	GGCGATATTG	CCCCTCGTGA	ACGCAAGCGA	ATCATGAATC	4020
AGGTGCAAAA	TCTGGATTTT	GAGTATATTG	TCGCAACAGA	TTTGGCAGCG	CGTGGGATTC	4080
ACATGAAGG	TGTCAGCCAT	GTCAATCAATG	ATGCCATTCC	GCAAGACTTA	TCTTTTTTTG	4140
TTCATCGTGT	TGGTCGTACT	GGACGAAATG	GCCTACCAGG	TACAGCTATT	ACCCTTTTATC	4200
AGCCAAGTGA	TGACTCGGAT	ATCCGTGAGT	TGGAGAAAT	GGGAATCAAG	TTTAGTCCTA	4260
AGATGGTCAA	AGACGGGGAA	TTCAAGATA	CCTATGACCG	TGATCGTCGT	GCCAACCGTG	4320
AGAAAAACA	AGATAAACTT	GATATCGAAA	TGATTGGTTT	GGTFAAAAAG	AAAAAGAAAA	4380
AAGTCAAACC	GGGTATAAG	AAGAAAATTC	AATGGCGGT	TGATGAAAAG	CGCCGTAAAA	4440
CCAAGCGTGC	TGAAAATCGC	GCTCGCGGTC	GTGCAGAGCG	TAAAGCTAAA	CGCCAAACAT	4500
TTAATAGAA	ATTGTTGGAG	TATTGAGCTC	CAACTTTTTT	ATTTATGAGA	ACGAACTATC	4560
TAAACCGAAA	CACTACATTA	AAGACTGCAA	ATTGCGATTA	AAAATGGTAT	AATGATAAAG	4620
TTATATAGTC	CCGATAAGAT	GGTAGGTATT	TATTACGAAG	AGTTTTCCCTA	TCAGTACTTT	4680
GTAACCTCTAT	AACAATATTT	TTTAAGGGGG	GACATTTTTA	TGTCAGAGCG	TAAATTATTC	4740
ACGTCTGAAT	CTGTATCTGA	GGGCATCCG	GATAAGATTG	CAGACCAAAT	TTCAGATGCG	4800
ATTTTGGATG	CTATTTTAGC	AAAGGATCCA	GAGGCGCACG	TTGCTGCTGA	AACAGCTGTA	4860
TATACTGGTT	CTGTCCACGT	TTTGGTGAA	ATTCTACAA	ATGCCTATGT	GGATATTAAC	4920
CGTGTGGTTC	GTGATACCAT	TGCAGAGATT	GGTATACCA	ATACAGAATA	TGGATTTTCT	4980
GCTGAGACGG	TGGGAGTACA	CCCATCTTTG	GTGGAACAAT	CTCCTGACAT	CGCTCAAGGT	5040
GTTAACGAAG	CCTTGGAGGT	TCGTGGAAAT	GCTGATCAAG	ATCCTACTGA	CTTGATTGGA	5100
GCAGGTGACC	AAGGGCTCAT	GTTTGGATTT	GCAGTAGATG	AAACAGAAGA	GCTTATGCCA	5160
TTGCCAATG	CACTCAGTCA	TAAATTGGTT	CGTCGTCTGG	CAGAACTTCG	TAAGTCTGGA	5220
GAAATTAGCT	ATCTCCGTCC	AGATGCAAAA	TCACAAGTTA	CAGTTGAGTA	CGATGAAAAT	5280
GACCGTCCGG	TACGTGTAGA	TACAGTCGTT	ATTTCTACTC	AGCATGATCC	AGAGGCCACT	5340
AATGAACAAA	TCCATCAAGA	TGTGATTGAC	AAGGTCATCA	AAGAAGTTAT	TCCATCTTCT	5400

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TATCTTGATG	ATAAGACAAA	ATTCTTTATC	AATCCGACAG	GTCGTTTTGT	AATCGGTGGT	5460
CCTCAAGGGG	ACTCAGGTTT	GACTGGTCGT	AAGATTATTG	TAGATACTTA	TGGTGGCTAC	5520
TCTCGTCATG	GTGGTGGTGC	CTTCTCTGGT	AAAGATGCGA	CTAAGGTGGA	TCGTTCAGCC	5580
TCTTATGCGG	CTCGCTATAT	TGCCAAGAAT	ATCGTTGCAG	CAGACCTTGC	TAAGAAGGCA	5640
GAAGTGCAGT	TGGCCTATGC	TATCGGTGTT	GCGCAACCTG	TTTCTGTTCG	TATCGATACT	5700
TTCGGTACAG	GAACAGTAGC	TGAAAGTCAA	CTTGAAAAAG	CGGCTCGTCA	AATCTTTGAC	5760
CTTCGCCCTG	CAGGGATTAT	CCAAATGCTG	GACCTCAAGC	GTCCAATTTA	CCGTCAAACA	5820
TCGGCTTACG	GTCACATGGG	ACGTACAGAT	ATTGATCTTC	CATGGGAACG	TTTGGATAAG	5880
GTAGATGCTT	TGAAAGAAGC	AGTAAAATAA	GATTTTAAAG	GGGAACGTC	CTCTCTTTTT	5940
TATAGTTTTT	AACTATACTG	GGATACTGTT	CTGAAAATCC	ATTTTGCGAA	AGTAGAGATT	6000
TACATGTATA	GTAGATTGAA	ACTAGAATAG	TACACCTCAA	CTTCTAAAAC	ATTGTTAGCA	6060
ATCAATTTGA	CTGTCCTGAT	CGATTTCTCC	TGTTCTTGTT	TCATTTTACT	ATATTTCTTT	6120
AAAAATGATA	AAGGTTAAGA	TTTCTCCTCG	TAATAGATAA	TCTTGGGGAT	ATTTCAATCC	6180
AAAGTTTTAT	TCGTTATCAC	TTGACTATTG	CAAGGTTTTC	TAGAGCAACA	GAGTCATGGA	6240
ATGGACTCAT	GTTTGAGATT	TCTCCTFGTT	GCTTGGACTT	CATTCAAAAAG	TCTGTTACCC	6300
AAGCCTTGTT	CAAACCTCTA	ATACACTAGC	TGTTTCCATA	GCATGACTTC	TGTACTIONG	6360
TTTCTTTTCC	GAATAAATAG	ATAGAACCAC	AGAATCTAGT	AAACCTAGAA	TTAAAAATTAT	6420
GGTATAATAT	TAGCAATAAA	AGAAATCTGG	AGGATTAGAA	TCATGGTATC	AACGAAAACA	6480
CAAATGCTG	GTTTTGAGTT	TGACAATTGC	TTGATGAATG	CAGCAGGTGT	GGCTTGATG	6540
ACGATAGAGG	AGTTAGAAGA	GGTCAAAAAC	TCAGCGGCAG	GAACCTTTGT	TACTAAGACA	6600
GCGACCTTGG	ACTTCCGTCA	GGGGAATCCT	GAGCCACGCT	ACCAAGATGT	TCCACTTGGT	6660
TCCATCAACT	CTATGGGCTT	GCCAAAATAAT	GGCTTAGACT	ATTATTTGGA	TTATCTTTTA	6720
GATTTGCAGG	AAAAAGAGTC	GAACCGAACT	TTCTTCTTAT	CTCTGGTCGG	CATGCTCCCA	6780
GAGGAAACCC	ATACTATTTT	GAAAAAAGTC	CAAGAGAGTG	ATTTTCGTGG	TCTGACTGAG	6840
CTAAATCTTT	CCTGTCCAAA	TGTTCCAGGT	AAACCTCAGA	TTGCCTATGA	TTTTGAGACA	6900
ACAGACCGGA	TTTTGGCAGA	AGTGTTTGCT	TACTTCACCA	AACCTCTTGG	AATTAATTTG	6960
CCACCTTATT	TTGATATTGT	TCACTTTGAC	CAAGCGGCAG	CTATTTTCAA	CAAATATCCG	7020
CTCAAGTTTG	TCAACTGCGT	TAACCTATATC	GGAAACGGCC	TCTATATAGA	AGACGAATCT	7080
GTCGTTATTC	GGCCTAAGAA	TGGTTTTGGT	GGAATTGGTG	GAGAATACAT	CAAACCGACT	7140
GCTTTAGCCA	ATGTTACAGC	CTTTTATCAA	CGTTTAAATC	CTCAAATCCA	AATTATCGGA	7200

1057

ACAGGTGGCG TTCTGACTGG TCGAGATGCC TTTGAACACA TCCTCTGTGG AGCAAGTATG 7260
 GTGCAGGTGG GAACGACCCT TCACAAAGAA GGCCTCAGTG CTTTGTGACCG CATTACCAAT 7320
 GAACTGAAAG CAATCATGGT GGAAAAAGGC TACGAGAGCT TAGAAGATTT CCGTGGGAAA 7380
 TTGCGCTATA TTGACTAAAT TAAATCGAAA AATCTGAAGA AAGGAGAGAC GATGCTAGCC 7440
 ATTGAAGAAA GTCAGAAGTT GACTTTATCA AATTTACCGA GCCTGAGCCT ATTTACAGGG 7500
 ACAGATCAGG GTCAGTTTGA AGTGATGAAG AGTCAAATGT TGAACAGAT TGGGTATGAT 7560
 TCTGCTGACC TCAACTTTGC CTA CTTTGGAT ATGAAAGAAG TAGTTTACAA GGATGTGGAA 7620
 CTGGAGTTGG TCAGCCTTCC TTTCTTTGCG GATGAGAAAA TCGTGATATF AGATTATTTT 7680
 ATGGATATCA C GACTGCTAA GAAACGCTTT TTGACAGATG ATGAGCTTAA GTCATTTGAG 7740
 GAATACCTTG ACAATCCTTC TCCAACAACC AAGTTGATAA TCTTTGCAGA AGGAAAGCTG 7800
 GATAGCAAAA GACGGTTAGT CAAATTACTT AAGCGTGATG CCAAGGCCTT CGATGCAGTA 7860
 GAAGTAAAAG AACAGAATT GCGCCAGTAC TTCCAAAAGT GGAGTCAGAA ACAAGGTCTG 7920
 CAGTTTACCA ATCATTCTTT TGAAAATCTC CTCATCAAGT CGGGGTTTCA ATTTAGCGAA 7980
 ATCCAGAAAA ATCTTCTCTT TTTACAGTCC TATAAGGCGA ATTCTGTTAT TGAGGAAGAG 8040
 GATATTGTTA ACGCAATTC CAAGACTTGC AGGACAATAT TTTTGATTTA ACTCAGTTTA 8100
 TTCTGACTAA AAAGATGGAT CAGGCGCGCG ATTTGGTGAG A GACTTGACC TTGCAAGGGG 8160
 AAGATGAAAT CAAACTGATT GCAGTCATGC TGGGACAATT TCGGACTTTT ACTCAGGTGA 8220
 AGATTTTGGC GGAGTCTGCC CAAACAGAAT CGCAGATTGC AAGTAGTTTA GGTAGTTATC 8280
 TGGGACGTAA CCAAATCCT TATCAAATCA AGTTTGCATT AAGAGATTCG AGAGGACTTT 8340
 CTTGAGCTT TTTGAAGCAA GCTATTTCTT ATTTGATTGA GACAGACTAT CAGATTAAGA 8400
 CAGGTCTTTA TGAAAAGGT TTCCTTTTGT AAAAGGCACT CTTACAGATT GCTAGTCAGG 8460
 TCAATTGACA TTTGTTGAAA CTACTAACC GCGG 8494

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CCGGTCAGTT CGTTCAGTAC AAGGAATCAT AATGAACGAT CAATCAGAAA AAAAGACTAG 60

1058

AAAGAAGACT	GTATGGATAA	TCGACCAATT	GGTTTTTTGG	ATTCGGGTGT	CGGGGGCTTG	120
ACCGTTGTGC	GCGAGCTCAT	GCGCCAGCTT	CCCCATGAAG	AAATCGTCTA	TATTGGAGAT	180
TCGGCGCGGG	CGCCCTATGG	CCCCCGTCCT	GCTGAGCAAA	TTCGTGAATA	TACTTGGCAG	240
CTGGTCAACT	TTCTCTTGAC	CAAGGATGTC	AAAATGATTG	TCATTGCTTG	TAACACTGCG	300
ACTGCGGTGC	TCTGGGAAGA	AATCAAGGCT	CAACTAGATA	TTCTGTCTT	GGGTGTAATT	360
TTGCCAGGAG	CTTCGGCAGC	CATCAAGTCC	AGTCAAGGTG	GGAAAATCGG	AGTGATTGGA	420
ACGCCCATGA	CGGTACAATC	AGACATATAC	CGTCAGAAAA	TCCATGATCT	GGATCCCGAC	480
TTACAGGTGG	AGAGCTTGGC	CTGTCCCAAG	TTTGCTCCCT	TGGTTGAGTC	AGGTGCCCTG	540
TCAACCAGTG	TTACCAAGAA	GGTGGTCTAT	GAAACCCTGC	GTCCCTTGGT	TGGAAAGGTG	600
GATAGCCTGA	TTTTGGGCTG	TACTCATTAT	CCACTCCTTC	GCCCTATTAT	CCAAAATGTG	660
ATGGGGCCAA	AGGTTTCAGCT	CATCGATAGT	GGGGCAGAGT	GCGTACGGGA	TATCTCAGTC	720
TTACTCAATT	ATTTTGAAAT	CAATCGTGGT	CGCGATGCTG	GACCACTCCA	TCACCGTTTT	780
TACACAACAG	CCAGTAGCCA	AAGTTTTGCA	CAAATTGGTG	AAGAATGGCT	GGAAAAAGAG	840
ATTCATGTGG	AGCATGTAGA	ATTATGACAA	ATAAAATTTA	TGAATATAAG	GATGACCAGG	900
ACTGGTATGT	TGGGTCTTAT	AGTATTTTTG	GTGGCGTTAA	CAGTTTGAGC	GAATAAAGA	960
CAGATTTTCC	TCTGTTTGAA	TTCTCCAAAA	TATTTGGAGA	TGAAGAGTAT	GGTTTCCCGC	1020
TTTCAGTTAC	TGTTTTACGC	TATGGTTCTA	TCTACCCTTT	GTTCTCCTTT	GTGGTAGACA	1080
TGCTTAATCA	AGAAATGGGA	CGAAACTTGG	AAGTTATTCA	ACGTCATGGG	GCCCTGCTCT	1140
TGGTTGAAAA	TGGGCAACTC	TTGTATGTAG	AATTGCCTAA	AGAAGGGGTC	AATGTTTCATG	1200
ATTTCTTTGA	GACAAGCAAG	GTCAGAGAAA	CCTTGTGAT	TGCGACTCGT	AACGAAGGTA	1260
AAACCAAGGA	ATTCCGAGCT	ATCTTTGATA	AGTTAGGCTA	CGATGTGGAA	AATCTTAATG	1320
ACTACCCTGA	CCTGCCTGAA	GTAGCAGAAA	CAGGTATGAC	CTTTGAAGAA	AATGCCCGCC	1380
TTAAGGCAGA	AACCATTCT	CAATTAACGG	GCAAGATGGT	TTTGGCAGAT	GATTCTGGTC	1440
TCAAAGTCGA	TGTCCTTGGT	GGCTTACCAG	GCGTCTGGTC	AGCTCGTTTC	GCAGGTGTGG	1500
GAGCAACTGA	CCGTGAAAAT	AATGCCAAAC	TCTTGACAGA	ATTGGCCATG	GTCTTTGAAC	1560
TCAAGGACCG	CTCGGCTCAG	TTCCACACAA	CCCTAGTCGT	AGCCAGCCCA	AATAAGGAAA	1620
GTTTAGTTGT	TGAAGCAGAC	TGGTCAGGTT	ATATTAACTT	TGAACCTAAG	GGTGAAAATG	1680
GCTTTGGCTA	TGATCCCTC	TTCTTGTAG	GAGAAACAGG	TGAGTCATCA	GCTGAATTAA	1740
CCCTGGAAGA	AAAAAATAGT	CAATCTCACC	GTGCCCTTAGC	CGTTAAGAAA	CTTTTGAGAG	1800
TATTTCCATC	ATGGCAAAGC	AAACCATCAT	TGTAATGAGC	GATTCCTCATG	GCGATAGCTT	1860

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GATTGTGGAA	GAAGTCCGTG	ATCGCTATGT	GGGCAAAGTC	GATGCTGTTT	TTCATAACGG	1920
CGATTCTGAA	CTACGTCCGG	ATTCTCCACT	TTGGGAGGGC	ATCCGCGTTG	TAAAGGGAA	1980
CATGGACTTC	TACGCCGGCT	ACCCAGAACG	TCTGGTGACT	GAGCTTGGTT	CGACCAAGAT	2040
TATCCAAACT	CATGGTCACT	TGTTTGACAT	CAATTTCAAC	TTTCAAAAGT	TGGACTACTG	2100
GGCTCAGGAG	GAAGAGGCCG	CTATCTGCCT	CTATGGTCAC	TTGCATGTGC	CAAGTGCTTG	2160
GTTGGAAGGC	AAGATCCTCT	TTCTAAATCC	AGGTTCTATC	AGTCAACCAC	GAGGTACCAT	2220
CAGAGAAATG	TCTATGCTC	GTGTGGAGAT	TGATGATAGT	TACTTCAAAG	TGGACTTTTT	2280
GACACGAGAT	CACGAGGTGT	ATCCAGGTTT	GTCCAAGGAG	TTTAGCCGAT	GATTGCCAAG	2340
GAGTTTGAGA	CTTCTTGTT	GGGGCAGGAG	GAAACTTTTT	TGACCCCTGC	TAAAAATCTA	2400
GCTGTGTTGA	TTGATACCCA	CAATGCCGAT	CATGCGACCC	TCTTGCTCAG	TCAGATGACC	2460
TATACCCGTG	TTCCCGTTGT	GACAGATGAA	AAACAGTTTG	TTGGGACGAT	TGGACTCAGA	2520
GATATTATGG	CTTATCAGAT	GGAGCATGAC	TTGAGCCAAG	AAATCATGGC	GGATACGGAT	2580
ATCGTTCATA	TGACAAAAAC	GGACGTAGCG	GTTGTTTCGC	CTGATTTTAC	CATTACGGAG	2640
GTCTTGCACA	AGCTAGTAGA	TGAGTCCTTC	TTACCGGTTG	TGGATGCAGA	GGGTATTTTC	2700
CAAGGGATTA	TTACGCGCAA	GTCCATCCTC	AAGGCCGTTA	ATGCCCTCTT	GCATGACTTT	2760
AGTAAGGAAT	ATGAGATTCG	ATGCCAATGA	GAGACAGGAT	TTCAGCCTTT	TTAGAGGAAA	2820
AGCAGGGCTT	GTCTGTCAAT	TCCAAGCAGT	CCTATAAGTA	TGATTTGGAG	CAATTTTATG	2880
ACATGGTAGG	TGAGCGGATT	TCTGAGACCA	GTCTCAAGAT	TTACCAAGCC	CAGCTAGCCA	2940
ATCTAAAAAT	CAGCGCCCAG	AAGCGAAAGA	TTTCGGCCTG	TAACCAATTT	CTATACTTTC	3000
TCTATCAAAA	AGGAGAGGTG	GACAGCTTTT	ACCGCTTGGA	ATTAGCCAAA	CAAGCTGAAA	3060
AGAAGACGGA	AAAGCCAGAG	ATTCTATACC	TAGACTCTTT	TTGGCAGGAA	AGCGACCATC	3120
CAGAGGGCCG	CTTGCTAGCG	CTCTTAATCC	TAGAAATGGG	GCTCTTGCCC	AGTGAGATTT	3180
TAGCCATCAA	GGTTGCGGAC	ATCAATCTGG	ATTTTCAGGT	GTTGCGAATC	AGCAAGGCTT	3240
CCCAACAGAG	GATTGTCAAC	ATTCCCACGG	CCTTGCTTTC	AGAATTGGAA	CCCTTGATGG	3300
GGCAGACCTA	TCTTTTGAAG	AGAGGAGAGA	AACCCTATTC	TCGTCAAGTG	GCCTTTCGTC	3360
AGTTAGAATC	TTTTGTCAAG	GAGAAAGGTT	TTCCATCCTT	ATCAGCTCAA	GTCTTACGTG	3420
AACAGTTTAT	TCTAAGACAA	ATAGAAAACA	AGGTCGATTT	GTACGAAATT	GCAAAAAAAT	3480
TAGGATTAAA	AACAGTCTCG	ACCTTAGAAA	AATATAGATA	ATGGATATTA	AATTAAAAGA	3540
TTTTGAAGGA	CCCCTGGACT	TGCTCTTGCA	TCTGGTTTCT	AAGTACCAGA	TGGATATCTA	3600

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CGATGTGCC	ATTACGGAAG	TCATCGAACA	GTATCTAGCC	TATGTCTCAA	CCCTGCAGGC	3660
CATGCGTCTG	GAAGTGACGG	GTGAGTACAT	GGTCATGGCT	AGTCAGCTCA	TGCTGATTAA	3720
GAGTCGTAAA	CTCCTTCCGA	AGGTAGCAGA	AGTGACAGAC	TTGGGGGATG	ACCTGGAGCA	3780
GGACCTCCTC	TCTCAAATCG	AAGAATATCG	CAAGTTCAAG	CTCTTGGGTG	AGCACTTGGA	3840
AGCCAAGCAC	CAAGAACGGG	CCCAGTATTA	TTCCAAAGCG	CCGACAGAGT	TGATTTACGA	3900
AGATGCGGAG	CTTGTGCATG	ACAAGACGAC	CATTGACCTC	TTTTTTGACTT	TTTCAAATAT	3960
CCTAGCCAAG	AAAAAAGAGG	AGTTTGACA	AAATCACACG	ACGATCTTGC	GGGATGAGTA	4020
TAAGATTGAG	GACATGATGA	TTATCGTGAA	AGAGTCCCTG	ATTGGACGAG	ATCAATTGCG	4080
CTGTCAGGAT	TTGTTCAAGG	AAGCCCAGAA	TGTCCAAGAG	GTCATCACCC	TCTTTTTGGC	4140
AACCCTAGAG	TTAATCAAAA	CCCAGGAGTT	GATCCTCGTG	CAAGAGGAGA	GTTTTGGAGA	4200
TATCTATCTC	ATGGAAAAGA	AGGAAGAAAG	TCAAGTGCCT	CAAAGCTAGA	CTTGATAGAG	4260
AGGAAAGATG	AGTACTTTAG	CAAAAATAGA	AGCGCTCTTG	TTTGTAGCGG	GTGAAGATGG	4320
GATTCGGGTC	CGCCAGTTAG	CTGAACTCCT	CTCTCTGCCA	CCGACAGGCA	TCCAGCAAAG	4380
TTTAGGAAAA	TTAGCCCAGA	AGTATGAAAA	GGACCCAGAT	TCCAGTTTGG	CTTTGATTGA	4440
GACAAGTGGT	GCTTATAGAT	TGGTGACCAA	GCCTCAATTT	GCAGAGATTT	TGAAGGAATA	4500
CTCTAAGGCG	CCTATCAACC	AGAGCTTGTG	TCGGGCTGCC	CTTGAGACCT	TGTCCATTAT	4560
TGCCTACAAA	CAGCCGATTA	CGCGGATAGA	AATTGATGCC	ATCCGTGGAG	TTAACTCGAG	4620
TGGAGCCTTG	GCAAAGTTGC	AGGCTTTTGA	CCTGATAAAG	GAAGACGGGA	AAAAGGAAGT	4680
ATTGGGGCGC	CCCAACCTCT	ATGTGACTAC	GGATTATTTT	CTAGATTACA	TGGGGATAAA	4740
CCATTTAGAA	GAATTACCAG	TGATTGATGA	GCTTGAGATT	CAAGCCCAAG	AAAGCCAATT	4800
ATTTGGTGAA	AGGATAGAAG	AAGATGAGAA	TCAATAAGTA	TATTGCCAC	GCAGGTGTGG	4860
CCAGTAGGAG	AAAAGCAGAA	GAGCTGATTA	AGCAAGGCTT	GGTGACGGTT	AACGGCCAAG	4920
TGGTGCGTGA	ACTAGCAACC	ACTATCAAGT	CAGGCGACAA	GGTCGAAGTT	GAAGGTCAAC	4980
CTATCTACAA	CGAAGAAAAG	GTCTACTATC	TGCTTAACAA	ACCACGCGGT	GTGATTTCCA	5040
GTGTGACAGA	TGATAAGGGT	CGCAAGACGG	TTGTGACCT	CTTGCCCAAT	GTCAAAGAGC	5100
GTATTTACCC	TGTGGGTCGT	TTGGACTGGG	ATACATCAGG	TGTCTTGATT	TTGACCAATG	5160
ATGGGGACTT	TACAGACGAG	ATGATTCACC	CTCGTAATGA	GATTGACAAG	GTTTATGTCG	5220
CGCGTGTAA	AGGTGTGGCC	AATAAGGACA	ATCTCCGCC	CTTGACCCGT	GGTCTTGAGA	5280
TTGATGGTAA	GAAAACCAAG	CCAGCTGTTT	ATGAAATFCT	CAAAGTGGAC	CCAGTCAAAA	5340
ATCGCTCTGT	GGTGCAGTTG	ACCATCCATG	AAGGGCGTAA	CCATCAGGTT	AAAAAGATGT	5400

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TTGAAGCTGT TGGTCTCCAA GTAGATAAGT TGTCTCGGAC TCGTTTCGGA CACCTAGACT	5460
TGACAGGACT CCGTCCAGGA GAATCCCGTC GTCTTAATAA AAAAGAAATC AGCCAACTAC	5520
ACACCATGGC TGTAACTAAG AAATAATGAA ACGAATTTTA ATAGCGCCTG TCGCCTTTTA	5580
CCAACGTTT ATCTCACCAG TCTTCCACC CTCTTGTCGC TTTGAGCTGA CTTGTTCCAA	5640
CTACATGATT CAGGCTATTG AAAAACATGG GTTTAAGGGG GTATTGATGG GCTTGGCTCG	5700
GATTTTACGT TGTTCATCCCT GGTGAAAAC AGGTAAGGAC CCCGTTCCAG ACCGCTTTTC	5760
CCTTAAACGA AATCAAGAAG GGAATGAGG TGGGGTAAAT AGATTTCAA ATGATAAAAA	5820
CGCATCCTAT CAGGTTTGAG TGAACCTGAT AGGATGCGTT TTAGAATGTC AAAATTTTAT	5880
ACTCTTCGAA AATCTCTCA AACCGCGTCA GCTTTCATCT GCAACCTCAA AACAGTGTTF	5940
TGAGCAACCT GCGGCTAGTT TCCTAGTTTG CTCTTTGATT TTCATTGAGT ATTAAATTGA	6000
GTTTGAAGTG GCTTATTTCA AAGCTTTTGT TATGTCTTCA ATCATGAGTT TTGTGATTC	6060
AAGTCCGCCT CCGCTTAGAT ACCAGAGGTC TGGTGTAGT TGGATAATCT TACCATTTTT	6120
AGCAGCAGGT GTTTCAGCGA TAAGGGCATT TTCTAGGACA CCGTCGTTGC TAGAGTTGTC	6180
CCCACCGATG GCAAGGGTAC GGTGATGAC AAAGAGGATG TCAGGGTTGA TTTCTTTGAC	6240
ACTTTCAAAG CTGACTTCTT GTCCGTGGCG TGAGTCTTCA AATTTTGTAT CAGTTGGTTT	6300
GAATTTCAAG GTTTGGTACA AGAAAGAGAA ACGAGATTG GCACCAAAG CTGCCATTTT	6360
TCCTTCATTA AGGAGGATCG CAAGGGCTTT TTGTGTCAGAG CTTTCATTTT TAGTAGCGAC	6420
TTCTTGATG CTCTTGCTA GCTTGGTCAA TTCTTCCTTG GCTTCTGTG TACCAGTTTC	6480
GCCGAAGCA CTTGCTAAGG ATTCGATATT AGCCTTGTA GAAGTCCAGT AGTCGTCCTT	6540
GCTTGCTTGG AAGAGAACGG TTGGGGCGAT TTCTTTGAAT TTGTCTACGA ATTTTGTGT	6600
ACGTGGCGAA GCGATAATCA AATCAGGCTC AAGGGCGCG ATAGCTTCTA AATCAGGTC	6660
TTTCATAGAA CCAACATTTT TGACAGTCC CACTAGGTCT TTTAGATAAG TCGGAACAGT	6720
TTTTGTAGG ATTCGACGA TATTTTTTTC AAATCCTAAA GCGCGAATAG TATCCGACG	6780
GCCGAGGTCA AAGGTCACAA TCTTTTCAGG AACTTTGAA AGTTTGACCT CGTCCAGTGA	6840
ACTTTAATG GTTACCTCTG TTGGAGCAGA GCTACTGGTC TCTGTCTGAC TAGTGCTTGA	6900
GTTTGTACTA CATGCACCAA GTAGGAGCAA GAAGCTGGCC ACTAGGGCAG TGAATAAAG	6960
TTTAAGGGAT GTTTTCATAA TTTCTCCTTT TTAAAATGTG ATAACGATTT AGGGAGTCTC	7020
TTAATCTTAT TGACTAAGAG ACTGAAGGTT CTCTAAGTTG AGCTTTTATG TTACTAGCTA	7080
TAGATACAGA TCTTTTTGTC ATTGATATCA GCTAGCGTGA TGGGAATCTC ATAAAGTTGA	7140

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CTGAGCAGGT	CAGCCTGCAT	GATTTGATCG	GTTCTTCCCT	TGCTAAAGAC	CTGGCCGTCC	7200
TTGAAGGCCA	CAATTTTCATC	TGCATACTGA	CTGGCCATGT	TGATATCGTG	GAGGACGATG	7260
ATAATGGTCT	TGCCGAGTTC	CTCCACCAGT	CGTCGAAGAA	TCTGCATCAT	GCTGACGCTT	7320
TGCTTGATAT	CGAGATTGTT	GAGTGGTTCG	TCCAGCAAGA	TAAAGTCCGT	ATCCTGGGCC	7380
AGTACCATAG	CGATAAAGAC	GCGCTGGAGT	TGCCCCCTG	ACAGGCTATT	GATGTAGCGG	7440
TCTTTTAAGT	TGGTCAGTTC	TAAATAGTTC	AGAGTTTCTC	GGATTTTTC	CCAGTCTTCT	7500
GATCTAAGTC	GACCTCGGCT	GTAGGGAAAA	CGTCCAAAAC	TGACCAGTTC	TTCAACAGTC	7560
AATTTGGCTT	GGTAATTGAT	TTTCTGTTTT	AGGATGGTTA	GTTCTTGGGC	CAGTCTTGC	7620
GAATTCACG	TCTCGATTTC	ACGTCCTTTG	ATACTGAGAA	CTCCCTGATC	TTTCTTGGTT	7680
AGCCTGCTCA	TGATGGAGAG	GAGAGTCGAT	TTTCCAGCAC	CATTTGGACC	AATAAAGGCT	7740
GTCAGTTTTT	GAGGACTGAC	TTCAAGCGAA	ATGCCTTGCA	AAATATCCTG	TTTTTGAATG	7800
GATTTGTCAA	TGTTTTCCAG	TTTCACTGAC	GAGACCTCCT	ATATAGTAAG	ATAAAGAATA	7860
AGAAGCCACC	CACACTCTCA	ATGATCATA	TGATACGAAT	TTCAGTGCA	AAGACTCGTT	7920
CAATCAAGGC	TGCCCCAAG	GTTAAGCTAA	TAAATCCAAC	CAGAATGGCC	ACTATAAAGA	7980
GTAAC TTGTG	CTGATAGTCT	TTGACAATCA	GGTAGGTGAG	GTTGGCCAGT	ATAAAGCCGA	8040
AGAAGGCCAT	AGGTCCTACC	AAGGCAGTGG	CCGTTGAGGT	CAAAGCACG	ATTCCCCAGA	8100
GGAGCTCTTT	CTGTTCTTTT	TCAACATCGA	GTCCCAATAT	CTGAGCCGTT	TCTCTTTGCA	8160
GGTGCAAGAC	ATCTAGAACG	ACTGCTTTTC	GAAAGAAAA	GATTGTCAA	GCGAGGATGA	8220
TCAGAGAACC	GATGGCTAGG	ATGGAAGTGT	TGAGATGTTG	AAAGGAGGCA	AAAAGACTAT	8280
TTTGCAGTTT	ATCGTATTCG	TTTGGATCCA	TTAGGACTTG	AAGGAAGGTG	CTGATATTTT	8340
GAAAGAGACT	TCTGAGCGCT	AGACAGATCA	GCAGGACGAA	GACCAGGTCT	TGCTTCATCA	8400
GTGTCTTCAA	GTAACCTTGT	AAGGCAGGAA	AGAAGAGGGA	CTGGACAAGA	AGTAAGACTA	8460
GGAATCTAA	GATAGGGGAT	TTGCCAAGTT	GAAGAACTT	GCTTTCAAAA	ACCAGTAGTA	8520
GGGTTTGTAG	TAGGACGTAG	AAGGATTCAA	TTCCCAAAAT	ACTAGGCGTC	AGGAAGCGAT	3580
TTTCCGTCAG	GGTTTGAAAA	CTAATGGTCG	AAATCCCAGT	CGCGATGGCT	ACCAAGAGAT	8640
AAACGATGAT	CTTTTGGGAA	CGCAACTTCC	AAGCAAAGGC	TGACAAGTGA	GTGATGGGCC	8700
AAAAGTAGAG	AAGACAAGCT	CCGATGGCAA	GAATAATGAG	AATCCAGAAG	AGCTTGGTAT	8760
GTTTGCTTTT	AGTCTGCATC	TTTTCGTCCC	CCTCTCCAGA	GAAGTAGGAT	AAAGACGAGA	8820
CTACCGATGA	TTCTTAGCAA	GAGACTGACA	GACAACTCAT	AGGGCCTAAT	CAGAACTCGG	8880
GATAGGATAT	CGCAAGCCAG	AACTAGATTG	GCACCAACCA	GTGCGACCAT	GAGTTTGGTT	8940

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TGACTTAGAT TATCTCCATA GCGCTTGCGA ACAAGATTGG GAACGATAAC TCCGAGAAAT 9000
 GGTAGGCCAC CCACGGTAAT CATGGTGACG CTTGTCGTTA GCGCCACCAG AAAGAGGGCC 9060
 AGTTTTTCAA GTAGGGAGTA GGAAATCCCC AAACCTCTCGC TGGTTTCTTT CCCTAGATTC 9120
 ATGATGGTGA AGGTTTGGGA TAATTTCCAA ACGGTTATCA GGATGATGAG GCCTAAGAAG 9180
 AGCCACTCAT ACTGATGGGT CTGAATCATG GAGAAGGAGC CCTGGGTCCA GGCAGTCATA 9240
 CTCTGAACCA GATTGAAACG ATAGGCGATA ACTTCTGTGA CTGAGCCGAT AATCCCGCTA 9300
 TAGATGATCC CAATCAGAGG CAACATCCAC CTTTCCTTTA CAGTAAAAAT GGTCATAAAG 9360
 GCTAGGAAGA AGAGGGTGAA TACGATGGAT GAAACAAAAG CGAAGAGCAT CTGTGGGTC 9420
 AGACTAGCCG ATGGAAAGAC AAAAAGGCTC AGCACCATTC CCAGTTTGGC GGCTTCAGTC 9480
 GTTCCAACCTG TACTCGGTGC AGCAAACCTGA TTTTGGGTAA TAGTCTGCAT GAGAAGGCCT 9540
 GCCATACTCA TACTAGAGGC AGTCAGGAGA ATACTGATAG TTCTTGGGAG ACGGGACTCT 9600
 TGAAAGAGGA GCCAGGTCTG CTGGTCGAAA TCAAATAGCT TTCCCATGA AAAATCACTG 9660
 GTCCCAATGC TAATAGAGAG AAAGACTAGG AGTAGAAGTA AGCCAGG 9707

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5910 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CCGCAATTAT GCTTGAAAAG GAGTATACTT ATAAGTAACG CAAACGTTTG CGTCTGAAAA 60
 ATACGCAACG TTCCATTATT TTAACACACG AGGTGCTATT ATGAAAAAAC GTCAAAGTGG 120
 TGTGTTGATG CACATCTCTT CTCTCCAGG AGCTTACGGA ATCGGATCAT TTGGTCAAAG 180
 TGCTTACGAC TTCGTGATT TCTTGGTCCG TACAAAACAA CGTTACTGGC AAATCCTTCC 240
 ATTAGGAGCA ACTAGTTACG GGGATCTCC TTACCAATCT TTCTCAGCCT TCGCAGGAAA 300
 CACTCATTTT ATCGATTTAG ATATCTTGGT GGAGCAAGGT TTGTTGGAAG CAAGTGACCT 360
 TGAAGGAGTT GACTTTGGTA GCGATGCGTC TGAAGTTGAC TATGCTAAAA TCTACTATGC 420
 ACGTCGTCCT CTTTTAGAAA AAGCGGTGAA ACGTTTCTTT GAAGTCGGAG ATGTTAAAGA 480
 TTTTGAGAAA TTTGCTCAAG ACAACCAATC ATGGCTTGAG CTCTTTGCTG AGTATATGGC 540
 TATCAAAGAG TATTTTGACA ATCTTGCTTG GACTGAATGG CCAGATGCAG ATGCTCGTGC 600

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TCGTAAAGCT	TCAGCACTTG	AAAGCTATCG	TGAGCAATTG	GCAGACAAGT	TGGTTTACCA	660
CCGTGTGACT	CAATACTTCT	TCTTCCAACA	ATGGTTGAAA	TTGAAAGCTT	ACGCTAACGA	720
CAACCACATC	GAAATCGTTG	GGGACATGCC	AATCTACGTA	GCGGAAGATT	CAAGTGATAT	780
GTGGGCAAAT	CCACATCTCT	TCAAAACAGA	TGTC AATGGT	AAGGCTACTT	GTATCGCAGG	840
ATGCCCACCA	GATGAGTTTT	CTGTA ACTGG	TCAGCTTTGG	GGTAATCCAA	TCTATGACTG	900
GGAAGCAATG	GACAAAGACG	GCTACAAATG	GTGGATTGAA	CGCTTGCCTG	AAAGCTTCAA	960
AATCTACGAT	ATCGTTTCGTA	TCGACCACTT	CCGTGGCTTC	GAATCTTACT	GGGAAATCCC	1020
TGCTGGTTCC	GATACAGCAG	CACCTGGTGA	GTGGGTGAAA	GGTCCAGGTT	ACAAGCTTTT	1080
TGCAGCCGTT	AAGGAAGAAC	TTGGTGAGCT	AAACATCATC	GCAGAAGACC	TTGGCTTCAT	1140
GACAGATGAA	GTGATCGAAT	TGCGTGAACG	TACTGGCTTC	CCAGGAATGA	AGATTCTTCA	1200
ATTTGCCTTC	AATCCAGAAG	ACGAAAGCAT	TGATAGCCCA	CACTTGGCAC	CTGCTA ACTC	1260
AGTTATGTAC	ACAGGAACAC	ACGATAACAA	TACGGTTCTT	GGTTGGTACC	GTAATGAGAT	1320
TGATGATGCG	ACTCGTGAGT	ACATGGCTCG	TTACACGAAC	CGTAAAGAAT	ACGAAACAGT	1380
GGTACACGCT	ATGCTTCGTA	CAGTATTTTC	ATCAGTTAGC	TTTATGGCAA	TTGCAACTAT	1440
GCAAGATTTA	CTAGAATTGG	ATGAGGCAGC	TCGTATGAAC	TTCCCATCTA	CCCTTGGTGG	1500
AAACTGGTCT	TGGCGTATGA	CTGAAGATCA	ATTGACACCA	GCTGTGAGG	AAGGTTTGCT	1560
TGACTTGACA	ACAATTTATC	GCCGAATTAA	TGAAAATTTG	GTAGATTTAA	AGAAATAAGA	1620
CAATAATCAG	GAGACA ACTA	AACATGTTAT	CACTACAAGA	ATTTGTACAA	AATCGTTACA	1680
ATAAAACCAT	TGCAGAATGT	AGCAATGAAG	AGCTTTACCT	TGCTCTTCTT	AACTACAGCA	1740
AGCTTGCAAG	CAGCCAAAAA	CCAGTCAACA	CTGGTAAGAA	AAAAGTTTAC	TACATCTCAG	1800
CTGAGTTCTT	GATTGGTAAA	CTCTTGTCAA	ACAACTTGAT	TAACTTGGT	CTTTACGACG	1860
ATGTTAAAAA	AGAACTTGCA	GCTGCAGGTA	AAGACTTGAT	CGAAGTTGAA	GAAGTTGAAT	1920
TGGAACCATC	TCTTGGTAAT	GGTGGTTTGG	GACGTTTGGC	TGCCTGCTTT	ATCGACTCAA	1980
TTGCTACTCT	TGGTTTGAAT	GGTGACGGTG	TTGGTCTTAA	CTACC ACTTT	GGTCTTTTCC	2040
AACAAGTTCT	TAAAAACAAC	CAACAAGAAA	CAATTCCAAA	TGCATGGTTG	ACAGAGCAAA	2100
ACTGGTTGGT	TCGCTCAAGC	CGTAGCTACC	AAGTACCATT	TGCAGACTTT	ACTTTGACAT	2160
CAACTCTTTA	CGATATTGAT	GTTACTGGTT	ATGAAACAGC	GACTAAAAAC	CGCTTGCCTT	2220
TGTTTGACTT	GGATT CAGTT	GATTCTTCTA	TTATTA AAGA	TGGTATCAAC	TTTGACAAGA	2280
CAGATATCGC	TCGCAACTTA	ACTCTCTTCC	TTTACCCAGA	TGATAGTGAC	CGTCAAGGTG	2340
AATTGCTCCG	TATCTTCCAA	CAATACTTCA	TGGTTTCAA	CGGTGCGCAA	TTGATCATCG	2400

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ACGAAGCAAT	CGAAAAAGGA	AGCAACTTGC	ATGACCTTGC	TGACTACGCA	GTTGTCCAAA	2460
TCAACGATAC	TCACCCATCA	ATGGTGATTC	CTGAATTGAT	TCGTCTTTTG	ACTGCACGTG	2520
GTATCGATCT	TGACGAAGCA	ATCTCAATTG	TTCGTAGCAT	GACTGCCTAC	ACTAACCACA	2580
CAATCCTTGC	TGAAGCGCTT	GAAAAATGGC	CTCTTGAATT	CTTGCAAGAA	GTGGTTCCCTC	2640
ACTTGGTACC	AATCATCGAA	GAATTGGACC	GTCGTGTGAA	GGCAGAGTAC	AAAGATCCAG	2700
CTGTTCAAAT	CATCGATGAG	AGCGGACGTG	TTCACATGGC	TCACATGGAT	ATCCACTACG	2760
GATACAGTGT	TAACGGGGTT	GCAGCACTCC	ATACTGAAAT	CTTGAAAAAT	TCTGAGTTGA	2820
AAGCCTTCTA	CGACCTTTAC	CCAGAAAAGT	TCAACAACAA	AACAAACGGT	ATCACTTTCC	2880
GTCGTGGCT	TATGCATGCT	AACCCAAGAT	TGTCTCACTA	CTTGGATGAG	ATTCTTGGAG	2940
ATGGTTGGCA	CCATGAAGCA	GATGAGCTTG	AAAACTTTT	GTCTTATGAA	GACAAAGCAG	3000
TTGTCAAAGA	AAAATTGGAA	AGCATCAAGG	CTCACAACAA	ACGTAAATFG	GCTCGTCACT	3060
TGAAAGAACA	CCAAGGTGTG	GAAATCAATC	CAAATTCTAT	CTTTGATATC	CAAATCAAAC	3120
GTCTTCACGA	GTACAAACGC	CAACAAATGA	ACGCTTTGTA	CGTGATCCAC	AAATACCTTG	3180
ACATCAAAGC	TGGTAACATC	CCTGCTCGTC	CAATCACAAT	CTTCTTTGGT	GGTAAAGCAG	3240
CTCCAGCCTA	CACAATCGCT	CAAGACATTA	TCCATTTAAT	CCTTTGCATG	TCAGAAGTTA	3300
TTGCTAACGA	TCCAGCAGTA	GCTCCACACT	TGCAAGTAGT	TATGGTTGAA	AACTACAACG	3360
TTACTGCAGC	AAGTTTCCTT	ATCCCAGCAT	GTGATATCTC	AGAACAAATC	TCACTTGCTT	3420
CTAAAGAAGC	TTCAGGTACT	GGTAACATGA	AATTCATGTT	GAACGGAGCT	TTGACACTTG	3480
GTAATATGGA	CGGTGCTAAC	GTGGAAATCG	CTGAGTTGGT	TGGAGAAGAA	AACATCTACA	3540
TCTTCGGTGA	AGATTCAGAA	ACTGTTATCG	ACCTTTACGC	AAAAGCAGCT	TACAAATCAA	3600
GCGAATCTTA	CGCTCGTGAA	GCTATCAAAC	CATTGGTTGA	CTTCATCGTT	AGTGATGCAG	3660
TTCTTGACGC	TGGAAACAAA	GAGCGCTTGG	AACGTTTTTA	CAATGAATTG	ATCAACAAAG	3720
ACTGGTTCAT	GACTCTTCTT	GATTTGGAAG	ACTACATCAA	AGTCAAAGAG	CAAATGCTTG	3780
CTGACTACGA	AGACCGTGAC	GCATGGTTGG	ATAAAGTCAT	CGTTAACATT	TCTAAAGCAG	3840
GATTCTTCTC	ATCTGACCGT	ACAATCGCTC	AGTATAACGA	AGACATCTGG	CACTTGAACT	3900
AATACTCTTC	GAAAATCTCT	TCAAACCACG	TCAGCTTTAT	CTGCAACCTC	AAAGCAGTGC	3960
TTTGAGCAAC	TGCGGCTAGC	TTCTTAGTTT	GCTCTTTGAT	TTTCATTGAG	TATAAGATAC	4020
AAATTTATAC	TAATACATTT	TGTAAAAAAG	CGAGTTTCGA	TGAAATTCG	CTTTTTTAAT	4080
GATGTAGATT	TGGGTCAATC	TTGTCTAAAA	ATAGGGAAAT	CCTAGATACA	GTGAAGGCTT	4140

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TAAATGCTGG	TTTTTACTGT	CCTCAGCCTT	ATATTTTTTC	GTAGTTGGTT	ACCTCATATC	4200
TATTATATTC	GCTTACATAA	AGTATTATAA	TATAATTGTA	GGAAAGAAGG	TGTTTTTATG	4260
ATATACACAC	TTAAATTGGT	GTTGTTTATT	ACCTTTCCTG	TAATAAGCTT	GTTACCTGAT	4320
AAGATTTTTG	GAAAAATAA	AAAAATTTGG	AAAATAGTTT	TTGCAATATT	GACGGCAGTG	4380
GCAGCATTGT	CATTTATGTA	CTAAGTTATT	TTAAGAATGT	AGGGAAATAA	ACCCTACATT	4440
CTTTTTAGTT	TTTCTGTTT	TCTAAATCTT	ATTTATCCAA	GCGATTCAAC	ATTTCTTGCT	4500
TCTTCGCTTC	AAGTTCGCA	CGCTTTTCTT	CGATTTCCGC	ATGTTTTTTC	TCGAGTTCAG	4560
AACAACCTGC	ACCATTGCTA	AATTCTTTTC	GCCATCAGGA	GATAGGGTGA	GTCGACATGT	4620
CTATTACTCA	CCCAAAGCAG	TCCTACAAAG	CAGGAATTTT	CTGTTACTTT	TTTGGAATAA	4680
GTAACGTTTA	TACAGCTTTG	ACACTTCGTA	TCAAAGCGCC	AAACACACTC	CGAGGGGTTT	4740
ACAGAAAGCA	GAAAAGGAAT	GATCTGGTAT	AAGATCATTC	CTTTTCyCTC	TTTTTCTTTA	4800
AGTAATTATA	TACAATGTAC	GACGAAGTCG	TCATTGCAAT	GCTGATCCAC	CACCTAAAGG	4860
GAACTTTAAA	CAACATTGAT	AAGATAAAGA	ATATAAACAA	CGAAAATACG	TTATACCCAA	4920
TTAATTTTAT	TGTATATCTC	ATGATTAAAA	GTTAATCCTT	CCGTTGTTAG	GAATGGCATC	4980
ATTTTTATCC	CATAATTGTG	CTAAATAAGT	CCCCGGTGAT	AATAAATTC	TAGCGAATTC	5040
TAAAGCAACA	TCATTTACAA	ACCAACTACC	TAGATATCTA	GAAATGCTG	AACGAATAGC	5100
ACTTTTTGCT	GCATGTTTTC	CTTTTACTTT	AATTAGATTT	GCAAGGCCTG	CAGTAGTTCC	5160
TCCTAATGCT	AAAGCTATTG	CAGTATCTAA	TAGAGCACCC	ATTTGATTAA	CTGTAATACC	5220
TTGCCAAACT	GCTCTAAATG	GAGAGTATGT	AGGTGGGATT	GTATAATCGC	CTTGTAATTG	5280
TCGGTTAATT	ACTTCTTTGA	TCCATTGTTG	TGAGACGCTC	GGATGAAAAG	ATTGGATTTC	5340
GTTTGCAAGT	GTATTGATTT	GTTCTTCTGT	TAGAGAAGTG	ACAGGTTGAA	GTTCCATATT	5400
TGTTTCAATT	TGTGATACTT	GTTTCAGAAGC	GTATACAGCT	GAAACACTTG	GAATCGCTGA	5460
TACAATTAAC	ACAATTGACG	TCAAAAAAAC	CGAAATAAAT	TTCATTAATT	TGTTCATGAG	5520
CTTTTCTCCT	TTTTATTGTC	ATCTGCTTAC	ATTTTATCAT	ATACTGTTAT	TATAGTCAAA	5580
AAAATATGCT	ATTATGTTAA	AAAAATATTT	TTCAAATAT	AAATGGACGG	ATTTATTTTG	5640
GATTTTATTT	GTTATTTTGA	CCTGCCTCTA	TATTTGGTAA	CATGATTTGT	TTACTCTCAA	5700
TCATCAAGAA	TTCTCTTTTC	GTGGTAGCGT	TTGGGGTCTG	GTAAGGCTCT	TATATCACTT	5760
ACTATTCATT	GATAAGTTTG	TTATATCGAA	TCGAAAATAA	AGATTAGAGC	TATGCTTGAC	5820
TGTGTACTTT	TAGGATTTAT	TTTGAGAGAA	GATTTTGTCT	CTATTATTTA	TTATTTTAAA	5880
TTTATTTATT	TTGTATAAGA	TCTATTCCTT				5910

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(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

GGCATAGCGA CTCATTTTTT CAACTGTCCA GGCTGGATAC CAGACTAATT TAACCTCAGT	60
ATCCGTTACT TCTGGAACCT CTATCATAGC ATCATAAATC TGGTCTGTCA AAAGGTCTGC	120
TAAGGGACAA CCCATAGTTG TCAAAGTCAT GTCAATCTCT GTTTGCCCTG TGTCCACGTC	180
AAAACGAATC TCATAGATCA AACCAAGATT GACAATATCG ATTCCCAACT CAGGGTCGAT	240
GACTTCTTCC AAGGCTGTTA AAATCCGTGT TTTGATGTTT TCAATTTGCT CTTCTGTATA	300
AGCCATATTT TCCTCACTCT TAGTCTTCAA TAAAATCACG AAGCGGTTTG CTACGACTTG	360
GTTGGCGTAG TTTTCTCAA GCCTTTGCTT CAATCTGACG GATACGCTCA CGAGTTACGT	420
TAAAGACTTT CCCCACATCT TCAAGTGTGC GCATTTTTTCC ATCATCTAGT CCAAACGTA	480
GACGCAGAAC ATTTTCTTCA CGGTCTGTAA GAGTATCTAA GATTTCATCC AATTGCTCAC	540
GCAAGACGAT ACGAGTCGTA TAATCCACTG GATTTTCAAT CACTTCATCT TCGATAAAGT	600
CTCCAAGGTG GCTATCGTCC TCTTCACCGA TAGGAGTTTC AAGAGATACT GGTTCTTGGG	660
CAATCTTCAA GATTTCACGA ACCTTATCAG GTGTATATC CATTGCTTCA GCAATCTGTT	720
CTGGTGTCGG ATCTTGCCCC AATTCTTGAA GGAGATTCGG CTGTTACGTA ACCAATTTAT	780
TGATAGTTTC AACCATGTGA ACTGGGATAC GGATGGTACG AGCTTGGTCC GCAATAGCAC	840
GAGTGATAGC CTGACGAATC CACCAAGTTG CATAAGTTGA AAAGTTGAAC CCTTTAGAAT	900
AGTCAAACCT GTCAACCGCC TTCATCAAGC CCATATTTCC TTCTTGAATC AAGTCAAGGA	960
ACTGCATACC ACGACCGACA TAGCGTTTGG CAATGGAAAC AACCAAACGA AGATTGGCTT	1020
CCGCAAGACG TTGTTTGGCT TCGATATCAC CAGCTTCAAC AGCCAGTGCC AACTCTTCT	1080
CCTCTTCATT GGTCAAGAGA GGAACGACCC CTATTTCTTT CAAGTACATA CGGACAGGCT	1140
CATTGACCTT AGCAGAAGTT GACCCAATCA AGTCCATC GCTGAGTTCT GGTCTTCTT	1200
CATTGCTGAG AACACGCGCA CTTGGATTTC CTTCGTTATC TGTGATAGAA ATGCCTGCAT	1260
CCTGAATCCG TTGCAAGAGA TCTTCAATCC CATCAGCGTC CAAGGTAAAA GGAATAACCA	1320
GACTTGCATT GATTTCATCA TCTGTTGCTG TCCCTTTTTG CTTATGATTA CGGATAAATT	1380

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CTGCTACCTG	TACGTCAAAT	GTGTTACTT	CTTTTTGTTT	TGTTGCCATT	ATTACTIONCAT	1440
TCTTCTCTTT	TGGGAAATTA	AACGTTCCAA	TTCTTCTAGG	GCTGTATCTG	TATCTCCTAC	1500
ATGGCTAGCT	TCCTGCACCT	TCTTTTTGAT	TCTCATATTG	TCCTGATTCA	AGAGAGCCTT	1560
GTTTCGAGTC	ATCTCTACTT	CACTAAGTTC	CTGCGGCGAT	ATCTCAGCAG	GCAAATCCTG	1620
AGCTAAACT	TGGTACCAAG	CTCTTCAAC	TTCTCTGTC	TGCTCTGCTA	AACTTCTGG	1680
AGGAAGATTT	CCATACTGGC	CAAGCAAGTC	ATATAAGACC	TGAAATTCAG	GTGTAGCAAA	1740
TGCAAAGTCT	TCTCGCAAAC	GGTAATCGTT	CAAAACAAGA	GGGGATTCCA	TCATCCGATA	1800
GAGTAGATGG	GCTTCTGCCC	TCATAATAGC	CGATAACTGC	TTGGTGACAG	GCATGGTGAT	1860
TGGCGTCGGT	CTGGAAATTC	CTTCCATGCG	ATTCTGCCTT	TGCACCTGAC	GACTCTCATT	1920
AACAATCTGC	TCAATCTGGG	TATAATCAAA	GGACGCCAGA	CTGTCAGCTA	AAATATGAAT	1980
ATAGCTGTTT	TGAGCAGCGA	TGGACTTTTC	TTGAACAATC	AAGGGAGCTA	TTTTTTCAAG	2040
AAACTCAATC	TGAGCCTGCA	GATTTTCACT	GTTTTCAGGT	TTGTACTGAT	GAATGTAGAA	2100
CTCAATCGGA	CTAATACGAG	TTTTCGTTAA	TAGATAGGCC	AAGTCTTCTG	GACCATTTTT	2160
TTGTAGATAC	TCATCAGGAT	CCAAGTTATC	AGGCATGCTG	ACGATTTGCA	CAGGCATATC	2220
ACCAATTTCA	TCCAATGCTT	TCAATGTCGC	GGCTTGCCCA	GCCTTATCTC	CATCGTAAAC	2280
AAGAACCAAT	TTCTTGTTA	ACCTTTTCAG	ATGCTCAACA	TGCTCTCGAC	TCAAGGCTGT	2340
TCCCATCGAC	GCCACAGCAT	TTTCGATTC	AGCCCGATAG	GCTGCAATAA	CATCCATGAA	2400
TCCTTCCATC	AGGTAAATCT	CACTAGCTTT	TCCAGAAGAT	CTTTTTGCCC	TATCCATATG	2460
ATATAATTCG	TAACTTTTGT	TAAAAATTGC	AGTCGATCGG	CTGTTTTTAT	ACTTAGAAGT	2520
TTGTGAATCC	GTTTTTTGCC	AGATACGACC	TGAGAAGGCA	ATGACCTTTC	CTTGGTCATT	2580
TGTCAGGGGA	AACATAATGC	GATTGTGAAA	GGTGTCTACA	AATTGATTGG	CATCCGAGAG	2640
ATAAACAGG	CCTGAATCCA	GTAAATCCTC	TTACAGATAC	TGATCAGACA	AACGTTGATA	2700
GAGATAGTTT	CGTTCTGGAG	GTGCTAAACC	AATCCAAAAA	TGTTTAAGCA	CTTCATCTGT	2760
CAACCCCGC	TGATAAAGGT	AATTTCTGGC	CTCTTCGCCC	ATAGTCGTTG	TCATGAGAAT	2820
AGCATGGTAA	AATTTGGCTG	CATCTTCGTG	CATATCATAA	AGAGCTTGGT	GAGGTGAGGC	2880
TGACTTCTGC	TCACTATAAA	GCGGTTTTTC	AACCTCAATT	CCAACACGCT	GACCTAAGAT	2940
TTGGACTGCT	TCTATAAAGG	GAACCCCTTG	GTACTCCTCG	ATGAACCTAA	AGACATCACC	3000
TGAGCGACCA	CAACCGAAAC	AGTGATAAAA	CTGCTTGTC	TCTACAACAT	TGAAAGATGG	3060
TGTTTTTTCA	CCATGAAAAG	GACAGAGCCC	TAGATAGTTC	CGTCTGCCT	TTTGTAAGA	3120
AATCACATCT	CCTATGACTT	CCACAATGTT	GGCATTGTTT	TTGATTTCTT	CAATGACTTG	3180

1069

TTTGTCAACC ATACACAATA CCTCCATGTT ATCATAGTTT ACTTTATATA GTATACTTTA 3240
 TTTTCAGAAA AAAGTAAACC ATTTCACTCA TTTTCCCTAC TTTATTCAAA GAGTTGATAA 3300
 TAATCAGAGA TTTTCATTTT TGCTTTTTCT TCTTGTTTTA AATCTTGAT AATTCGTCCT 3360
 TCTTTCATGA CAATCAAGCG ATTGCCGTAT TTGAGAGCAT CTTCATATG ATGAGTAATC 3420
 ATAAGGGCTG TTAGCTGATC TTTCTTAACA AATTCATCTG TCAATTCAT CAAAGCAACA 3480
 CTAGTCTTTG GATCCAGGGC AGCAGTATGC TCATCTAACA GGAGTAATTC AGGTCGCTTC 3540
 AAGGTTGCCA TCAAGAGACT CAAAGCCTGT CTTTGTCCAC CTGATAAGAA CTCATCGGT 3600
 GTATTCAAGT GTTCTCAAG ACCATTTCCCT ACTTTTTCAA TGGTTGCCTG AAATTCATCC 3660
 TTATAGCTAG TCAAGCGTCG TGGTAACAAT CCACGCTTTT CACCACGAAA CTTGGCGATT 3720
 AAAAGATTTT CAGCGACCGT CATACGGGGA GCTGTCCCA TCTTTGGATC TTGGAAGACA 3780
 CGAGACAGGT ACTTGGCAGC CTTCTCGGGT GAAAACCTAG TGAGATCTTC ACCTAAAATA 3840
 CGGATAGTTC CACTAGTTAG TGATAAGGTC CCTGCTATAG TGTTAAAGAG AGTTGATTTT 3900
 CCAGCACCAT TTCGCCCAA AATCGTGATA AAGTCCCGTT CAAAAATTC TAAGGAAACA 3960
 TCATTTAAAA TAATCTTTTTC TTCATCAAAG CCATTTTAA CGATTTTGGT TGCATTTTTT 4020
 AATTCTACAA TTGTGTCAAT TTGTTAACF TGGCTCCTTT CAAGATTGTT TGCTTAAATG 4080
 TTGGAATCAT GAGGCAGACT GCTAAAATCA AGGCACTGTA TAAACGAAG TAACTTGTAT 4140
 TAAAGCCAAG TGCATAACT GCCCACACTA AAAATTGATA AGCGATAGAA CCTACAACGA 4200
 TAGTAACCAA ACGCTCTGCC AAGCTCAAC TCTTGAAAAT AACTTCTCCA ATAATCAAAC 4260
 TTGCAAGCCC CACAACGATA ACCCCGATCC CTCGAGACAC ATCGGCATAA CCTTCTTGCT 4320
 GAGCAATGAG GGCACCTGCA AGGGCAATCA CACCATTGTA TAAGACCAAG CCCATGAGCT 4380
 CCATGCGTCC AGTATGAATC CCGAAACTTC TAGCCATATC AGGATTATCC CCTGTAGCAA 4440
 TATAGGCTTG TCCGAGTTTA GTGTCCAAGA AAAAGAGCAT GAGAGCAATA ACAATACTCA 4500
 CAAAGATGAG ACCTGTCAAG AGTTGATTCA AATCCGAATC AAAAGGCAA ACATCCTGAA 4560
 TTTGCTTGGT TCCAAGCAGG CTTAAATTCG CACGTCCCAT AATCAAGAGC ATGATTGAGT 4620
 GACAAGAAGT CATCACAAA ATCCCTGAGA GCAAGGTTGG GATCTTCCCT TTTGTATAAA 4680
 GAAGGCCTGC TGCCATTCCA GCCAAACAAC CTGCTCCTAC AGCAACAAGT GTCGCTAAAA 4740
 ATGGGTTTAC GCCTTTGGTT ATCAAAGTGA CAGCAACAGC TCCCCAAGA GGAAGGAAC 4800
 CTTCTGTGCT CATATCTGGA AAGTTTAAAA TCCTAAATGT CATAAAGATT CCCAGACCTA 4860
 GAATAGCCCA GACAAATCCT TGAGAAATAA TGGAAACAAT CATATTTTAT TTAATCCTTT 4920

1070

CTATATTCAT CTTTTTAAAA AATGGGAAGA GTCTCCTCCT CCCTACCTTA TTTATTTCGAT	4980
GACTTGTCCCT GCTTCTTTGA GAACAGACTC AGGAATAGTA ATACCTAGTT CTGTGTCTAT	5040
TTTTTTATTG ATGACTGACT TACCAGTTGA AAAGACATTG ACTGGGGTAT CGGCTGGTTT	5100
TGCACCTTC AAGACTTGCA CAATCATTTT ACCTGTTGCC ACACCAAGGT CATGTTGGTC	5160
AATTACAAC GATGCCAAAC CACCTACTTC TACCATAGCT GTCGCACTGG GATAAATTGG	5220
TTTCTTAGAA CTTTGATTGC TAGAGACAAC CGTTGGAAAT CCTGATGCAA TGGTGTATC	5280
AATTGGAACC CAAATAGCAT CTACCTTGCT AGTCATAACA GTGACAGTTG AGGCAATTC	5340
ATTTGTTGAA GGAAGTCAA ATGTTTCCAC TGTCAGACCT GCCTTTTCAG CATAAGCCTT	5400
AAATTC	5406

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAGCTTGCTC TTA CTATTAT AGCAGATGTT ATAGCTGGAA TTATCTTGTA TTTCGTCTGC	60
AAATGGCTAG ATGGTAAGAA GTAGACCGAA TGACTAGCCT ATAAACACCC GTTAAATCGC	120
TAAGATACGT CAAAAAAGCC CTTAACTATG GCACTAGTTA GGGGCTTTGG TGTTC TAATG	180
AACCTTATAC ACTAACTACA TTCTAGCATA TAAGCCCAGA TATTTCAAGA GTTTTATTTA	240
TTGTTTAAAG TTCTGAAAGG TCTATAATGA AGTTAGCCAT CTAGTATCAA AAAACCGACT	300
AGCTCTTATG AACTAGTCGA TTTCTCATCA ATGCGCCAAC ATTTCTTGGG CGATTTCTTG	360
GCCAGATAGG TTATCTGGGT AGTAGGTTGG CCAGTTGTCC ATTTCTTCAA AGAGGGCTTC	420
TTGGCTTGTG CCTCCAAAGA AGATATGGAA ATGTTCTGCC TTAAGTGGGG CAACATTTGG	480
GTCACTAAAC TGAACATACT TGAATTGTCC AGCGTCAGCA TCTGTGGCTT CAAAGAGGAA	540
ACGCACGCCA CGATTGCCTT TCTTGTAAAGT CAAAATTTTC TTACCGACAT ACTTGTAAGT	600
GTATTTCTTG CTTTGTCCAC CTTGAACAAA TTCCATAGTA TTATCAGTAA TGTTAATCTT	660
AGTCACATCT GTATGATAGC CTTTGTATA GTAAGCCTTG TACTCAGCCT GGGTCATCTT	720
ACCAGTCAAC TTAGCCTTGT AGTCAAAGAC TTGGTCAAAC GTGCCGTCTT CAAGGAAAGG	780
ATAAAGTATG TGCCAGTTAC CTGCATAGTC ACTCAAAGTG CGGTCCTTGA CAGCTGCATC	840
CTCGAAGTAA CCATTTTGA CTGTCTTGGT ATCCTCTGCC TTTTCAGGTT CAATGCTGG	900

1071

GCCTTCTTGG TCTGTGTGTTT GTTTCAAAGC CTTGAGGTTT TTCTCCATCA CGGAAATGTA	960
GTTTTCTCCA GCCTTGGTGT CCTCTTCTGT CAGACTTTCT AAAGGATTGA GGACATCAGT	1020
TTTGACACCT GCTTCTTTTG AAAGTGTGTT AGCAAGGGCT TGTGAGGCAT TTCTTCAAAA	1080
TAGATATAGG CGATTTTATF TTCTCTGACA TACTCTGTCA ATTCTGCCAA GCGAGCAGCT	1140
GATGGCTCTG CATCTGGAGA AAGTCCTGAG ATTGCGACTT GTTTGAGTCC ATAGTCCAAG	1200
GCAAGATAGT TAAAGGCTGC GTGTGAGTC ACAAAGCTCT TTTGTTTTGC TTGAGACAAA	1260
CCTTCTGCGT AAGCCTTATC CAAGGCTTGC AATTTTTTCGA TATAGGCAGC TGCATTCTTC	1320
TCAAAGGTCT CTTTTTTATC AGGATAATCT GCTGACAAGC TGTGCGGAT GTGCTCTACT	1380
AGTTTAATGG CACGAACTGG TGATAACCAA ACATGGGGGT CAAACTCATG GTGATGACCT	1440
TCTTCTCCAT GGTTCATGGTC TCCCTCTTCT TCCTCGCCAC CTGGCAAGAG CAACATATCG	1500
CCTGTCGCCT TGATGGTTTT CACTTTTTTC TTATCCAAGG TATCTAGCAA TTTAGGTACC	1560
CATGTTTCCA TGTTTTCATF TTCATAAAGC AAGGTATCTG CATCTTGGAT TTTGGCAACT	1620
GCCTTGGCAG ATGGTTCGTA TTCATGAGGT TCTGTCCCAG CACCGATTAG GAGTCTTACA	1680
TTAGCCGTAT CTCCTGCGAC TTGCTTGGTA AATTCATAGA CAGGGTAAAA GGTGTGCACG	1740
ATATTGAGTT TACCATCTGC CTGTTTTTGA TTGGAACAAG CCACTAAAA CAAGGCACAT	1800
AGACTGGCTA GTAATAAGCT AATTTTTTTC ACGTTCGTCT CCTATTTGAT AAAACGCTCTT	1860
ACTAAACTGA TTAGTATAAA GACAGTTACA AAAATAATGG TAATACTTGC ACTTGCAGGT	1920
GTTTCTGCAT AGTAGGAAAT GTAAAGTCCT GCTACCATTTC CAAAAAGCC AATCGCACTG	1980
GCAAGCAGCA TAACCGATTT AAAGTTTTTC CCCAGACGCA GGGCAATACT AGCTGGCAAG	2040
ACCATAATGG TCGATAACCAG AAGAGCTCCT GCTGCAGGAA TCATAAGGGC AATAGCCACC	2100
CCTGTCACCA TGTAAAAAAG AATGGACATG GTACGAACTG GCAAGCCATC CACAAAGGCC	2160
GTATCTTCGT CAAAAGTTAA GATATACATA GGACGAAGAA AGAGAAAGGT CAAAATCAAA	2220
ACAACCGCCG CAATGACAAA GAGGGAAATG ACCTGTTCTT CACTGATAGT CACGATCGAA	2280
CCAAAGAGAT ATTGGTCCAA ACTCATTGAA CTCGAGCTTT TACCCTTGCT CATGACAATC	2340
AGAGAAACAG CCAGACCTGT TGACATGAGG ATAGCTGTCC CGATTTCCAT AAAGCTCTTG	2400
TAAACCGTAC GGAGATACTC CAGAAAGACC GCCGCAATCA AGACAATGGC AATAGTAGAA	2460
ACAGTTGGAG AAATCCCCAA AACCAGACCA AAGGCTACAC CTGAAAGTGA GACGTGGCTA	2520
AGGGTATCAC TCATCAAACCT CTGACGACGC AAGATGAGGA AGGTTCCCAA TACCGGTGAG	2580
AAAAGACTCA TAGCAATAAC CGCCAAAAAG GCGCGTTGTA TAAAGTCGTA AGATAATAAA	2640

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CTAAGCATGG	CCCACCTCCT	GGCCATTCTC	ATGAACATPG	AAACAACGCC	ATGGCGAGTC	2700
TTGGTTACGG	ACTAGATGAA	TATTGCGATC	CGCATAATCC	TTAACTTCTT	CAGGGTCATG	2760
GGTAATCATC	AAAACAGCCT	TGCCATGATG	ATGGGCGCTG	TGGTGCATGA	GTTTCGTA AAA	2820
TTCATTTTTA	CTTCCTGCAT	CCATCCCCGT	TGTCGGCTCG	TCTAGGATAA	ACACATCAGG	2880
GTCAGAAGCA	AACATACGCG	CAATTACCGC	TCGCTGCTTT	TGTC CCCCAG	ATAGAGACCC	2940
CAAGCGTTTG	TCTCGATGTT	CCCACATGCC	AACTGAGTCC	AGACTAGCCT	TGATATGCTC	3000
CTCATCATGA	GCATTCAAAC	GACGGAACCA	GCCTTTTCTC	GGATAGCGAC	CCGACTTGAC	3060
AAATTCATAG	ACCGTACTTG	GAAAACCAGC	ATTAAACTG	GCAATTTGTT	GAGGAAGATA	3120
GGCTATTCTC	AATTCCTTAC	CTTGCGTATT	TGCTTTTGAA	ATAGCCACCT	TTCCAATGCG	3180
TGGTTGCAGA	ATTC CAAGAC	TAGCCTTGAT	GAGCGTCGTC	TTAGCCGCTC	CATTTTCCCC	3240
AGTCAAGGTA	ACAAATPCCC	CACTATCAAC	ACAATAATTG	ATATGTTCAA	GAACAGGCTC	3300
CTTATCATAA	TAGAAGGACA	AATCCTCTAC	CGTAATATAT	CTCATTATTT	GATTTCTCCT	3360
ACTAAAGCAG	TCAAAAACCG	CTGAATCACT	TTTTGTTCAT	TTGGAGTAAA	CTGAGTCGCC	3420
ACTTGTFCAT	AGGTTAAAAG	TGTATGCTCA	TGGTGATGGT	GGTGCTCCTC	AGCGATTGGA	3480
CGAGCCAAGT	CAGTCAACTG	ATAAAAAATC	ACACGCGCAT	CTTTAGAATC	TTTAGATGTT	3540
TCCAACATCC	CTTCCTTGAC	CAAAGACTTA	ATGGCCTTGG	TAAGTCCCGC	CTGACTGACA	3600
TTGAGACGAC	GGGCCAATTC	TGAATTTGTT	AAAGATTCCT	CTGACAAGAG	CATAAGGATA	3660
TGCTCCTGAG	TATTGGTCAG	GGCCACCTCG	CTAGTGCAAT	GACCTATTAG	GATTTTCATGC	3720
TGATTTTCCG	CCTGCAAAAT	CACCTCATTC	AAAAAAGCAT	TGATATCCTT	TGCTAGCTGT	3780
CTCATATCTG	ACTCCTTTCC	TTTTAGACTT	CTCTTTTTTA	AGAGAAAAAT	ACTATTCTTT	3840
GACATTTTGT	TTACCAGTTA	ATTATATCAC	AAGCAAAAAA	AGAGTCAAGA	AAAAACGTGA	3900
AAACTAGTTT	CATTCTTGAA	CTCTTCTATA	TTATATTATC	TATTGAAATT	CTTTGACATC	3960
TCCATCATAA	GTCGCCCAAT	CTTTGCTGAA	AAAGCGCTCA	TTCAGATGGT	AAGTCGGAGC	4020
TGGTGTGGGA	TTGGATAGGA	AAGGATCAAC	TGCCTTGTC	AAAGCCAACC	AACCCAACCA	4080
ACCAAGGTGA	ATGGTGTCTC	TCATAAAGAA	AGGCTCCCCG	CCGTCTTAG	AAAAATCTGC	4140
TATATTGGTA	AAACCTTGAC	TTTCTAACTG	GTAGCGAATC	TTCTGCACCG	TTTGTGGTA	4200
CATATCTCT	CGTAGACCAG	CATAGTTCAT	CCATTTTTTA	TTAACAGGTG	GAATGATAAA	4260
AATCGGGTTT	ACCTTAGATT	TAGAAAACCTG	TGTTAAAACC	AACTGCAAGT	CATTATACTC	4320
TGGCGACTTG	AGATAGGTAA	AGCTTTTCTG	AGAATCCTTT	AATTTCTTCA	AATCCTTCTT	4380
GATCTGCTCA	TTATAGAAAT	AATTTTCCAT	TCCCATCTCA	TTATTGGAAG	TATTTTTTTC	4440

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AGCATCTGCT	TTGACAACAT	CTTCTATTGC	CTGATAAGAA	AACTGGTCTG	GCAAGATTTT	4500
TAAATACTTA	GCTACATGCT	TATCGTAGTT	AACATAGCCT	CTAACCGAAA	ACTGACCAAA	4560
AAAGGAAGCT	TGGCGTTCAT	TAAAACGAGC	CAATAATTCA	ATCATTTTCAT	TGTCTGCTGT	4620
CGACAATTCT	TCTTTACTTG	CCAACTTCTG	AACCAGGTCC	TTCATAGCTA	CGTTTGGGAA	4680
CTGTTGCAGT	AAGCGAGTCG	CTGCATATTG	ACTAGCCTGA	TCCCCAGATF	GATGTTTCAG	4740
AAAAGTAGTC	AACTGGTCTC	CATTAAAATA	CTGCTGGAAG	GCTGCTGGAT	CATAGCCATT	4800
TTTACTGAAC	CACGAGGTG	AGATAACATA	CACAACTTGT	TTATTCCTCA	GCTGTGGTAA	4860
CATCTGTTGC	ATTCCAAAAT	ATTGGTTAAG	CGATGCAGCT	CCCCCTGTC	CTAAAAGATA	4920
AGGACGGTAG	GAACGATTGT	ATTTCTCAGC	TAATACCGCA	GGATGAGCAC	CGTCAAAACG	4980
AAGCCATTCA	CTAGAGCCAA	AGAAGGGAAC	AAAACGCACA	TTTGATCAG	ATAGTGCTCT	5040
GACTTTTTGA	CTTCGCTCCT	TAAAATAATC	GATAGTAGTA	GCCACTGCTG	AACGCTTTTC	5100
AGTCCTAGA	TTATGATGCA	TCTCAGTAGG	ATAAAAGAAA	ATGAGCAGAA	AAACCAACAA	5160
ACCAGCGATC	AAGACCGGTC	CGAAGATCAT	CCATAAGCGT	TTAAGCATTT	TGTAGCTCCA	5220
CAATACCAGC	TATGATTTTA	TTAGCTGTAT	TCCAGTCGTC	ACGACCAAAC	TCTGTTACAG	5280
GGACACGAAT	GTCAAAACGG	TTCTCAATCT	CCACAATCAA	CTCAACCGTT	CCCATACTAT	5340
CCAAGACACC	TGCATCAAAA	AGATCTTCAT	CCATCATGTC	AGAAACATCT	TCCATAAACA	5400
ACTCATCAAT	AATTTCAATA	ACTTCTGATT	TGATATCCAT	ATTTTATTTT	CTTTTATTTT	5460
TTAAACCATA	GATTATTCAA	GAATCCAGAA	AAGATTAAGA	ATGACAACAT	GACAACATGG	5520
AAAGTGACAA	CCATGCCAAG	CAACTGAATC	CAGCGATTCT	CAGGTAGGGC	AGCCTTCCCT	5580
GCTTTTTTCC	GTTCCTTATT	GAGCGTTTTT	TTCTTGCGAA	CCCAGGCATC	ATTGATGACC	5640
AAGCCTAGTC	CATGAAAGAG	TCCATAGGCG	ATATAGTACC	AGGTCACACC	ATGCCAAAAT	5700
CCCATAATCA	GCATATTTAC	AATGTAGGCC	ATGCTTGAGG	TTACATTACG	ATTTTAAAG	5760
ACTTTCCTTC	TGGTTAACAC	CATCACCATT	CGCATAAAGA	CAAAGTCACG	GAACCAGAAG	5820
GACAGACTCA	TATGCCAGCG	ATTCCAAAAC	TCCTTTAAAT	CCCTTGATAA	AAAGGGCTTG	5880
TTAAAGTTGA	TAGGGCTACG	GATTCCCATC	AAGTTTGAGA	TGGCCAAAGC	AAACATAGAA	5940
TAACCTGCAA	AGTCAAAGAA	GAGTTCAGAA	CCAAAAGTAT	ACATAACTGC	CAAGGCATAG	6000
AGATTAAGA	AGCCACCTGA	CTGCAAGGCT	AAATCTTCA	GAGGAGGTAG	TAAGGTCTCT	6060
CCTAAAACAT	GAGCTAGGAT	AACTTATAC	AAAAGCCCC	ACATGATATA	GCGGACAGAT	6120
TCATCCAGCA	TATCCATCAA	CTCATCTCGC	TCAGGAATAG	CCTGATAATT	TTTATTAAAT	6180

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CGCTTAAAGC	GATCGATTGG	ACCACTCGAG	AAAGTTGGCA	TGAAGAGAAG	GAAACGGAGG	6240
AAT'TCCCAGA	GGGTAAAATC	CTTAATCACT	CCATCTCTCA	GCTCGATGAC	AAT'TCCAACC	6300
GAACGAAAGG	TCAGGTAAGA	AAT'TCCCAAG	AACCCAAGCA	AAGACTGCGT	TCCATTGATA	6360
GCTGGTTGCA	CCTTGACAAA	GATAATCGGA	AGTAGGGACA	GAAAACCTAAC	TAAGTAGAAG	6420
ACCCACTTGC	CATCCTTGCT	TTTTTCGATAA	TGCTTGTAGA	AAAGCAGGAG	CAATATTTCC	6480
CAGCAAAGGT	AAATACCCAA	GGCAGCTAGT	TGATTGGTCT	TTCCACCCAC	CAACATGGTG	6540
ACAATAAAGA	AGAGACTTAC	CAACACTTCA	TACCAGGCAA	AGCGTTTCTT	GAAAAAGAGA	6600
CCTATAAAGA	TGGGCAAGGT	TGCAGCAATC	ACATAAACAA	AATACTGAGG	ATTGCCATAT	6660
GGCTCTAAAT	GAGGAAGCTG	TTGAAAAAAC	TCCATCATCT	CTTATTCACC	TCGTTAATCA	6720
ATCCTTTGAT	GTCAATCTTT	CCATTTGGAG	TTAGTGGCAA	ACTGTCTCGG	TAAAGGAATT	6780
TAGATGGCAT	CATATAGGAC	ATCATGATGT	CTGTCAGGTC	TTCCCTTGATG	GCCTTGGTAA	6840
TATCGATATC	TCGCTCAAAC	TGCTCACGAA	CACCGTCTTT	TAAGATGACA	TAAGCCAATA	6900
GATTTTGTAC	CTTGTGGTCC	TTGTTATAGC	GCGTACTGTC	GACAGCAGAT	TCGATAAAGC	6960
GAGACTTGTT	GAGGTTTTGA	GAGACATCTT	CTAACTCAAT	GCGGTAACCG	TTAAACTTAA	7020
TCTGGAAGTC	CATGCGTCCG	CCGTAGAGAA	GCAAGCCCTC	ATCTGTCATG	GTTCCACAT	7080
CGCCTGTGTG	ATAGGCTGGC	AGATCTTCAA	ACTCAAAGAA	GGCTTCTGCT	GTTTTTTCAG	7140
GAT'TGTTTCA	ATAACCTTTT	GAAACAGCTG	GCCCAGAAAC	AATGATTTCT	CCCTGCTCAC	7200
CATTTGGCAG	TTTATTTCCCT	TCCTCGTCAA	TGATAAAGGT	TGGAGAATCA	GCCTTGGTAT	7260
AGCCGATTGG	TAGGCGTTTG	AGAGTCGCTA	ACATCTCGTC	TGTCACGGCA	ACTGCTGACA	7320
GAGCTACTGT	CGCTTCTGTT	GGGCCGTAAG	CATTGATGAT	ACGGGCATTT	GGGAAACGCT	7380
CGCGCAGTTT	TTGAGCTGTT	TTGACCGTCA	ATTCTTCACC	ATCAAAGTAG	AAATGCGTGA	7440
TTCCAGGCAT	TTTCTCACTG	TTGAAGTATP	CAGACAACAT	GGCCATATCT	GCAAAGGATG	7500
GTGTTGATGT	CCAGATAGCG	ATTGGCAATG	AAAAGATAGC	CGCAAAGAGT	TGCTTAAACT	7560
CCTGAGTGAT	GACTIONAAGGA	AGAGTGAAAA	GCGTACCACC	AAGTGCCAAG	GTCGGTGCCC	7620
AATACATGAC	AGACAAGTCA	AAAGAATAAG	GTGGCTGTGC	CAGCATTGTC	GGACGACTCG	7680
GTGTCGCAAA	TTCTTATCC	GTAATCATCC	AGTTTGTAAG	GCTGAGGAGA	TTATCATGTG	7740
AAATCTGCAC	TCCCTTAGGC	TTACCAGTCG	TACCAGAAGT	AAAGATAATG	TAGTAATTAT	7800
CATCTCCCTT	GACTIONGATGC	GTGATTTTCA	AGTTATTTCC	TTGGGCAAAG	GCTTCTTGAA	7860
CCTGAGCTAG	ATTTATCATT	GGTGTAGAAA	CCTGCTCCAA	GGGAAAGGCT	GAAATGGCAA	7920
TAATCAAGCT	TGGCTCTGCT	ACTTCTAAAA	TAGCTGAAAC	TCGCTCCAAG	GCCGAATGGC	7980

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TATCAATTGG	AATGTAGGCA	TGACCTGACT	TAGTCAGCGC	TACAAAGGTT	GCCAACATTT	8040
CATATTCCTG	GCCACCAAAA	ACAACCACAG	GAGACTTCTC	AGGCAAGCCT	AGTTGGTCAA	8100
TGACTGCAGC	CAAACATATCC	GAATCAGCCT	TTAAATCGCC	ATAAGTGTGT	TCCTGCCCCA	8160
AAACATTATA	GACAGGATAG	CTAGGCTGTG	TCTGAGCAAA	ATGCTCAATG	GTTTCAATCA	8220
TATCTGCTAT	TGGTTTATTT	GACACAATAG	GGATTCTCCT	TCAAGTTAAA	ATTCATTATA	8280
GATAAAGCTT	CCTTGACCCT	GACCAAGATA	GCTAAAGAAG	TAAAGCAGCC	CTAGAAAGAT	8340
AAGAAAATAC	AAGGCTGTCC	GACCAAGAAA	GAGGTACAAT	TCTTTTCTCT	GTTTCATCAA	8400
GAAAAACCAT	TCATTTCTGT	AATTTTTTCGC	TAAAATAAGA	GTGATTCTTA	CTAGCTTATT	8460
TTTCTACCAT	TGTACCACTT	TATATAGTAT	CTTTTCAATT	GTTTACCGTA	TGTTTCCAAT	8520
AGATTTGAGC	TTATTTAAG	GATTATACAG	TTTTTCTATG	TATATTTTCA	AATAGAGTGA	8580
TCCTGCTTCA	AAACTCCATT	TCAGGAGACA	ATGAAGTAAA	TCTTCCCATA	ATAAAACACA	8640
CAATATCAAG	TTTTTTCAAC	ACCTGATACT	ATGCGCTTTT	CTGATTTTFA	AAGACTTTTT	8700
AACCACTCTC	TCATTTAAAA	TAATCTCGTC	TGATATAAAT	TAAAATAGCT	TCTATCATCA	8760
GACAAATGGC	TGATAGCCAA	AAACTGATGC	TAATACCAA	ACTCTCAGTA	ATATAGCTCA	8820
TTAGCAAAAC	AAATACTGAA	AATGCTAATG	TAGAAATCAC	TTCFAAGAACG	GAATAGACAT	8880
TAACTAAATG	ATTTTCTCT	ACTGTTTCT	GAAGAAATAC	ACTTTCAGGA	ACTTCTTTTA	8940
GTTGCGATAA	CATACCAACT	AAAGCTGAAA	ATAATAAAAA	CATCTGTGCG	TTTGGAAAAT	9000
ATAGAATAGT	CAGTGTCACT	ATTTCCATAG	CTACAAGAGG	AAAAAGAATA	CTTTCCCCC	9060
AAATCATTCA	TACCTCTCTC	AACTAGATGT	AACTTACAAA	ACCCCTGACC	TCATGAGCCA	9120
CTTTCTTCCT	CCTCATGAGG	TCAGTTTAC	TTTCTGCTGT	TCCAGTATCG	TTTTTCTTCG	9180
CTAGATTTCC	TCAAAAGGGC	AGACTCCTCC	CTTGGTGCCT	CACACGATTT	TTTCATCTCG	9240
ACTGTCTTTT	AATGCATCAT	TAACGACGCT	TTTCTTCTAG	GTGGTTCATA	AGGAACAGGA	9300
AGATTCAGGT	TGACTTTTCT	AATCCTAGAA	TAAAGTGCTG	AAAACAATTC	GGAATAGGCA	9360
TAGAGACTAG	ACAATTTGAG	GAGCTGCTTG	CGTCTGTTC	GAACACATTT	TCCCACCACG	9420
TGAAGAAAAA	GATGGCGGAA	GCGTTTGATT	GTTAAAGTTT	GGAAGTCACC	TCCAGCTAGA	9480
TGTTTGAGAA	AAAGATAGAG	ATTGTAGGCG	ATACAGCTCA	TCATCATACG	AACTTCGTTT	9540
TTGATTAAGG	TTGAACTATC	CGTTTTATCG	CCAAAAATC	CCTCCTTCAT	CTCCTTGATG	9600
AAATTCCTCG	CTTGACCACG	TCCACGATAA	AGCTGAAACT	GGTCTTGGcT	gTTCCACTCG	9660
TCATATTTGT	AACGAGAGAA	ATAACATCGT	AGAACAAGTA	TCCTTCTTTT	C	9711

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(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3025 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CCCCTTTGTC AAAACTGTAA AATTAACGAC TCAACAATTC ATCTTTACAC CAATCTCAAT	60
GGAAAACAAA AACAAATTGA CCTCTGTCAA AACTGCTATA AGATTATCAA AACAGATCCT	120
AACAATAGCC TCTTCAAAGG TATGACGGAT CTGAACAATC GTGACTTCGA TCCCTTTGGT	180
GATTTCTTCA ATGATCTAAA CAATTTGAGA CCTTCTAGCA ATACTCCTCC TATTCCCCCA	240
ACCCAATCAG GTGGAGGTTA CGGTGGAAAC GGCGGTTATG GTTCCCAAAA TCGTGGATCT	300
GCTCAAATC CGCCACCTAG CCAAGAAAAA GGCCTGCTGG AAGAATTTGG TATTAATGTA	360
ACTGAAATG CCCGTCGTGG AGACATTGAC CCCGTTATG GCGCGACGA TGAGATTATC	420
CGTGTATCG AGATTCTCAA TCGTAGAACC AAGAATAATC CTGTCCTTAT CGGTGAACCT	480
GGTGTGCGAA AACCGCCGT TGTCGAAGGT CTAGCTCAGA AAATGTGCGA TGGCGATGTG	540
CCACATAAAC TCCAAGGTAA ACAAGTCATC CGTCTGGATG TGGTTAGCTT AGTCAAGGA	600
ACGGGGATTC GAGACAATT TGAAGAACGC ATGCAAAAAC TCATGGAAGA AATTCGCAA	660
CGTGAAGACA TCATCCTCTT TATCGATGAA ATCCATGAAA TTGTTGGTGC TGGTTCTGCG	720
AGTGATGGTA ATATGGACGC AGGAAATATC CTCAAGCCAG CCCTTGCTCG TGGAGAACTG	780
CAACTAGTCG GTGCTACTAC CCTCAATGAA TACCGTATCA TTGAAAAGGA TGCTGCCCTC	840
GAGCGTCGTA TGCAGCCTGT TAAAGTCGAT GAACCAACGG TGGACGAAAC AATCACTATT	900
CTCAAAGGGA TTCAAAGAA ATACGAAGAT TACCACCACG TTCAATATAC AGATGCTGCG	960
ATTGAAGCAG CTGCAACTCT TTCCAATCGC TACATCCAAG ATCGCTTCTT GCCTGACAAG	1020
GCCATTGACC TCCTAGATGA AGCTGGTTCT AAGATGAACT TGACCTTGAA TTTTGTGGAT	1080
CCTAAAGTAA TTGATCAGCG CTTGATTGAG GCTGAAAATC TCAAGTCTCA AGCTACACGA	1140
GAAGAAGATT TTGAGAAGGC GGCTACTTTC CGCGACCAGA TTGCCAAGTA TAAGGAAATG	1200
CAAAAGAAAA AGATCACAGA CCAGGATACT CCTAGCATCA GCGAGAAAAC TATPGAGCAC	1260
ATTATCGAGC AGAAAACCAA TATCCCTGTT GGTGATTTGA AAGAGAAAGA ACAATCTCAA	1320
CTCATCCATC TAGCCGAAGA TCTCAAGTCT CATGTTATTTG GTCAAGATGA TGCAGTCGAT	1380
AAGATTGCCA AGGCTATTTC CCGTAATCGT GTCGGACTTG GTACCCCTAA CCGCCAATC	1440

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GGAAGCTTCC TCTTCGTTGG GCCAACTGGT GTCGGTAAGA CAGAACTTTC CAAACAAC TG 1500
 GCTATCGAAC TTTTGGTTC TGCTGATAGT ATGATTCGCT TTGATATGAG TGAATACATG 1560
 GAAAAACATA GTGTGGCTAA GTTGGTCGGC GCTCCTCCAG GTTATGTTGG CTATGATGAG 1620
 GCTGGTCAAT TAACTGAAAA AGTTCGCCAC AATCCATATT CTCTCATCCT TCTCGATGAA 1680
 GTGGAAAAAG CTCACCCAGA TGTATGCAC ATGTTTCTTC AAGTCTTGA CGATGGTCGT 1740
 TTGACAGACG GGCAAGGACG CACCGTTAGC TTCAAGGATG CCATCATTAT CATGACCTCA 1800
 AATGCAGGTA CAGGAAAGAC CGAAGCTAGC GTTGGATTTC GTGCTGCTAG AGAAGGACGT 1860
 ACCAATTCTG TCCTCGGTGA ACTCGGTAAC TTCTTTAGCC CAGAGTTTAT GAACCGTTTT 1920
 GATGGCATT TCGAATTTAA GGCTCTCAGC AAGGATAACC TCCTTCAGAT TGTGAGCTC 1980
 ATGCTAGCAG ATGTTAACA GCGCCTCTCT AGCAACAACA TTCGTTTGA TGTAACTGAT 2040
 AAGGTCAAGG AAAAGTTGGT TGACCTAGGT TATGATCCAA AAATGGGAGC ACGCCCACTT 2100
 CGTCGGACTA TTCAAGACTA TATTGAGGAC ACAATCACTG ACTACTACCT TGAAAATCCA 2160
 AGCGAAAAAG ATCTCAAAGC AGTTATGACT AGCAAGGGAA ACATTCAGAT TAAATCTGCC 2220
 AAAAAAGCTG AAGTTAAAAG TTCTGAAAA GAAAAATAA TCCTATAAAA AAGGAGTAGA 2280
 AAATGAAAT TTCTGCTTC TTTTTTACT AAAATAACTG TAATTTCTTG ACAGCTTGCC 2340
 CTTTGTCCAT TATGATATAT AGTAGACTGA ATCTGAAATA GTACGAAACA ATTGCTAAAA 2400
 CATTTATAGA AATTAATTTT ACTTTCCCAA TCGATTTGTT CTCATCTTAT TTCAATCTGC 2460
 TATAGTCAAT TGAACAAGA ACAAGACAAA AGAGCCTCAT AAAAGGTATT GCAACTTGGT 2520
 AATACCTTT TGAGGTGCTT TTGATATGA GCCCATGTTT TCTCAATAGG ATTGTACTCA 2580
 GGTGAGTAGG GAGGAAGAGG TAAAAGTTA TACCCAAACT CTTCACACAA GAGTTCTAAC 2640
 TTACCCATTC TATGGAATCT TGCATTATCC ATAATAATAA CCGATGGTGT GGTAAATGTT 2700
 GGTAAGAGAA ACTTCTGAAA CCAAGCTTCA AAAAAGTCGC TCGTCATCGT CTCTTCGTAA 2760
 GTCATTGGAG CGATTAATC ACCATTCATT TGTTAGACCT GCAACCAAAG AAATCTCTCTG 2820
 ATATCTTCTT CCAGATACTT TGCTCTTCT TAACTGACCT TTTAATGAGC GACCATATTC 2880
 TCGATAAAAA TAAGTATCGA ATCCTGTTC GTCAATCTAA ACAGGTGCTA GGTGCTTTAA 2940
 ACTATTAATA TTCTTAAGAA ATAAGGCTAC TTTTCTGGG TCTTGTTCAT AGTAGGTGTA 3000
 GTTCTTTTTT TTTTCGAGTG TAGCC 3025

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4104 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TTTAAGGTTT TAAAAAAGT TTTCGAAAGG TTTCTTCTTT ATTTTTTAAG GGAGAGATAA	60
CGTTGATATC TAAATCGTGG TCAAAGCCGG CAATTTTCC TTTAGATGTG TATTGGTGAA	120
TATCATAATC TAAATCAGTT TTAGGACTGC TCTCCAAAA TCCTGAGTCT GAGCCGTAGA	180
CGGAATCCAA ACAGAGGTAA ACTTGCCTGT ATCAATACTG TGTCTTCCA TGAAGTAGAC	240
ACCAACGTAG ATGCCGATGT TTTTAGCACC CAGTGATGCT AGTTTTGCTC GAAAGTTTC	300
GACACCTCG TTCATATFAG ACATGGTFTT GTCTTCCACG TCAAGCCAAT AGTAACTAGG	360
GCTGTAAGGA GAGGCAGCAT TGTAGAAAA TTCGGCAGCC TTTTCCATT CTGGGACT	420
TTTTCCAGCT ACATAAGCGT AGACAGCAAC TGGGACATTC CGCTTTTGAA GTTCAGTGAT	480
ATGACTCTTA TAGGCCTTGT CTATTCCATT GATAAATGAA GCATCATTTT CTTTGTGCGT	540
TTGAGCACCA CTGTGAACAC GAACAATAGC ACCTGAAATA TTTTGTGAGA GGCATCGTA	600
GTTGATTTCC TCAGGACGCT GCCAGCCAGA GAGGTCAATA ATCGGTTTGT CTAAGTGT	660
CAAAGCCTGT GCTTCAATCT GTGCTATATT GGATTTTGT TAAACGATT GGCTGTCATT	720
AAGTGGCGCA TTGATGATTA AAATGAACAT CATAATCCCA AAAAACTAA ATAAAATAAG	780
TGGATGAATT TGTTTTCTCA TATCTTATAA TTCTACCCTA AAAATCAAAA AAAATCAAAA	840
AAATGGGTTA AGGAAGAGAC TTTAGAGCAT TTTTTCATTC AAGAGTGCGG AATGATTTGA	900
AATATGGTAT AATAAAGGG AATTTCTACA GAAAAGAGAA GATTATGTCA AATTTGCCA	960
TTATTTTAGC AGCGGGTAAA GGGACTCGCA TGAAATCTGA TTTGCCAAAA GTTTTGACA	1020
AGGTTGCGGG TATTTCTATG TTGGAACATG TTTCCGTAG TGTGGGAGCT ATCCAACCTG	1080
AAAAGACAGT AACAGTTGTA GGACACAAGG CAGAATTGGT TGAGGAGGTC TTGGCTGGAC	1140
AGACAGAATT TGTGACTCAA TCTGAACAGT TGGGAACCTG TCATGCAGTT ATGATGACAG	1200
AGCCTATCTT AGAAGTTTG TCAGGACACA CCTTGGTCAT TGCAGGAGAT ACTCCTTTAA	1260
TCACTGGTGA AAGCTTGAAA AACTTGATTG ATTTCCATAT CAATCATAAA AATGTGGCCA	1320
CTATCTTGAC TGCTGAAACG GATAATCCTT TTGGTTATGG ACGAATTGTT CGTAATGACA	1380
ATGCTGAGGT TCTTCGTATT GTTGAAGAGA AGGATGCTAC AGATTTTGAA AAGCAAATCA	1440
AGGAAATCAA CACTGGAACA TACGTCTTG ACAACGAGCG TTTGTTGAG GCTTTGAAAA	1500
ATATCAATAC CAATAACGCT CAAGCGAAT ACTATATTAC AGACGTCATT GGTATTTTCC	1560

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GTGAACTGG	TGAAAAAGTT	GGCGCTTATA	CTTTGAAAGA	TTTTGATGAA	AGTCTTGGGG	1620
TAAATGACCG	TGTGGCGCTT	GCGACAGCTG	AGTCAGTTAT	GCGTCGTGCG	ATCAATCATA	1680
AACACATGGT	CAACGGTGT	AGCTTTGTCA	ATCCAGAAGC	AACTTATATC	GATATTGATG	1740
TTGAGATTGC	TTCGGAAGTT	CAAATCGAAG	CCAATGTAC	CTTGAAAGGG	CAAACGAAAA	1800
TTGGTGTGA	GACTGTTTTG	ACAAACGGTA	CTTATGTAGT	GGACAGCACT	ATCGGAGCAG	1860
GAGCGGTCAT	TACCAATTCT	ATGATTGAGG	AAAGTAGTGT	TGCAGACGGT	GTGATAGTCG	1920
GTCCTTATGC	TCACATTCGT	CCAAATTCAA	GCTGCGGTGC	CCAAGTTCAT	ATTGGTAACT	1980
TTGTTGAGGT	GAAAGGATCT	TCAATCGGTG	AGAATACCAA	GGCTGGTCAT	TTGACTTATA	2040
TCCGAAACTG	TGAAGTGGGA	AGCAACGTTA	ATTTCCGGTGC	TGGAACATAT	ACAGTCAACT	2100
ATGACGGCAA	AAACAAATAC	AAGACAGTCA	TTGGAAACAA	TGCTTTTGT	GGTTCAAATT	2160
CAACCATTAT	TGCACCAGTA	GAACTTGGTG	ACAATTCCT	CGTTGGTGT	GGTTCAACTA	2220
TTACTAAAGA	CGTGCCAGCA	GATGCTATTG	CTATTGGTCG	CGGTCGTGAG	ATCAATAAAG	2280
ACGAATATGC	AACACGTCTT	CCTCATCATC	CTAAGAACCA	GTAGGAGCCT	ATCATGGAGT	2340
TTGAAGAAAA	AACGCTTAGC	CGAAAAGAAA	TCTATCAAGG	ACCAATATTT	AAACTGGTCC	2400
AAGATCAGGT	TGAATTACCA	GAAGGCAAGG	GAAGTCCCA	ACGGGATTTG	ATTTTCCACA	2460
ATGGGGCTGT	CTGTGTTT	GCAGTAACGG	ATGAACAAAA	ACTTATCTTG	GTCAAGCAGT	2520
ACCGCAAAGC	TATCGAGGCT	GTCTCTTACG	AAATTCAGC	CGGAAAATTG	GAAGTAGGAG	2580
AAAACACAGC	CCCTGTGGCA	GCTGCCCTTC	GTGAATTAGA	GGAAGAAACA	GCCTATACAG	2640
GGAAATTAGA	ACTCTGTAC	GATTTTTATT	CAGCTATTGG	CTTTTGTAA	GAGAAGTTAA	2700
AACTATATTT	AGCAAGCGAT	TTGACAAAAG	TGGAAAATCC	GCGTCCGCAG	GATGAGGATG	2760
AAACCTTGA	AGTCCTTGAA	GTGAGCTTAG	AAGAAGCGAA	AGAATTAATC	CAATCAGGTC	2820
ATATCTGTGA	TGCCAAGACA	ATTATGGCTG	TTCAGTATTG	GGAGTTGCAG	AAAAAATAGA	2880
GGAGGTCAGT	ATGGGTAAAT	CTTTATTAAC	GGATGAAATG	ATTGAAAGAG	CTAATAGAGG	2940
CGAAAAAATT	TCAGGTCTC	CTTTGCTAGA	TGATAATGAG	GAAACTAAGA	TTTTACCAAC	3000
CTCTCTCTCC	CGTTTTGGTT	ATGCCAATCC	TAAGGATCAT	GGTTTTAGCC	AGGAAACCTT	3060
GAAGATTCAG	GTCGAACCAT	CTATTCATAA	AAGCCGTCGT	ATTGAAAATA	CCAAGAGAAA	3120
TGTCTTCAAT	TCTAAGTTGA	ATAAAATCTT	ATTTGCGGTC	ATCTTCTCT	TGATTTTGCT	3180
TGTTTTAGCA	ATGAACTTT	TGTAATAGAA	AAGGAATTGA	AATGAAAATA	GGAATTATTG	3240
CTGCTATGCC	AGAAGAACTG	GCTTATCTGG	TCCAGCATTT	AGATAATGCC	CAGGAGCAAG	3300

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TTGTTTTTGG GAATACCTAT CATAACGGAA CCATTGCTTC TCATGAAGTC GTTCTTGTAG	3360
AAAGTGGAAAT TGGTAAGGTC ATGTCTGCTA TGAGTGTGGC GATTTTGGCT GATCATTTCC	3420
AGGTGGATGC CCTTATTAAT ACGGGTTCAG CTGGGGCAGT AGCAGAAGGT ATCGCTGTTG	3480
GGGATGTCTGT GATTGCTGAC AAATTAGCCT ATCATGACGT GGATGTCACA GCTTTTGGCT	3540
ATGCTTATGG ACAAAATGGCG CAACAACCGC TTTATTTCTGA ATCAGACAAA ACCTTTGTTG	3600
CTCAAATCCA AAAGAGTTTA TCTCAATTGG ACCAAAACCTG GCATCTTGGT TTGATTGCTA	3660
CAGGAGATAG TTTTGTGCA GGAAATGACA AGATAGAAGC GATTAAGTCC CATTCCCAG	3720
AAGTTTTAGC CGTGGAGATG GAGGGGGCAG CTATTGCTCA AGCAGCGCAT GCCCTCAATC	3780
TCCCAGTCTT AGTCATCCGA GCTATGAGTG ACAATGCCAA CCATGAAGCA AACATCTTTT	3840
TTGATGAGTT TATTATCGAA GCTGGACGTC GCTCTGCCCA AGTCTTGTG ACCTTTTGA	3900
AGGCTTTAGA TTAAGCGGAA ATTTGACAGT TTTTCTAGCT TATGATAAGA TTTAAGTAAA	3960
GAAAAGCTAG AAAACGTTTC AGAGGATATT ATGAGTATTG AAATGACCGT CAGTGAGATT	4020
GCAGAGGTCT TAGGATTATC TCGCCAAGCA ATCAATAACC GTGTCAAAGA ATTACCAGAA	4080
GAAGACACAG ATAAAAATGA CAAG	4104

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8876 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CACGGATAGG CTCGGCTTTC ATCAGTCCTC AGGCTGATTT ACTAATAGCA ACTTTCCTCG	60
ACAAAGTCCA CAGCGATACG TnTGGGTATC AATCCTACGC TTACGCTGAT ACCTTTGCTG	120
GCAGGATTGG CAACGATAGA GCTTGATTGG CTTGGAGTTA CTATTGGGCA AGGATGGTAC	180
AAACCGTAAT CCATCCACTG CTTTCAACAG TTCCTTAAAA TCCCAGATCCT TGTGTTGATA	240
GCCTTTCCCT TGAAAATAGA GGTGATAATG ACAGAGTTCA TGTCGGACAA TTTTCCTAAA	300
AACGTCCAAC CCCAGTTCCT GATAAACCTT GGGATTAAAA TCCAAATGCC CATCTTTGGG	360
GAAAAATCGC CCACCTGTCG AACGTAGACG CCTATTCCAC TGGACATGAT GGATAAAAGG	420
TCTGCCGAAG TCTTCTAGTG AAACCTGCTT GACGTAATCA GTCAGTTTCA TTTGGAGCTA	480
GGAGAGACAG ATTAACTTTT TCACGTTTCTG TATCAATTTT CTTAACCCAA ACGCTCACCA	540
AATCTCCAAC TGCCACCACT TGACTAGGGT GTTTGATAAA CTGCGACTC ATATGGGAAA	600

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TATGGATGAG	ACCGTCCTCA	TGAATCCGA	TATCAACAAA	AGCACCGAAA	TCAACAACGT	660
TACGCACCAC	TCCTTCTAGC	TTTTGTCCAA	CCACTAAGTC	CTTGATATCT	AGGACATCTT	720
GGCGAaCACA	GGTGCGTCAA	AGGAATCACG	GAAATCTCGA	CCTGGTTTGA	GAAGATCTGC	780
AATGATATCT	TTAAGAGTTT	CTGGACCAAG	GTCTAACTCT	TGCGCCATTT	CCTTGACTGA	840
AAGCGACTTG	AGTTTGCTTT	GGCCTCTTC	GTTTAGGTCT	TTAATATCTA	AACGTTTGAA	900
GAGTTCCTTA	ACTGCAGTGT	AATTCCTGG	GTGAACTCCT	GTATTATCAA	GGATATTGCT	960
ACTTTCAGGG	ATACGAAGGA	AACCAGCAGC	CTGCTCAAAG	GCCTTGGCTC	CCAGACGAGG	1020
AACTTCTTG	ATTTGGGCGC	GTGAAGTGAT	TTTTCTTCT	TCCTCGCGGT	ATTTGACAAT	1080
ATTTTCAGAG	ATAGTTTGT	TGAGTCCAGC	TACGTGTGAA	AGAAGAGCTG	GGCTAGCTGT	1140
ATTGACATTG	ACACCAACTT	GGTTAACCAC	TGTATCGACA	ACAAAGTCCA	GACTCTCAGA	1200
TAGTTCTTC	TGACTGACAT	CGTGTGGTA	TTGACCGACA	CCAATTGACT	TAGGATCGAT	1260
TTTGACCAAT	TCCGCAAGAG	GATCTTGCAA	ACGACGGCG	ATAGAAATGG	CAGAGCGTTT	1320
TTCAACGGTC	AAGTCTGGAA	ACTCCTGACG	AGCAAGTTCG	CTGGCAGAA	AGACAGAAGC	1380
ACCACTTTCA	TTAACGATAA	CATAGCTGAC	TTCAGGGAAA	TCTTTCAGAA	CTTCCGCTAC	1440
AAAAGCTTCA	CTTTCACGAC	TGGCCGTTC	ATTTCCAATG	GCAATAATCT	CTACACCGTA	1500
TTGACCAATT	AAATCTGCTA	AATCTTCTT	GGCTTCTTCG	ATTTGACGAG	CTGATGCTGG	1560
TTTAACAGGA	TAAATAACCT	GAGTTGTCAG	CATTTTCTCT	GTTGCATCCA	CGACAGCTAG	1620
CTTGGCACCT	GTACGAAAGG	CTGGGTCAA	TCCAAGAACC	ACGCGCCCTT	TCAGTGAGC	1680
AACCAAGAGG	AGATTGCGCA	GATTGTCAGA	AAAAAGTTGG	ATAGCTCCTT	CTTCAGCTTT	1740
CTCAGTTAAT	TCTGTCCGAA	TACGACGCTC	GATAGCAGGC	AAGACCTTTT	TCTTAACGGA	1800
TTGCTGAACA	ACTTCATCAA	TATAAGCATT	TTTCACCTTG	AAACGAGTAG	CAAAGAAGGC	1860
AAGAATACGG	TCCGTGCGAT	GTTCAAAACC	GATCTTCAAG	ACACCAAGTT	TCTCCCCACG	1920
ATTGAGAGCC	AAGGTACGAT	AGCCTTGAT	AGTTCCAAC	GTCTCTGAAA	AATCATAATA	1980
AATCTGAAAA	ACCTGCTTTT	CATCAAGACT	TTTATCCTTG	GCTTGAGAAG	TAAGTTTAGA	2040
GTGTCTCAGC	ACTTCTGAT	AAGTCATAGA	ACGCAAGGTC	ACATCTTCCG	ATAAGGCTTC	2100
GACCAAAATA	TCAACTGCAC	CGGTCAAGGC	TTCTTGGCCA	GTCGCAAATC	CTTCACAGAC	2160
GAACTTTTCA	GCTTCTTCT	CTAAGTCAAC	TATATTCTGC	AAAATCAAGC	GAGCAAGAGG	2220
AAAGAGTCCA	GCTTACGGG	CAATGGTTGC	CTTGGTACGA	CGCTTTCTCT	TATAAGGAAG	2280
ATAGAGTTCT	TCAACGTCTG	CTAATTTTTT	GGCAACTAAG	ATAGCTTCTT	CCAATTCCTT	2340

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GGTCAACTTA CCTTGTCTT GAATCTTAGC TAAGACAGCT TCCTTACGGT CATTGAGATT	2400
TGTCAGACTT TTATCCAAAT CAATAATAGC CTTAATCGCC ACCTCATCCA GACTACCAGT	2460
CATGTCCTTG CGATAACGCG CGATAAAGGG AATAGTCGCC CCTTCAGCTG TCAAACCTTAG	2520
AACGGTATCA ATTTGCTTTA ACGTCACTCC CAAATCCTGA GAGATTTTTT CATATTTTTT	2580
ATCCATAAAT CTATTATACC ACAAGCTAAA CGTTTCAAAT TAACTCGTAG AACATTTAAA	2640
AAATATGTAG GAAATAGATT TATATGCTAC AGCGCAATAA CTTGCACCTA AAGAGCATTG	2700
CCACCTTTTT TTAACCAAGC CATGATATCA AAAGTATTTA ATGGATCAGA CATAATAGCC	2760
AGTTCTGGAA GATGTTCCCTG ACCTGGAATA ACACATTGAC TTTTCAAAT TTTATATGGA	2820
CGATTGACTA AAATTAATTT ATTAGAATAA GGAAGATTAT CCATCTTATT TAAAATTTCT	2880
TCACTAGCTG AATCTTTATT ATCAAATTTA AAATAAAGAT TATFCCAATT TATGCGTTTT	2940
TTTCTTTTTT CCCACTTAGT TCGTGCTTCT TCAATACTAG AATAATGTAG AAAATGAATA	3000
TCTATATCTC CTAAGTGCCC CAAAGGATAA ACTTCATGAG TCCAGCTCGG TGAATAAAGT	3060
TCCTCTTCGA AAACAAGTTC TTGTTCCATA TAATAACGAA AATGCTTTGT AAGTTTATAA	3120
TAATCATCAG GAAGAATAAA TAAACCAACA AAAGGTGTTT TATATTGAAA ACCAAGCTGT	3180
TTATAAATTA ATCCTCCAAC ACAATTATTA CTTATAATCG TAAAATCTAA TCTATCAAGC	3240
TCAAGAAAAG GGAAAATTC TTTCTCTGCA GCTATTAACT TATGATAAAC AATATCAGAA	3300
TCTAAATATT CACCGTCATT TTTTAACCAA GCACTAAAAT TTGCCAATTC TTGAATATAT	3360
TGTTTTTCG CTCTTTCTAT ATCATAGTTT TCTAAGACGG CGCAATCTTT GATTCTATTT	3420
TCATAATTTT CTAATATGAT TTTGTAGGAG TCTTTTAGAG GTTTAGCATC TATAACAGGT	3480
TTATAGATAT ATGTCGGGAA ATTAATATAG GTTGCAGTTT TAGAGTGAAT ATAAAGTCTC	3540
CAAATAAGGT TGTTTATATC AAATTGATTT ATTTTTCGTA AAAGCTTACT ATTGAATAAT	3600
TTFCAAATA ATGAGCGATA TTGTTTTCTA ATFCGATGAT CTGTATCATC CATCTTTTGT	3660
AAAACCTGAA CATTCGTAA ATTTTCTGTC AACCAATTAT CCCCCAAAA AGGATAAAAAG	3720
TAAAATACTC CATCAACCAA ATCAGCAAAA TGACCAAGAA CAACATCAGA ATCGGATAAT	3780
TTTATCGCAT GATACATCTT TTCAAATGTC CAATCAAATA ATGAATCATT TGAAGATAGA	3840
AACGTAATAT AATCTCCTGT AATCATATCA GACAACTCAG CAAAAGAATT CTCATCTATA	3900
ATCTTAATAT TAAATGATAG ATTCATCTGT TGGCTAATGG AAGCTATCTC CTCTGTAGAT	3960
TGATTTACAA TAATAACTTC TATATCTTTT AATGTTTGTG TCTCCACTAT TGACAAAGAC	4020
TCTAATAAAC TATTTTTATC TCCTTGATGT AACAAAACAA CACTAATTGA GTAAGTCAGT	4080
TTGACTACCT CCCATAATTT TCTGATAATG ATTTTCTTTT TATTTAATTA TAGCACAATT	4140

ATGATATATA TCAGGTAATA TCAAGCTATA TTATCTCTTA GCTACTCAAT TTGAAATTTT 4200
 AACTTTTCCC TTTTCCGCAA AATAATAGTA TAATAGAGGT AGAATCTAGA ATCGAGGTAC 4260
 ACCTATGGCT GTCAAATTTA CAAAACGAGA CGACTTGGAC AAGATGTTTG AAGAGTTTGC 4320
 TAAACTCCCT GATTTGAAAC AAGTTACTTT CCCTGATGAC AAAGAGAAAA AAGTCAAAGC 4380
 AGAAAAGAAA AACTAGATGA CTGCTTTTCA ACAACTCCCA TCTAGTGTAC TTCAAACTGG 4440
 AGCCATTTTT CTCTCCATTA TCATTGAAGC CCTTCCCTTC GTTCTGATAG GAAGCATTGT 4500
 CTCAGGGCTG ATTGAAGTTT ATATCACACC TGACAAGGT TATCATTTC TCCCTCGAAA 4560
 TCGTTGGGGG AGAATCTTTT TTGGGACCTT TGTCGGTATA CTTTTCCCTT CTGTGTGAATG 4620
 TGAATCGTC CCCATCATCA ATCGTTTCTT GGAAAAAAG GTTCCAAGTT ACACGGCCGT 4680
 TCCTTTTCTT GTGACAGCAC CTGTTATCAA TCCCATGTGT CTTTTTGCGA CCTATTCTGC 4740
 CTTTGGCAAC TCCTTCCATG TCGCCCTATT ACGAGCTCTG GGTTCCATTC TTGTGGCTGT 4800
 AATACTAGGA ATTTTTCTAG GATTTTTCTG GCAAGAACCG ATTCAGAAA AAAATCGTCT 4860
 GGCTTGTCAT GAGCATGATT TTTCTTACTT GAGTTCGTCA AAAAAAGTTT TTCAAGTCTT 4920
 TGTGCAGGCC ATTGATGAAT TTTTGTGATC GGGGCGTTAT TTGGTATTTG GCTGCCTCTT 4980
 TGCTTCTATA ATACAGGTCT ACGTTCCGAC TCGGATTCTG ACCTCTATCA GTGCGACCCC 5040
 TCTTTTGTCC ATCCTGCTCT TGATGATTTT AGCCTTCTT CTTTCGCTCT GTAGTGAGGC 5100
 GGATGCCTTT ATAGGTGCTT CTCTTCTCTC GAGTTTCGGT TTGGCACCAG TTCTGGCCTT 5160
 TCTCGTCATT GGTCCAATGC TGATATCAA AAATATCTC ATGATGAAAA ATTACTTGAA 5220
 AGCACGATTT ATCAGTCACT TCATAACAAT TGTAACTCTT GTCGTCTTAG TCTATTCTCT 5280
 CTTGATTGGA GTTATCCTAT GATTCGATTT TTAGTTT TAGCTGCTATTT TGAAGTACT 5340
 ATTTACCTCC ATCTGTCGGG CAAACTAAAC CAGTACATCA ACATGCACTA TTCCATCTG 5400
 GCCTATATCT CCATGGTGCT TTCTTTTATC TTGGCTATCG TTCAATTGTA TATCTGGATG 5460
 AAGCAAGTCA AAACCCACAG TCATCTGAAC AGCCGATTAG CCAAGATAAC GAGTATTTCT 5520
 CTCTGGCTA TTCCAATTGT CATCGGCTTA ACTTTCCCAA CTGTTAGCTT GGATTCTCAG 5580
 ACTGTTTCTG CTAAAGGTTA TCATTTCCCC CTATCGGAAG GAACGGATCT AGCCATTCAG 5640
 ACAAGCGAAG GGACGACAAG CCAATATTTG AAACCAGATA CCAGTCTTA TTTTTCAAAA 5700
 TCAGCCTATG AAAAGGAAAT GCGAACGGCG GCGGATAAAT ACTTATCCCA AGATAGTATT 5760
 CAGATCACTA ATGAAAATA TATGGAAGTC ATGGAGGCTA TCTACGACTA TCCAGATGAG 5820
 TTTGAGGCA AGACAATCCA GTTTACAGGC TTTGTCTATA ACGACCCAG TCATGCCAAT 5880

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AGTCAATTTC	TGTTCCGATT	CGGCATTATC	CACTGTATCG	CAGATTCTGG	TGTCTATGGA	5940
TTGCTGACCA	AGGGCAATAC	CCGGCAGTAT	GAAAACAACA	CTTGATAAC	AGCCAAAGGA	6000
AAACTGGTCA	ATCACTACCA	TAAAGAACTC	AAACAAAACC	TTCCAACCTT	GGAAATCGAC	6060
AGCTTTACCA	AAGTCGATAA	ACCAGAAAAT	CCCTATGTAT	ATAGAGCTTT	TTAAGAAAAT	6120
CAAGATAAAA	ACGAACAAGT	TCTCTTCTGA	ATAACAGAAA	AAGAGCCTGT	TCGTTTTTTG	6180
TTATATGAAA	ATTAGTGACT	TGTAGATTTT	CATCTTATAC	CATTCCCAGC	AATACAAGTA	6240
GCTCATAGAA	AATAAGCGAG	CCACTCATTC	ATTAGACTAG	CGATTTCTTT	AGGTGCTTGA	6300
GTATAAAGCT	CATGGCCAAA	GTTTTCTAAA	AAAATAGTAT	CAAATAGTTC	TGGCAATTCT	6360
TTTAGGGCTT	CCTCTCTCCA	TGTAGCTTCA	TTAGGATAGC	GAGGACTAAT	AAACAAGGTA	6420
TCTCCCCTT	CTCTCTTAAA	AGCTTGTATT	TTTCTCCGTA	GcGGAGTATC	GCTTCTATAT	6480
TTTCATAATT	TATAGCCAAC	TCATATCTAT	TATACTCAAC	ATTCCAGTGA	TAAGACTGTC	6540
TTACAGCTTT	CTCCATATTT	TCTGACCAAT	GCTTTGCTTC	AGATTTTCT	TTAGAAGTAA	6600
GAACATCTAA	GTCCGAAACA	ATTTGAGATT	TGATATAATT	TTTAGTTTCC	TCTAACTCTG	6660
TATCCAAAGG	TAAAATCTTA	TCTAAATCTA	GATAGCCACC	ATCCAAAAGA	ATCAGTTTCT	6720
TTACTTCTTC	AAATTCCGAT	GCGAAATAAC	GAGCTAAATC	TCCTCCAAGA	GAATGGCCTA	6780
TCAGACAGAT	AGATTCTTCC	TCTACAATTT	CATTTTTAAA	CCATGATTTT	AATTCTGTTT	6840
CATCTCGAAG	ATGCTTTTCA	TATGGATTTA	GAAAATAGAC	CTGCGAATCT	AGTTCTTGAA	6900
GAAAATCCTT	GCTATGATAG	GCATTGCTTC	CAAACCGCC	AATAAAATAT	TTTTTCATTC	6960
TCTACTTAAT	ACTATGCTTA	TTCATCTTTT	GTTCAAAGAT	AGTTGTGATA	ATCTGACGCA	7020
ATTCTTCGCG	TTTTTTTTTCT	GGAATCTCAC	CACTTGTTTG	AGCTACAGCG	TAGAGTTCAG	7080
GGTATTC AAT	TGAAATGCGT	TTAATCGTAC	GTGTTGTAGC	ATGTTTTCTG	ACAAAAACG	7140
GGATTCGCTT	AATCAAGTCT	TGTGGGACTA	GCGCCAGAAT	CTTCTCAGTA	GTTCTTTTGT	7200
CACTAATATT	AGACATGTA	AGCCTTTTCT	TAATCATTTT	CTGTTCTTTT	TCTGTAAAAT	7260
CTTTTAATTC	CATTGATTA	GTCCTCCTAT	TTTCTCTAAG	TTAAATTATG	TACTAATACA	7320
GATGAAACTA	CAAAGAATAA	ACTTTAAGAA	ATCTTCTCAC	TGATAAGATT	TTAGCATTAG	7380
ACTTCCTGCG	AAACAAAATA	TGGTATAGTA	GTTCTATGAA	TTATGAAGCA	AGTAAACAAC	7440
TAACCTGATG	ACGATTTAAA	CGTCTTGTTG	GTGTTGAGCG	CACGACTTTT	GAAGAGATAT	7500
TAGCTGTATT	AAAAACAGCT	TATCAACTTA	AACACGAAA	AGGTGGACGA	AAACCTAAAT	7560
TAAGCCTAGA	AGACCTTCTT	ATGGCCACTC	TTCAATATGT	GCGAGAATAC	CGCACTTATG	7620
AAGAAATTGC	GGCTGATTTT	GGTATTCACG	AAAGCAACTT	AATCCGTCGG	AGCCAATGGG	7680

1085

TTTAAGTAAC TCTTGTTC AA AGTGGTGTTA CGATTTCAAG AACTCCTCTC AGTTCTGAGG 7740
 ACACGGTAAT GATTGATAGC CATTCCCATC AATATCGTAT CTTTGGACAT AGCCAATAAA 7800
 TGTTTCATTT TTGCGTGGTT TCTGGCTATT AACGATGAA ATAACCCACC AACTTATCAA 7860
 AAATAGAAAT AAAAATCCCTA AGATTACTGT CATATCATAA CACTATTAAA GTTTAACCCA 7920
 CTTATCATT A TCCATGATAA AAGGCTTAGC CAGTCCCTCG CCTGTATAAT CCGCATACTT 7980
 GGTGCCAAA TACTTGTAGC AATCTTCCTT ACTAGCAAAT TTAATCGCTT GGTAGGGCTC 8040
 TTCGAAAGTC AATTTCTCTA CAAATAAGAA ACCGTCATCA GCAGGFACTA AGACCCCAAC 8100
 GTGGCCTACA AACAGATACT CGCCATCCAA ATTGTCGTGC AAGACTACAG ACAGCATTCG 8160
 AGCTTTTTCA TTGAATTGAA ATTGTGAGAA GAATGCTTCC ATCTTTTCAG CGTGAACCTT 8220
 GACATCTGTA GTTGACTCAG TTGGAAGTCT CGAAAATAGA ATATCAAACCT CTTCTTATC 8280
 TTGTGAATCA AAGACCTTTC CTTTATCAAT CGCATCATT TCTAGGAAAA GCAACTGGTC 8340
 ATTCTTTTCA AGCTTTGGAA TGGTGACTGA ATTTTTCAAA AGACAATAAC TATTGATACG 8400
 GCAGTTGGTC CCAACAAAAT CGCCCTTCTT TTGATTCCAG AGATGACTGA TTTTCTCAAC 8460
 ATCGTATTCG GTGTGAGTAA AGGAAGTGAA ATCTCCTGAT AAGCCAGTTG AGCCGACAAT 8520
 GGTATTATAG TCATTAACGA GATTAATAAAA TGCATCAACA CTATTTGGAT CCAAGTGAGC 8580
 TGATAAGAGA GATTTGACCT CTTCTGACT TACCTGGTTG TTTAGGTTGG TGTATGAAGC 8640
 TTTCCATGGA ACTTTCGCTG AACTGCTTTG CCTTTGATTC GTCCCCTCAG AAGTAGCATG 8700
 TTGTGTGTA CAAGCAGCCA AGCCTAAAA CAAGCTGAA CAGATTCCTA ATGTGGCTAA 8760
 TTTTCTTGAT TTCTTCATTT CTTTCTCCTA AATGTCTTGG ATTAAAGTTT CTTTAACTAT 8820
 TGCTTTACAG ATATTGATTA CTTTCTCATT TAATGTGTTT ATCGTCTTTC CTCCGG 8876

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

CGCAAACCTT CGCGGTCGGA AGGTAGTTTT ATGACACGAT TTGAGATACG AGATGATTTT 60
 TATCTCGATG GAAAATCATT TAAGATTTTA TCTGGTGCCA TTCATTATTT TAGGGTTTCT 120
 CCAGAGGATT GGTATCATT C GCTCTATAAC TTGAAGGCTC TTGGTTTAA TACGGTAGAG 180

1086

ACTTATGTTG	CTTGGAATTT	ACACGAGCCT	TGTGAAGGTG	AGTTTCATTT	TGAAGGTGAT	240
CTGGATTTAG	AGAAATTTCT	CCAAATAGCG	CAGGATTTGG	GTCTCTACGC	AATTGTGCGT	300
CCGTCTCCAT	TTATCTGTGC	GGAATGGGAA	TTCGGTGGCT	TACCAGCTTG	GCTCTTGACC	360
AAGAACATGC	GAATTCGCTC	ATCCGACCCA	GCATATATCG	AGGCAGTTGG	TCGCTACTAT	420
GATCAGTTAT	TGCCAAGACT	GGTGCCTCGT	TTGTTGGACA	ATGGTGGCAA	TATTCTCATG	480
ATGCAGGTTG	AAAATGAGTA	TGGTCTTAC	GGAGAAGATA	AGGCTTACCT	GAGAGCGATT	540
CGACAGCTAA	TGGAAGAGTG	TGGCGTAACC	TGTCCCTCT	TTACATCAGA	TGGTCCATGG	600
CGAGCTACTC	TGAAAGCTGG	AACCTTAATT	GAAGAGGACC	TCTTTGTAAC	AGGAACTTT	660
GGTTCTAAGG	CACCTTACAA	CTTTTCGCAG	ATGCAGGAAT	TCTTTGATGA	ACATGGTAAG	720
AAATGGCCAC	TCATGTGTAT	GGAGTCTGG	GATGGTTGGT	TCAATCGCTG	GAAAGAACCG	780
ATTATCACAC	GGGATCCATA	GGAATTGGCA	GATGCAGTTC	GAGAGTTTTT	GGAACAAGGC	840
TCTATCAATC	TTTACATGTT	CCACGGTGGT	ACAACTTTG	GTTTCATGAA	TGGTTGCTCA	900
GCTCGAGGAA	CTTTGACCT	GCCACAAGTT	ACGTCTTATG	ATTACGATGC	CCTTCTGGAT	960
GAAGAAGGAA	ATCCAAGTGC	TAAATATCTT	GCAGTCAAGA	AGATGATGGC	AACACATTTT	1020
TCAGAGTATC	CGCAGTTGGA	ACCACTCTAC	AAAGAGAGTA	TGGAGTTGGA	TGCTATTCCA	1080
CTAGTTGAAA	AAGTTTCTTT	GTTTGAAACC	TTAGATAGCT	TGTCAAGTCC	TGTAGAAAGT	1140
CTCTATCCTC	AAAAGATGGA	GGAGCTGGGA	CAAAGTTATG	GCTACCTACT	TTATCGAACA	1200
GAAACAAACT	GGGATGCAGA	AGAAGAAAGA	CTTCGTATCA	TTGATGGTCG	AGATAGGGCC	1260
CAGCTGTATG	TCGATGGTCA	GTGGGTAAAA	ACTCAATATC	AGACAGAGAT	TGGGGAAGAT	1320
ATTTTTTATC	AAGTAAAAA	GAAAGGGCTA	TCTAGGTTAG	ATATCTTGAT	AGAAAATATG	1380
GGGCTGTGCA	ACTATGGGCA	TAAGTTCTTA	GCGGATACGC	AACGTAAGGG	AATTCGGACA	1440
GGGGTCTGTA	AGGATCTGCA	TTTCTTACTA	AACTGGAAAC	ACTATCCACT	CCCCTAGAC	1500
AATCCTGAGA	AAATTGATTT	TTCAAAAAGGA	TGGACTCAAG	GACAACCAGC	CTTTTACGCT	1560
TATGACTTTA	CAGTCGAAGA	GCCAAAAGAT	ACTTACCTAG	ACTTGCTGTA	GTTTGGTAAG	1620
GGGGTTGCCCT	TTGTCAATGG	GCAGAATCTA	GGACGTTTTT	GGAACGTTGG	CCCAACTCTC	1680
TCACCTTATA	TCCCTCATAG	CTATCTCAAG	GAAGGTGCCA	ACCGCATCAT	TATCTTTGAA	1740
ACAGAAGGTC	AATATAAAGA	AGAGATTCAT	TTAACTCGTA	AACCTACACT	AAAACATATA	1800
AAGGGGGAAA	ACTTATGACA	ATTGTAGGAT	GCCGTATTGA	TGGACGTTTG	ATCCACGGAC	1860
AAGTAGCCAA	TCTTTGGGCT	GGAAAATAA	ATGTTTCACG	CATTATGGTT	GTAGACGACG	1920
AAGTTGTCAA	CAACGATATT	GAAAAGAGTG	GTTTGAAACT	TGCGACACCA	CCAGGTGTGA	1980

1087

AATTGAGTAT	TTTGCCAGTT	GAGAAAGCTG	CAGCCAATAT	TCTTGGTGGC	AAATACGATA	2040
GCCAACGTCT	CTTTATCGTG	GCTCGTAAAC	CAGACCGCTT	CCTTGGTTTG	GTAGAAGCAG	2100
GTGTACCACT	TGAAACCCTT	AATGTTGGGA	ATATGTCTCA	AACACCAGAA	ACTCGTTCTA	2160
TTACACGTTC	TATCAACGTA	GTAGACAAGG	ATGTGGAAGA	CTTCCACAAA	CTGGCAGAAA	2220
AAGGTGTTAA	ACTTACTGCT	CAGATGGTTC	CAAATGATCC	AATTTTCAGAC	TTTTTGTAGCT	2280
TATTAATAATA	GGAAAAAAT	TTTGTAGGAG	TCATTGTTAT	GATACAATGG	TGGCAAATTT	2340
TACTTCTCAC	TTGTACTCA	GCTTATCAA	TCTGTGATGA	GTGACGATC	GTTCATCTG	2400
CAGGTTCCCC	TGATTTTGT	GGTTTCATTA	CTGGTTTAAAT	CATGGGAGAT	GTGACTACTG	2460
GTTTACTTAT	CGGTGGTAAC	TTGCAACTGT	TCGTTCTTGG	GGTGGTACC	TTCGGTGGTG	2520
CTTCTCGTAT	CGACGCAACT	TCTGGTGC	TTCTTGC	ACCTTCTCTG	TTTACAAGG	2580
AATTGATGCA	CCGCTTGCCA	TTACTACAAT	CGTGATACCA	GTAGCAGCTC	TCTTGACTTA	2640
CTTCGACGTT	CTTGGTCGTA	TGACTACTAC	CTTCTTCGCT	CACCGTGTGG	ATGCTGCAAT	2700
CGAACGCTTT	GACTATAAAG	GTATTGAACG	CAACTACTTG	CTTGGTGC	TTCGTTGGG	2760
TCTATCTCGT	GCCCTTCCAG	TCTTCTTTGC	CCTTGCTTTT	GGTGGTGCCT	TTGTACAATC	2820
AGTAGTAGAC	TTGCTTGAAG	CCTACAAATG	GGTGCAGAT	GGCTTGACAC	TTGCAGGACG	2880
TATGCTTCCA	GGTCTTGGAT	TTGCAATCTT	GCTTCGTTAC	CTTCCAGTTA	AACGTAACCT	2940
TCACTACCTT	GCTATGGGAT	TTGGTTTGAC	AGCTATGTTG	ACTGTTCTTT	ACTCATATGT	3000
AACAGGTCTT	GGTGGCGCTG	TTGCTGGTAT	CGTAGGTACT	CTTCTGCTG	AAGTTGCTGA	3060
AAAAATTGGT	TTGCTGAACA	ACTTCAAAGG	TTTGTCTATG	ATTGGTATTT	CTATCGTAGG	3120
TATTTTCCTT	GCAGTGCTTC	ACTTCAAAAA	TAGCCAAAAA	GTAGCTGTAG	CAGCACCTTC	3180
TACACCATCA	GAAAGTGGGG	AAATCGAAGA	TGACGAATTC	TAATTACAAA	CTTACAAAAG	3240
AAGATTTTAA	TCAAATCAAC	AAACGTAGCT	TGTTTACTTT	CCAATTAGGT	TGGAAC TACG	3300
AACGTATGCA	AGCTTCTGGT	TACCTTTACA	TGATCTTGCC	TCAGTTGCGT	AAAATGTATG	3360
GTGATGGAAC	TCCTGAATTG	AAAGAAATGA	TGAAAGTTCA	TACTCAATTC	TTCAATACTT	3420
CACCATTCTT	CCATACCATT	ATCGCTGGTT	TTGACCTTGC	CATGGAAGAA	AAAGATGGTG	3480
TAGGTTCAAA	AGACGCCGTT	AACGGTATCA	AGACAGGTTT	GATGGGACCA	TTGCTCCTC	3540
TTGGGGATAC	AATCTTTGGT	TCACTTGTAC	CTGCTATCAT	GGGGTCAGTC	GCAGCAACTA	3600
TGGCTATCGC	TGGCCAACCT	TGGGGGATCT	TCCTTTGGAT	TGCAGTTGCA	GTAGCGTATG	3660
ACATCTTCCG	TTGGAAACAG	TTGGAATTTG	CTTACAAAGA	AGGGGTTAAC	CTTATCAACA	3720

1088

ACATGCAAAG	TACCTTGACA	GCTTTGATTG	ACGCTGCATC	TGTA CT TGGT	GTCTTCATGA	3780
TGGGTGCTCT	TGTAGCAACA	GTGATTA ACT	TTGAAATTC	TTACAAGTTG	CCAATCGGTG	3840
AAAAGATGAT	TGATTTCCAA	GACATCTTGA	ACCAAATCTT	CCCACGTTTG	CTTCCAGCAA	3900
TCTTTACTGC	CTTTATCTTC	TGGTTGCTTG	GTAAGAAAGG	TATGAACTCT	ACTAAAGCTA	3960
TCGGTATTAT	TATCGTACTT	GCTTTGGCTC	TTTCTGCCCT	TGGTCACTTT	GCACTTGAA	4020
TGTAATTCCT	TATGACTAAA	TCATTAATTT	TGGTGAGCCA	TGGTCGCTTC	TGTGAGGAGC	4080
TTAGAGGTAG	CACAGAAATG	ATTATGGGCC	CACAAGACAA	CATTTACACA	GTAGCTCTTC	4140
TTCCAGAAGA	TGGCCCAGAA	GAATTTACTG	CTAAATTTGA	AGCTGTTATF	GAAGGATTGG	4200
ATGATTTCCCT	AGTCTTTGCG	GATCTTCTCG	GTGGGACACC	TTGTAATGTG	GTGAGTCGCT	4260
TGATCATGGA	AGGTCGTGAT	ATTGACCTTT	ACGCGGGAT	GAATCTTCCA	ATGGTGATTG	4320
AATTTATCAA	TGCAGCCTT	ACAGGCGCAG	ATGCGGACTA	CAAGAGCCGT	GCTGCAGAAA	4380
GCATTGTGAA	AGTTAATGAC	CTGTTAGCGG	GCTTCGATGA	TGACGAAGAT	GAATAACT	4440
CTTCGAAAAT	CTCTTCAAAC	TACGTCAACG	TCGCCCTGCC	GTAGgTATAT	GTTACTGACT	4500
TCGTCAGTCT	TATCCGGCAA	CCTCAAAACG	GTGTTTTGAG	CTGACTTCGT	CAGTCTTATC	4560
CGGCAACCTC	AAAGCAGTGC	TTTGAGCAGC	CTGCGGCTAG	TTTCCTACAG	ATTTTAGTTG	4620
GAACTCGATT	CAATTCATGT	GACAACGTGA	AAATCGTTAG	AGCATTTTAT	ATAGAATATA	4680
CATGGGAATG	TAGCTTACTC	CCATTCCCAT	ATTTAATAGA	AAAAGAGGAA	CTCAATGCTA	4740
CATTATACAA	AAGAAGACTT	GCTCGAATTG	GGTGCAGAAA	TCACTACGCG	TGAAATCTAC	4800
CAACAGCCTG	ATGTATGGAG	AGAAGCTTTT	GAATTTTATC	AAGCAAAACG	TGAAGAAATT	4860
GCAGCCTTCC	TACAAGAAAT	CGCTGATAAA	CATGACTATA	TTAAGGTTAT	CTTGACAGGT	4920
GCTGGGACTT	CTGCTTATGT	GGGAGATACC	TTGCTACCTT	ATTTTAAGGA	AGTCTATGAC	4980
GAACGCAAAT	GGAATTTCAA	TGCTATTGCG	ACAACAGATA	TCGTTGCCAA	TCCAGCAACC	5040
TATTTGAAAA	AAGATGTGGC	AACTGTCCCT	GTGTCTTTTG	CTCGTAGTGG	GAATTCGCCCT	5100
GAAAGTTTGG	C GACTGTGA	TTTGGCCAAA	TCCTTGGTGG	ATGAGCTTTA	TCAAGTGACC	5160
ATTACTTGTG	CAGCAGATGG	TAAATTGGCT	CTTCAAGCTC	ACGGTGATGA	TCGTAATCTC	5220
TTGCTCTTGC	AACCAGCTGT	CTCTAATGAT	GCTGGATTTG	CCATGACTTC	TAGCTTTACG	5280
TCTATGATGT	TGACA ACTCT	CTTGGTCTTT	GATCCTACAG	AATTTGCTGT	TAAGTCTGAA	5340
CGTTTTGAAG	TTGTATCTAG	TCTTGCCCCGT	AAAGTTTTAG	ACAAGGCAGA	AGATGTCAAA	5400
GAGCTCGTTG	ATTTAGACTT	TAACCGTGTC	ATCTATCTAG	GCGCTGGTCC	TTTCTTTGGA	5460
CTTGCTCATG	AAGCTCAGCT	CAAGATTTTG	GAATTA ACTG	CTGGTCAAGT	TGCGACCATG	5520

1089

TATGAAAGCC	CAGTTGGCTT	CCGTCACGGT	CCAAAATCTC	TTATCAACGA	CAATACAGTT	5580
GTTTTGGTCT	TTGGTACAAC	GACAGACTAC	ACTCGTAAGT	ACGACTTGGA	CTTGGTTCGT	5640
GAAGTTGCTG	GTGACCAGAT	TGCTCGTCGT	GTTGTGCTTT	TGAGTGATCA	AGCTTTTGGT	5700
CTTGAAAATG	TCAAAGAAGT	GGCCCTTGGT	TGTGGCGGTG	TCTTGAATGA	TATTTACCGT	5760
GTCTTCCCTT	ACATCGTTTA	TGCCCAACTC	TTTGCCTTAT	TGACTTCACT	CAAGGTAGAA	5820
AATAAACCCAG	ATACACCGTC	TCCTACAGGT	ACAGTAAACC	GTGTAGTACA	AGGTGTCATA	5880
ATTACGGAAT	ATCAAAAGTA	AGACAGTGTT	TATGAATTCT	TGACAAGAGG	ATTTGTAAT	5940
TATCAGATAA	ACCATAGATT	GTCAGTACGC	TTTCTATGGT	TTGTTTGCTT	GAGAGAAATA	6000
GTAAGAGGAG	AACAGAATGA	AAGCATAAC	AGAGCGTGTA	TTTGGAAATG	TTGAGGGTGA	6060
GGATGTCTTG	GCCTATCGAT	TTGAGACAGA	CGGTGGCTAC	CAACTTGAGG	TTATGACTTA	6120
TGGTGCAGCT	ATCTTGCCT	ATGTCGCACC	TGACAAGGCT	GGAAATTTTG	CCAATGTTAT	6180
CTTGGGATTT	GATGACTTTG	ATAGTTATGT	AGGCAATAGT	CCCAAGCATG	GAGCAAGTGT	6240
AGGTCTGTGA	GCGGGTCGTA	TTGCAGGTGC	GACCTTTGAG	CTCAATGGTA	AGACCTATGA	6300
CCTTGAGGTT	AATAATGCTA	GCAACTGTAA	TCACAGTGGT	TCAACTGGTT	GGGATTCAG	6360
CTTGTTTGAA	GTTGAAGAAG	TAAGCGATCA	TGGCTTGACT	CTCTACACAG	AGCGTACAGA	6420
TGGGACAGGA	GGGTTCCTTG	GAAATCTCAA	GATTTGGATC	AGTTATCACT	TGGAAGAAAC	6480
TGGTGCCTAT	GAAATCAGCT	ACAAGGTAAC	GACCGATCAG	GATACGCTGG	TCAATCCAAC	6540
CAACCACAGC	TATTTCAACT	TGTCTGGTGA	TTTCACGCAG	ACGATTGACC	GTCATGTCTT	6600
CCAACTAAAC	ACAGAGGGCA	TTTACTCAAT	CGCTCCTGAC	GGTGTTCCTG	CCAAAACCTCC	6660
AGAAGCCAAC	CGTGATGTGG	TCAAACACGT	CTACAATGGT	ACCTTGTGTA	AGGATATCTT	6720
TGCAGAAGAA	GATGAGCAAA	TCCAGCTGGC	ATCAGGTTTG	GATCATCCAT	TTGCCCTTCC	6780
TGCAGGCCAT	GACAATGCTG	GATTCCTTTA	TGACCAAAT	TCAGGTCGCT	TCCTGCTTTT	6840
CAAGACAGAA	GCTCCTTGCT	TTGTGGTCTA	CACAGCAAAC	TTTGTGGATG	AAAGTGTGAT	6900
CATAGGAGGT	CAGCCAATGC	TACAGCACAA	TGGGATTGCT	CTTGAAGCGC	AAGCTTTACC	6960
AGATGCCATT	CACAGTGACC	TTAAAGGCCA	AGTCATTCTT	AAAGCTGGTC	AAACCTTCAC	7020
CAGTAAGACA	CGTTATGAAC	TTGTTGTGAA	GTAAGAGAGT	CATTGCGCCT	ACTTTTGGGA	7080
GCTAGGAATA	GGTACGCAGA	GACAAATAGT	AGGAAAATAT	GATATAACTA	AGCGTTGAAA	7140
GCTATCTGTT	AATATAATAT	TCAAACCTACA	ATAAGGAGTA	AGAAAGAAAC	GAAGAAAATT	7200
GTATTTGCTA	GTGCCTTGGC	TTTGACCTTG	GCTGGAGCAG	TTTTGACAAA	TGATGTTTTT	7260

1090

GCGAACGACA	GACTTGTGGC	AACACAAACT	ACTGATGGTA	AAAATGAAA	TGTATTGACC	7320
TCAGAGGTGC	TAAAACCTTC	TAGTGGCAAT	GTTTTGGTTG	GAATCAAAGG	AGAATTTGTG	7380
GCTCCTCATC	AACAATCTAT	TTTGGATGCC	ATCAATGCTA	TCTGTAAAGA	AGCGGCTGAC	7440
GAAGGTTTGG	TAGATAAGTA	TGTCCCTATC	AAATGATCAA	CTGACCTAGA	AAAGGCAGCT	7500
TTTGCCAGAG	CTACAGAAGC	ATCTATAACC	ATGGATCATA	CCCGTCTTTC	TAGCAAAGAT	7560
CTTTGGAGTG	CCTTTCCAAC	TTCTAATAGT	ATAATGGGAG	AAAATTTGGC	ATGGAATCAT	7620
GACGGTTTTTC	TAAAAGCTAT	TGAACAATGG	CGTGCTGAAA	AAGCAGATTA	TGTGGAGAAA	7680
AAAATAGTGG	TTCAGACAAC	GGGAAATCTG	GTCACTATGA	GTCGCTAATT	AACCCTAAAT	7740
TTACACACAT	GGGGATGGCA	GCTTTTAAAA	ATCCTAACAA	TCAATACAAA	GCTATTACAA	7800
TTGCTCAAAC	TCTAGGTGAT	GATGCTTCTT	CAGAGGAATT	GGCTGGTAGA	TATGGTTCTG	7860
CTGTTCAGTG	TACAGAAGTG	ACTGCCTCAA	ACCTTTCAAC	AGTTAAAACT	AAAGCTACGG	7920
TTGTAGAAAA	ACCACTGAAA	GATTTTAGAG	CGTCTACGTC	TGATCAGTCT	GGTTGGGTGG	7980
AATCTAATGG	TAAATGGTAT	TTCTATGAGT	CTGGTGATGT	GAAGACAGGT	TGGGTGAAAA	8040
CAGATGGTAA	ATGGTACTAT	TTGAATGACT	TAGGTGTCTAT	GCAGACTGGA	TTTGTAATAAT	8100
TTTCTGGTAG	CTGGTATTAC	TTGAGCAATT	CAGGTGCTAT	GTTTACAGGC	TGGGGAACAG	8160
ATGGTAGCAG	ATGGTTCAC	TTTGACGGCT	CAGGAGCTAT	GAAGACAGGC	TGGTACAAGG	8220
AAAATGGCAC	TTGGTATTAC	CTTGACGAAG	CAGGTATCAT	GAAGACAGGT	TGGTTTAAAG	8280
TCGGACCACA	CTGGTACTAT	GCCTACGGTT	CAGGAGCTTT	GGCTGTGAGC	ACAACAACAC	8340
CAGATGGTTA	CCGTGTAAT	GGTAATGGTG	AATGGGTAAA	CTAGGCTCAG	GCCATAGGTA	8400
AAGCATTCAT	CTTACTTAGC	AAAAAGAATG	AACGATAAGA	AAGAGGTGA	TGGCGAACAT	8460
TGGCCTCTTT	TGATTTATAA	AGATTGGATT	CTTGTCGCCT	CAATTTCAGA	CTTTTCTATT	8520
GTAAGCTAAT	ATTTTATAGC	CCATTAATAAG	CATAAGCGGT	AATCTAATTT	AAAAAATGCT	8580
GTAATTAGTC	TGAAGTCCAC	ACTTACTTGT	TGAGATGTTA	TCTCTGTTTT	TTATCGTTA	8640
AATTTACTGT	ATTTTTTATA	GTATGCAGAA	TATTTTTAAG	TATATTTCAA	TAGAAATPFC	8700
TATCGATTTA	TGTATAATG	ATAAGTAATT	GTTGAAAAGT	ACTCAGAAAA	TTCCATACTA	8760
TATTATTTTT	ATGTTTATAC	TTTTATGCTA	TAAAATATAG	ATTGATATAA	AGAATATAGA	8820
AAAAGCGAGG	TAAATATGAG	CCGAAAAAGC	ATTGGTGAGA	AACGCCATAG	TTTCTCGATG	8880
AGAAAGTTGT	CAGTGGGATT	GGTATCAGTT	ACTGTATCTA	GTTTCTTTTT	GATGAGTCAA	8940
GGGATTC AAT	CGGTATCGGC	CGATAATATG	GAAAGTCCAA	TTCATTATAA	GTATATGACC	9000
GAGGGTAAAT	TGACAGACGA	GGAAAAATCC	TTGCTGGTAG	AGGCCCTTCC	ACAACTGGCT	9060

1091

GAAGAATCAG ATGATACTTA TTA	TTACTTGGTT TATAGATCTC AACAGTTTTT	ACCGAATACA	9120
GGTTTTAACC CAACTGTTGG TACTTTCCTT	TTTACTGCAG GATTGAGCTT GTTAGTTTTA		9180
TTGGTTTTCTA AAAGGAAAA TGGAAAGAAA	CGACTTGTTC ATTTTCTGCT GTTGACTAGC		9240
ATGGGAGTTC AATGTTGCC GGCCAGTGCT	TTTGGGTGA CCAGCCAGAT TTTATCTGCC		9300
TATAATAGTC AGCTTCTAT CGGAGTCGGG	GAACATTTAC CAGAGCCTCT GAAAAATCGAA		9360
GGTTATCAAT ATATTGGTTA TATCAAACT	AAGAAACAGG ATAATACAGA GCTTCAAGG		9420
ACAGTTGATG GGAATACTC TGCTCAAAGA	GATAGTCAAC CAACTCTAC AAAACATCA		9480
GATGTAGTTC ATTCAGCTGA TTTAGAATGG	AACCAAGGAC AGGGGAAGGT TAGTTACAA		9540
GGTGAAGCAT CAGGGGATGA TGGACTTCA	GAAAAATCTT CTATAGCAGC AGACAATCTA		9600
TCTTCTAATG ATTCATTCGC AAGTCAAGTT	GAGCAGAATC CGGATCACAA AGGAGAATCT		9660
GTAGTTCGAC CAACAGTGCC AGAACAAGGA	AATCCTGTGT CTGCTACAAC GGTGCAGAGT		9720
GCGGAAGAGG AAGTATTGGC GACGACAAAT	GATCGACCAG AGTATAAACT TCCATTGGAA		9780
ACCAAAGGCA CGCAAGAACC CGTTCATGAG	GGTGAAGCCG CAGTCCGTGA AGACTTACCA		9840
GTCTACACTA AGCCACTAGA AACCAAGGT	ACACAAGGAC CCGGACATGA AGGTGAAGCT		9900
GCAGTTCGCG AGGAAGAACC AGCTTACACA	GAACCGTTAG CAACGAAAGG CACGCAAGAG		9960
CCAGGTCATG AGGGCAAAGC TACAGTCCGC	GAAGAGACTC TAGAGTACAC GGAACCGTA		10020
GCGACAAAAG GCACACAAGA ACCCGAACAT	GAGGGCGAAG cGGCAGTAGA AGAAGAACTT		10080
CCGGCTTTAG AGGTCACTAC ACGAAATAGA	ACGGAAATCC AGAATATTCC TTATACAACA		10140
GAAGAAATTC AGGATCCAAC ACTTCTGAAA	AATCGTCGTA AGATTGAACG ACAAGGGCAA		10200
GCAGGGACAC GTACAATTCA ATATGAAGAC	TACATCGTAA ATGGTAATGT CGTAGAACT		10260
AAAGAAGTGT CACGAACTGA AGTAGCTCCG	GTCACGGAAG TCGTTAAAGT AGGAACACTT		10320
GTGAAAGTTA AACCTACAGT AGAAATTACA	AACTTAACAA AAGTTGAGAA CAAAAATCT		10380
ATAACTGTAA GTTATAACTT AATAGACACT	ACCTCAGCAT ATGTTTCTGC AAAACGCAA		10440
GTTTTCCATG GAGACAAGCT AGTTAAAGAG	GTGGATATAG AAAATCCTGC CAAAGAGCAA		10500
GTAATATCAG GTTTAGATTA CTACACACCG	TATACAGTTA AAACACACCT AACTTATAAT		10560
TTGGGTGAAA ATAATGAGGA AAATACTGAA	ACATCAACTC AAGATTTCCA ATTAGAGTAT		10620
AAGAAAATAG AGATTAAAGA TATTGATTCA	GTAGAATTAT ACGGTAAAGA AAATGATCGT		10680
TATCGTAGAT ATTTAAGTCT AAGTGAAGCG	CCGACTGATA CGGCTAAATA CTTTGTAATA		10740
GTGAAATCAG ATCGCTTCAA AGAAATGTAC	CTACCTGTAA AATCTATTAC AGAAAATACG		10800

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GATGGAACGT ATAAAGTGAC GGTAGCCGTT GATCAACTTG TCGAAGAAGG TACAGACGGT 10860
TACAAAGATG ATTACACATT TACTGTAGCT AAATCTAAAG CAGAGCAACC AGGAGTTTAC 10920
ACATCCTTTA AACAGCTGGT AACAGCCATG CAAAGCAATC TGTCTGGTGT CTATACATTG 10980
GCTTCAGATA TGACCGCAGA TGAGGTGAGC TTAGGCGATA AGCAGACAAG TTATCTCACA 11040
GGTGCATTTA CAGGGAGCTT GATCGGTTCT GATGGAACAA AATCGTATGC CATTTATGAT 11100
TTGAAGAAAC CATTATTTGA TACATTAAT GGTGCTACAG TTAGAGATTT GGATATTAAT 11160
ACTGTTTCTG CTGATAGTAA AGAAAATGTC GCAGCGCTGG CGAAGGCAGC GAATAGCGCG 11220
AATATTAATA ATGTTGCAGT AGAAGGAAAA ATCTCAGGTG CGAAATCTGT TGCGGGATTA 11280
GTAGCGAGCG CAACAAATAC AGTGATAGAA AACAGCTCGT TTACAGGGAA ACTTATCGCA 11340
AATCACCAGG ACAGTAATAA AAATGATACT GGAGGAATAG TAGGTAATAT AACAGGAAAT 11400
AGTTCGAGAG TTAATAAAGT TAGGGTAGAT GCCTTAATCT CTACTAATGC ACGCAATAAT 11460
AACCAAACAG CTGGAGGGAT AGTAGGTAGA TTAGAAAATG GTGCATTGAT ATCTAATTCG 11520
GTTGCTACTG GAGAAATACG AAATGGTCAA GGATATTCTA GAGTCGGAGG AATAGTAGGA 11580
TCTACGTGGC AAAACGGTCG AGTAAATAAT GTTGTGAGTA ACGTAGATGT TGGAGATGGT 11640
TATGTTATCA CCGGTGATCA ATACGCAGCA GCAGATGTGA AAAATGCAAG TACATCAGTT 11700
GATAATAGAA AAGCAGACAG ATTCGCTACA AAATTATCAA AAGACCAAAT AGACGCGAAA 11760
GTTGCTGATF ATGGAATCAC AGTAACTCTT GATGATACTG GGCAAGATTT AAAACGTAAT 11820
CTAAGAGAAG TTGATTATAC AAGACTAAAT AAAGCAGAAG CTGAAAAGAAA AGTAGCTTAT 11880
AGCAACATAG AAAAAGTAT GCCATTCTAC AATAAAGACC TAGTAGTTCA CTATGGTAAC 11940
AAAGTAGCGA CAACAGATAA ACTTTACTACT ACAGAATTGT TAGATGTTGT GCCGATGAAA 12000
GATGATGAAG TAGTAACGGA TATTAATAAT AAGAAAAATT CAATAAATAA AGTTATGTTA 12060
CATTTCAAAG ATAATACAGT AGAATACCTA GATGTAACAT TCAAAGAAA CTTCATAAAC 12120
AGTCAAGTAA TCGAATACAA TGTACAGGA AAAGAATATA TATTCACACC AGAAGCATT 12180
GTTTCAGACT ATACAGCGAT AACGAATAAC GTECTAAGCG ACTTGCAAAA TGTAACACTT 12240
AACTCAGAAG CTAATAAAAA AGTACTAGGA GCAGCGAATG ATGCAGCCTT AGATAACCTA 12300
TACTTAGATA GACAATTTGA AGAAGTTAAA GCTAATATAG CAGAACACCT AAGAAAAGTA 12360
TTAGCGATGG ATAAATCAAT CAATACTACA GGAGACGGTG TAGTTGAATA CGTAAGTGAG 12420
AAAAACAATA ATAAACAAGA AGCATTATATG CTAGGTCTTA CTTATATGAA CCGTTGGTAC 12480
GATATTAATT ATGGTAAAAA GAATACAAAA GATTTATCTA CGTACAAGTT TGACTTTAAC 12540
GGAAATAATG AGACTTCAAC GTTGATACT ATGTGCGCAT TAGGAAATAG TGGACTAGAT 12600

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AACCTGAGAG	CTTCAAATAC	TGTAGGTTTA	TATGCGAATA	AACTTGCATC	GGTAAAAGGA	12660
GAAGATTCAG	TCTTTGACTT	CGTAGAAGCG	TATAGAAAAC	TGTTCTTACC	AAACAAAACA	12720
AATAACGAGT	GGTTTAAAGA	AAATACAAAG	GCATATATAG	TCGAAATGAA	GTCTGATATT	12780
GCAGAAGTAC	GAGAAAAACA	AGAATCACCA	ACAGCCGATA	GAAAATATTC	ATTAGGAGTT	12840
TACGATAGAA	TATCAGCACC	AAGTTGGGGG	CATAAGAGTA	TGTTATTACC	ACTACTAACT	12900
TTACCTGAAG	AATCTGTGTA	TATTTTCATCG	AATATGTCTA	CACTTGCATT	CGGTTCTGAT	12960
GAAAGATATC	GTGATAGTGT	GGATGGAGTT	ATTCTTTCAG	GAGATGCTTT	ACGAACTTAT	13020
GTAAGAAATA	GAGTTGATAT	AGCAGCGAAA	AGGCATAGAG	ACCATTATGA	TATTTGGTAC	13080
AATCTTCTTG	ACAGTGCTTC	AAAAGAAAAA	CTTTTCCGTT	CTGTGATAGT	TTATGATGGA	13140
TTCAATGTAA	AAGATGAGAC	AGGAAGAACT	TATTTGGCAA	GGTTAACGGA	TAAAAACATC	13200
GGCTCTATTA	AAGAATTCTT	CGGACCTGTT	GGGAAATGGT	ATGAGTATAA	TAGTAGTGCA	13260
GGAGCGTATG	CGyAtGGAAG	TTTAACGCAC	TTTGTGTTAG	ATAGATTATT	AGATGCTTAT	13320
GGAACGTCGG	TTTATACTCA	TGAAATGGTT	CATAATTC TG	ATTCTGCAAT	CTACTTTGAA	13380
GGAAATGGTA	GACGTGAAGG	ATTGGGAGCG	GAGTTATACG	CACTTGGTTT	ACTGCAATCT	13440
GTAGATAGTG	TAAATTCTCA	TATTTTAGCT	TAAATACGT	TATATAAAGC	AGAAAAAGAT	13500
GATTTGAATA	GATTCATAC	ATATAATCCG	GTGGAACGTT	TCGATTCCGA	TGAGGCGCTT	13560
CAAAGTTATA	TGCATGGATC	ATATGATGTA	ATGTATACAC	TTGATGCGAT	GGAAGCAAAA	13620
GCGATATFAG	CTCAAAATAA	TGATGTTAAG	AAAAAATGGT	TTAGAAAAAT	AGAAAATTAT	13680
TACGTTCTGT	ATACTAGACA	TAATAAAGAT	ACACATGCAG	GAAATAAAGT	CCGTCCATTA	13740
ACAGATGAAG	AAGTAGCTAA	CTTAACATCG	TTAAACTCAT	TAATCGACAA	CGACATCATA	13800
AATAGACGTA	GCTATGATGA	TAGTAGAGAA	TATAAACGAA	ATGGCTACTA	TACTATAAGT	13860
ATGTTCTCTC	CTGTATACGC	AGCGCTAAGC	AATTCGAAAG	GTGCTCCTGG	AGATATTATG	13920
TTTAGAAAAA	TAGCTTATGA	ATTACTTGCG	GAAAAAGGTT	ATCACAAAGG	ATTCCTACCT	13980
TATGTTTCTA	ATCAGTACCG	AGCAGAAGCA	TTTGCCAGCG	GAAGCAAAAC	ATTCTCATCA	14040
TGGCATGGAA	GAGATGTTGC	TTTAGTGACA	GATGATTTAG	TATTTAAGAA	AGTATTCAAT	14100
GGTGAGTACT	CATCATGGGC	TGATTTCAAA	AAAGCAATGT	TTAAACAACG	TATAGATAAA	14160
CAAGATAATC	TGAAACCAAT	AACAATTCAA	TACGAATTAG	GTAATCCTAA	TAGTACAAAA	14220
GAAGTAACTA	TAACAACGGC	TGCACAAATG	CAACAATTAA	TTAATGAAGC	GGCTGCGAAA	14280
GATATTACTA	ATATAGATCG	TGCAACGAGT	CATACCCAG	CAAGTTGGGT	GCATTTATTA	14340

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AAACAAAAA TCTATAATGC ATATCTTCGC ACTACAGATG ACTTTAGAAA TTCTATATAT 14400
 AAATAAGATT GTAGAGTTTC ATTGTTGAGT AGTGTTCCTT GTAAGGATGA GGAGTCAGAT 14460
 GACAAATCGA CTCCTTTTTC TTATGGATCG ATGTAGAGAT TTGATTGAAT GCAGATTGCA 14520
 GGAATCATCT TCAACTCATC AACGACCAAT GGTGACAAGG TGGATTTCAA TCCCACAGAA 14580
 AATGTTGATT TGAGAAATAA CTTTGCTAGT CTAGTAAAAT AAATACAAA CAATCCTAGA 14640
 AGATTTTTC TGGGATFGTT TTTTGCTGAG TGGGATGCTT CAAGTTGTCT GGCTTGACTT 14700
 TCTTGAGGGA AGTTATATAA TAGTTGTAAT AATTAG 14736

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

ACAGGAAAGC ACGATAGCAA TCTCTTTGGA AGATTTAAAA AATATTCCTC AAAGTTTCGC 60
 TGTTGCTTAC GGTGATACGA AAGTATCTTC GATTCTCTCT GTCTTGCGTG CTAATTTAGT 120
 AAATCATTTG ATTACAGACA AAAATACAAT TTTAAAAGTT TTGGAAGAAG ATGGGGATTT 180
 GACTTTTAGA GAGATTCTAG GTGAGTGAAA ATGATAGACT GATTCAGTTT ATCGTTTTC 240
 TTTTLAGTTG ATTGCACATT TGTGCTTATA TAAACAAAA TAGTTTATCT GTTGTTTTTC 300
 GATTGACAAC TTTATTATGT AGTTGTATTC TATAGTTACA AAAGAAAATT TTAAAAATTC 360
 AAATGAAAA AGCTTTTTAC ATAGTAAAAT GAGGAGGAAT TTATGGAAAT GATTGTTCCT 420
 GATCAAATTA TCATGGGTTT AATTTTATAT GCTGGTGATG CGAAACAACA TATTTATAAA 480
 GCGTTAGATT ACATAAAAA TGGTACATGT GAACGGTGTG AAGAAGAAAT ACAGTTAGCT 540
 GATGCAGCCT TATTAGAAGC TCATAATCTA CAAACAAAAT TTTTGGCACA GGAAGCGTCT 600
 GGTACAAAGA CAGAAATTAC AGCTCTCTTT GTTCATTCAC AAGATCATCT CATGACCAGT 660
 ATGACGGAGA TTAATTTAAT CAAAGAAAT ATTAGTTTGA GAAAAGAACT TCATAAAAA 720
 TAATACTAGA GTATTATCAT TGTTATTAAC ATAGAGGAGG AAAACATAAT GGTGAAGATT 780
 GGTTTGTTTT GTGCAGCAGG TTTTCTACT GGTATGCTTG TAAATAATAT GAAAATGCA 840
 GCGCAATCTA GTGGAGTTGA GGCAGAAATA GAGGCGTTTT CTCAGTCTAA ATTAGCGGAT 900
 TATGCCCAA ATATAGATGT TGCCTATTG GGTCCACAAG TTGCTTATAC ATTAGATAAA 960
 TCAAAAGAAA TTTGTGATAA GTGTGATGTT CCGATAGCTG TTATTCCGAT GATGGACTAT 1020

GGTATGTTAG	ATGGGAAAAA	AGTATTAGAT	TTGGCCCTAT	CTTTGATTAG	TGGGTAAGAA	1080
AAGGAGATTT	ATTATGTCAA	AGATGGATGT	TCAGAAAATC	ATTGCACCGA	TGATGAAGTT	1140
TGTGAATATG	CGTGGCATT	TAGCTCTAAA	AGATGGGATG	TTAGCAATTT	TGCCATTGAC	1200
AGTAGTTGGT	AGTTTGTCT	TGATTATGGG	ACAATTGCCG	TTCGAAGGAT	TAAATAAGAG	1260
CATTGCTAGT	GTTTTTGGAG	CTAATTGGAC	AGAGCCGTTT	ATGCAAGTAT	ATTCAGGAAC	1320
TTTTGCTATT	ATGGGTCTAA	TTTCTTGTTT	TTCAATGCC	TATTCTTATG	CTAAGAATAG	1380
CGGAGTAGAG	GCTTTACCAG	CTGGAGTTCT	ATCTGTATCT	GCATTCTTTA	TTTTGCTAAG	1440
ATCATCTTAT	ATCCCTAAAC	AAGGTGAGGC	GATTGGGGAC	GCTATTAGTA	AAGTTTGGTT	1500
TGGAGGCCAA	GGAATTATCG	GTGCTATCAT	TATAGGTTTG	GTAGTAGGAA	GTATTTATAC	1560
CTTCTTTATA	AAGAGAAAAA	TTGTTATTAA	GATGCCAGAA	CAAGTCCAC	AAGCTATTGC	1620
CAAACAGTTT	GAAGCAATGA	TTCCAGCATT	TGTAATTTTC	TTATCTTCTA	TGATTGTATA	1680
TATTTTAGCG	AAGTCATTGA	CTAATGGCGG	AACATTCATA	GAAATGATTT	ATTCTGCTAT	1740
TCAAGTCCG	TTGCAAGGTT	TAACGGATC	TTTGTATGGT	GCTATTGGAA	TTGCATTCTT	1800
TATATCATTT	TTGTGGTGGT	TTGGTGTTC	TGGGCAATCG	GTAGTAAATG	GAGTAGTGAC	1860
AGCTCTGCTT	TTATCTAATC	TTGATGCTAA	TAAAGCTATG	TTAGCCTCTG	CTAATCTATC	1920
ATTAGAAAAA	GGTGCACATA	TTGTTACTCA	ACAATTTTTA	GATTCATTTT	TAATTCATAC	1980
AGGFTCAGGG	ATTACGTTTG	GTCTTGTAGT	TGCCATGCCT	TTTGCAGCAA	AATCAAAAACA	2040
ATACCAAGCC	TTAGAAAAG	TTGCAGCTTT	TCCAGCAATA	TTTAAACGTAA	ATGAGCCAGT	2100
TGTATTTGGA	TTTCCGATTG	TCATGAATCC	AGTTATGTTT	GTACCTTTCA	TTCTTGTTC	2160
TGTACTTGCA	GCTGTGATAG	TATATGGAGC	TATTGCAACA	GGTTTCATGC	AGCCATTCCTC	2220
AGGGTAACA	TTGCCTTGGA	GTACACCAGC	TATTTTATCA	GGATTTTGG	TGGGTGGATG	2280
GCAAGGAGTT	ATTACTCAGC	TGGTGATATT	AGCGATGTCT	ACATTTGGTTT	ATTTTCCATT	2340
CTTTAAAGTA	CAGGATCGTT	TAGCTTACCA	AAATGAAATC	AAACAATCTT	AGAGGTATTT	2400
GTGTGTTACT	GTTAAACTCA	CACATTTGTG	CTAAAAATTA	GAGAGTTAAA	ATTTTCTAG	2460
TTAAAAGCTT	GAAAATTTCT	ATAAAAATCG	GTATTATATT	TTCGAAAGAA	ATAAAAATAT	2520
TTTCGAAAGA	AAGGTGCTTA	CGATGGTAAA	TACAGAAGTA	GCAAGAACAA	CAATCAAGAC	2580
AGAATATTTT	GGCAGCCTTA	CTGAAAGGAT	GAACAAATAT	CGAGAAGATG	TTTTAAATAA	2640
AAAACCTTAT	ATTGATGCTG	AGAGAGCAGT	TCTAGCAACA	CGCGCCTATG	AACGATACAA	2700
GGAACAACCT	AATGTCCTAA	AACGTGCATA	TATGCTGAAA	GAAATTTTGG	AAAATATGAC	2760

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TATCTATATT	GAAGAAGAAT	CTATGATTGC	GGGAAATCAA	GCTTCTTCCA	ATAAAGATGC	2820
TCCTATTTTT	CCGGAATATA	CGCTAGAATT	TGTTCTCAAT	GAGTTGGATC	TTTTTGAAAA	2880
GCGTGATGGA	GATGTTTTCT	ATATTACAGA	AGAAACAAAA	GAACAACCTA	GAAGTATTGC	2940
TCCGTTTTGG	GAAAATAATA	ATTTACGTGC	TAGAGCTGGT	GCCTTATTAC	CTGAAGAAGT	3000
GTCTGTTTAT	ATGGAACAG	GATTCTTCGG	TATGGAAGGT	AAGATGAATT	CTGGAGATGC	3060
TCACTTAGCA	GTTAACTATC	AGAACTTTT	GCAATTTGGT	TTAAGAGGTT	TTGAAGAGCG	3120
GGCTCGTAAA	GCAAAAGTAG	CTCTAGATTT	AACAGATCCA	GCAAGTATTG	ATAAATATCA	3180
TTTTTACGAC	TCTATATTTA	TCGTAATCGA	TGCTATTAAA	GTATATGCAA	AGCGCTTTGT	3240
TGCTCTTGCT	AAAAGTTTAG	CCGAAAATGC	AAATCCTAAA	CGTAAGAAAAG	AATTACTTGA	3300
GATTGCAGAT	ATTTGCTCTA	GAGTCCCAT	TGAACCGCA	ACTACTTTTG	CAGAAGCTAT	3360
TCAATCAGTT	TGGTTTATTC	AATGTATTTT	ACAAATGAA	TCTAATGGCC	ACTCTCTTTC	3420
ATATGGCCGT	TTTGATCAAT	ATATGTATCC	ATATATGAAG	GCTGATTTAG	AAAGTGGTAA	3480
AGAAACAGAA	GATAGCATTG	TTGAACGTCT	GACAAATCTT	TGGATTAAGA	CAATTACAAT	3540
TAATAAGGTT	CGCAGTCAAT	CACATACATT	TTCTTCAGCA	GGAAGTCCTT	TATATCAAAA	3600
TGTTACAATT	GGTGGACAGA	CTCGAGATAA	GAAGGATGCT	GTTAACCCAT	TATCTTATTT	3660
GGTATTA AAA	TCAGTTGCAC	AAACCCATCT	ACCGCAACCT	AATCTAACTG	TACGTTACCA	3720
TGCAGGTTTA	GATGCTCGTT	TCATGAATGA	GTGTATTGAA	GTGATGAAAC	TTGGTTTTGG	3780
FATGCCTGCA	TTTAATAATG	ATGAGATTAT	TATTCCTTCT	TTTATTGCAA	AAGGAGTATT	3840
GGAAGATGAT	GCTTATGATT	ACAGTGCCAT	TGGATGTGTT	GAAACGGCAG	TTCCAGGGAA	3900
ATGGGGCTAT	CGTTGCACAG	GTATGAGTTA	TATGAACTTC	CCTAAGGTTT	TACTTATCAC	3960
GATGAATGAT	GGAATTGATC	CGGCTTCGGG	TAAACGGTTT	GCACCAAGCT	TTGGTCGTTT	4020
TAAGGATATG	AAGAACTTTT	CTGAATTAGA	AAATGCTTGG	GATAAAACAC	TAAGATATTT	4080
GACACGAATG	AGTGTATTG	TTGAAAATTC	TATTGATTTA	TCATTGGAAC	GAGAAGTTCC	4140
TGATATTCTA	TGTTTCAGCAT	TGACTGATGA	TTGTATTGGT	CGTGGAAAAC	ACCTTAAAGA	4200
AGGTGGAGCA	GTATATGATT	ATATATCAGG	ATTGCAAGTT	GGAATTGCAA	ATTTGTCCGA	4260
TTCATTAGCT	GCAATTA AAA	AATTGGTGTT	TGAGGAAGAA	CGTATAAGCC	CAAGTCAGCT	4320
TTGGCATGCA	CTGAAAACAG	ATTATGCCGG	AGAAGAAGGT	AAGGTCATTC	AAGAAATGTT	4380
GATTCATGAT	GCACCTAAGT	ATGGTAATGA	TGATGATTAT	GCTGACAAAT	TGGTTACTGC	4440
TGCTTATGAC	ATTTATGTTG	ATGAAATTGC	TAAATATCCT	AATACACGTT	ATGGAAGAGG	4500
GCCTATTGGA	GGAATTCGTT	ATTCAGGAAC	ATCTTCTATC	TCAGCCAACG	TAGGGCAGGG	4560

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ACGTGGAACA	TTAGCAACTC	CAGATGGACG	CAACGCGGGT	ACACCGTTAG	CAGAGGGTTG	4620
TTCACCATCA	CATAATATGG	ATCAACACGG	CCCTACATCT	GTTTAAAAAT	CTGTTTCAAA	4680
ATTACCAACA	GATGAAATCG	TAGGTGGGGT	TCTCTTAAAT	CAGAAAGTAA	ATCCTCAAAC	4740
GTTAGCCAAA	GAAGAAGATA	AATTAAAACT	AATTGCTTTG	TTACGAACAT	TCTTTAATCG	4800
TTTACATGGG	TACCATATTC	AATACAATGT	TGTTTCCAGA	GAGACGCTGA	TTGACGCTCA	4860
GAAACATCCT	GAAAAACACA	GAGACTTAAT	TGTTTCGTGT	GCAGGATACT	CTGCATTCTT	4920
CAATGTTCTT	TCTAAGGCAA	CCCAAGATGA	CATTATAGGA	CGTACTGAGC	ATACTTTGTA	4980
AAATAAAGAG	GTTCTTTTTA	TGGAATTTAT	GCTTGACACA	TTAAATTTAG	ATGAGATTAA	5040
AAAGTGGTCT	GAAATTTTGC	CGTAGCTGG	GGTAACTTCA	AATCCCACTA	TTGCAAAAAG	5100
AGAGGGTCT	ATTAATTTTT	TTGAACGAAT	CAAAGATGTA	AGAGAATTGA	TTGGCTCTAC	5160
ACCCTCTATT	CATGTTTCAG	TGATTTCTCA	AGATTTTGAA	GGCATCTTAA	AGGATGCTCA	5220
TAAAATTCGA	AGACAAGCAG	GAGATGATAT	ATTTATCAAA	GTACCTGTTA	CTCCAGCTGG	5280
ATTACGTGCA	ATAAAGGCGC	TAAAAAAGA	GGGCTACCAT	ATCACTGCAA	CAGCTATTTA	5340
TACAGTTATT	CAGGGATTAT	TAGCTATCGA	AGCAGGAGCG	GATTACCTAG	CTCCATATTA	5400
TAATAGAATG	GAAAATCTGA	ACATTGATTC	AAATCTGTCT	ATTCGTCAAT	TAGCTCTTGC	5460
TATTGATAGA	CAGAACTCTC	CTAGTAAGAT	TTTAGCTGCA	TCCTTTAAAA	ATGTAGCACA	5520
AGTAAATAAT	GCTTTAGCTG	CAGGTGCGCA	TGCTGTTACA	GCAGGAGCGG	ATGTTTTTGA	5580
ATCAGCTTTC	GCCATGCCAT	CTATCCAAAA	GGCGGTTGAT	GATTTTTCTG	ACGATTGGTT	5640
TGTTATTCAA	AATAGTCGTT	CCATTTAGAT	AGAGAGGAAA	TACATATGAG	AATTTTTGCT	5700
AGTCCTTCTA	GATATATTCA	GGGGAAAAT	GCCTTGTTTG	AAAATGCCAA	ATCAATTTTG	5760
GATTTGGGAA	ATTGCCCTAT	TCTATTATGC	GATCAGTTGG	TTTATGATAT	TGTTGGAAAA	5820
CGATTTGAAG	ATTACCTACA	TAGGTATGGT	TTCCATATTG	TTCTGGCGCT	ATTTAATGGT	5880
GAAGCTTCTG	ACAATGAAAT	CAATCGAGTT	GTTGCCTTGG	CTGAGAAAAG	AAATGTGTAT	5940
AGTATTATCG	GTCTTGGTGG	GGGAAAGACG	ATTGATAGCG	CAAAGCTAT	TGCAGATTTG	6000
ATTGAAAAGC	CTGTTATTAT	TGCTCCAACA	ATTGCATCGA	CCGACGCACC	TGTATCTGCT	6060
TTATCTGTTA	TTTATACAGA	TGAAGGTGCA	TTTGATCATT	ATCTATTTTA	TTCTAAAAAT	6120
CCAGATTTAG	TTTTGGTTGA	TACAAAAGTT	ATTCACAAG	CCCCTAAGCG	TTTATTAGCG	6180
TCTGGTATTG	CAGATGGTTT	AGCAACTTGG	GTTGAGGCGC	GTGCGGTTAT	GCAGGCAAA	6240
GGAAAACTA	TGTTGGGACA	ACAGCAAACA	TTGGCTGGAG	TTGCAATTGC	GAAGAAATGT	6300

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GAAGAAACGC	TGTTTGCAGA	TGGTTTACAG	GCTATGGCAG	CTTGTGAAGC	TAAAGTGGTG	6360
ACACCAGCAT	TAGAAAATAT	TGTTGAAGCT	AATACTTTAT	TGAGTGGTCT	AGGTTTTGAA	6420
AGTGGAGGAT	TAGCTGCGGC	GCATGCAATT	CATAATGGTT	TTACTGCATT	GACAGGTGAC	6480
ATTCATCATT	TAAACATGG	TGAAAAAGTA	GCTTATGGAA	CTTTAGTACA	ACTATTATTG	6540
GAAAATAGAC	CTAAAGAAGA	ACTTGATAAG	TATATTGAGT	TTTACAAAAA	AATTGGTATG	6600
CCAACAATC	TAAAAGAAAT	GCATTGGGAT	CAAGTTGGAT	ATGATGATTT	AATAAAAGTT	6660
GGTAAACAAG	CAACTATGGA	GGGTGAGACA	ATTCATCAGA	TGCCGTTTAA	GATTTGCGCT	6720
TCAGATGTTG	CTCAAGCTAT	TATCGCTGTA	GATGCCTATG	TAAATTCAAA	ATAAACAATA	6780
AGGACTACTG	TTTCCCAAAT	GGTAGCTTTT	TATTGATCCC	TGTATTGAAT	TCTATAGAAG	6840
ATTGAAATAG	GATGAGAACA	AATCGATTGG	GAAAGTAAAA	TTAATTTCTA	TAAATGTTTT	6900
AGCAATTGTT	TCGTACTATT	TCAGATTCAG	TCTACTATAT	GTTCTTCATA	AATCAAAAAG	6960
CGACATAGGT	TGTCGGCTAT	TTATTGTGAA	TACATTAATT	AGCATCCAG	TTTATCTTC	7020
GGTCTAAAAT	AAGTATTTTG	TGCTATACGA	GATAAGCTTC	TTGACTTACT	CCTTGATTTA	7080
CTGCATAACA	ATGGGATAAA	AAGTGGGAGA	TAGAGCAATT	CATAGTCATC	AAAATTAATG	7140
AGATACAGTA	TACAGTTTTT	CCTTTAAACA	CATTTCAAAT	TCCCTCAAAA	ATGGTATAAT	7200
AGTAACATCA	CAAAATTGGA	GAGAGACCAT	GAGTTTTTAC	AATCATAAAG	AAATTGAGCC	7260
TAAGTGGCAG	GGTACTGGG	CAGAACATCA	TACATTTAAG	ACAGGAACAG	ATACATCAAA	7320
ACCTAAGTTT	TATGCGCTTG	ATATGTTCCC	TTATCCGCTC	GGAGCTGGTC	TGCACGTAGG	7380
ACACCCAGAA	GGTTATACTG	CAACCGATAT	CCTCAGTCGT	TACAAACGTG	CGCAAGGCTA	7440
CAATGTCCTT	CACCCAATGG	GTTGGGATGC	TTTTGGTTTG	CCTGCAGAGC	AATACGCTAT	7500
GGATACTGGT	AATGACCCAG	CAGAATTTAC	AGCGGAAAAC	ATTGCCAACT	TCAAACGTCA	7560
AATTAATGCG	CTTGGATTTT	CTTATGACTG	GGATCGTGAA	GTCAACACAA	CAGATCCAAA	7620
CTACTACAAG	TGGACTCAAT	GGATTTTCAC	CAAGCTTTAC	GAAAAAGGCT	TGGCCTATCA	7680
AGCTGAAGTG	CCAGTAAACT	GGGTGAGGA	ATTGGGAACT	GCCATTGCCA	ATGAAGAAGT	7740
GCTTCCTGAC	GGAACCTCTG	AGCGTGGAGG	CTATCCAGTT	GTCCGCAAAC	CAATGCGCCA	7800
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CACACTTTTC	GGTGCGACTT	TCACTGTCTT	GGCTCCTGAA	CATGAATTAG	TAGACGCTAT	8040
CACAAGTTCA	GAGCAAGCAG	AAGCTGTAGC	AGACTATAAA	CACCAAGCCA	GCCTTAAGTC	8100

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TGACTTGGCT	CGTACAGACC	TTGCTAAAGA	AAAAACAGGG	GTTTGGACTG	GTGCTTATGC	8160
CATCAACCCT	GTCAATGGTA	AGGAAATGCC	AATCTGGATT	GCAGACTATG	TCCTTGCTAG	8220
TTATGGAACA	GGTGC GGTTA	TGGCTGTGCC	TGCCACGAC	CAACGTGACT	GGGAATTTGC	8280
CAAACAATTT	GACCTTCCAA	TCGTGGAAGT	ACTTGAAGGT	GGAAATGTCG	AAGAAGCTGC	8340
CTACACAGAG	GATGGCCTGC	ATGTCAATTC	AGACTTCCTA	GATGGATTGA	ACAAAGAAGA	8400
CGCTATTGCC	AAGATTGTGG	CTTGGTTGGA	AGAAAAAGGC	TGTGGTCAGG	AGAAGGTTAC	8460
CTACCGTCTC	CGCGACTGGC	TCTTTAGCCG	TCAACGTTAC	TGGGGTGAGC	CAATTCCAAT	8520
CATTCATTGG	GAAGATGGAA	CTTCAACAGC	TGTTCTGAA	ACTGAATTCG	CGCTTGCTTT	8580
GCCTGTAACC	AAGGATATCC	GTCCTTCAGG	TACTGGTGAA	AGTCCACTAG	CTAACTTGAC	8640
AGATTGGCTT	GAAGTGACTC	GTGAAGATGG	TGTCAAAGGT	CGTCGTGAAA	CCAACACTAT	8700
GCCACAATGG	GCTGGTTCAA	GCTGGTACTA	CCTCCGCTAT	ATTGACCCGC	ACAATACTGA	8760
GAAATTGGCT	GATGAGGACC	TCCTCAAACA	ATGGTTGCCA	GTAGATATCT	ACGTGGGTGG	8820
TGCGGAACAT	GCTGTACTTC	ACTTGCTTTA	TGCTCGTTTC	TGGCATAAAT	TCCTCTATGA	8880
CCTCGGTGTT	GTTCCGACTA	AGGAACCATT	CCAAAACTC	TTTAACCAAG	GGATGATTTT	8940
GGGAACAAGC	TACCGTGACC	ACCGTGGTGC	TCTTGTGGCA	ACCGACAAGG	TGAAAAACG	9000
TGATGGTTCC	TTCTTCCATG	TAGAAACAGG	GGAAGAGTTG	GAGCAAGCGC	CAGCCAAGAT	9060
GTCTAAATCG	CTCAAGAACG	TTGTTAACCC	AGACGATGTG	GTGGAACAAT	ACGGTGCCGA	9120
TACCCTTCTG	GTTTATGAAA	TGTTTATGGG	ACCACTCGAT	GCTTCGATTG	CTTGGTCAGA	9180
AGAAGGTTTG	GAAGGAAGCC	GTAAGTTCCT	TGACCGAGTT	TACCGTPTGA	TTACAAGTAA	9240
AGAAATCCTT	GCGGAAAACA	ATGGTGCTCT	TGACAAGGTT	TACAACGAAA	CAGTCAAAGC	9300
TGTTACTGAG	CAAATGAGT	CTCTCAAAT	CAACACAGCT	ATTGCCCAAC	TTATGGTCTT	9360
TGTCAATGCT	GCTAACAAGG	AAGATAAGCT	TTATGTTGAC	TATGCCAAAG	GCTTTATTCA	9420
ATTGATTGCA	CCATTTGCAC	CTCACTTGGC	AGAAGAACTC	TGGCAAACAG	TCGCAGAAAC	9480
AGGTGAGTCA	ATCTCTTATG	TAGCTTGGCC	AACTTGGGAC	GAAAGCAAAT	TGGTTGAAGA	9540
TGAAATTGAA	ATTGTCTGTC	AAATCAAAGG	AAAAGTTCGT	GCCAAACTCA	TGGTTGCTAA	9600
AGATCTATCA	CGTGAAGAAT	TACAAGAAAT	CGCTTTAGCT	GATGAAAAAG	TCAAAGCAGA	9660
AATTGACGGT	AAGGAAATCG	TGAAAGTAAT	TGCGGTACCG	AATAAACTCG	TTAATATCGT	9720
CGTTAAATAA	CGAGTTTATT	AGCTCTATCT	GCCACCTTCA	ATAGTCCACT	GGACTATTGA	9780
AsCCAACTAA	ATTAGTTAAC	ATTGTTGTGA	AATAAGATAG	GAGTCCTTCA	GAGTAGAATC	9840

1100

TGGAGGATTT TTTGAATCTT CTTATGAAAG TATGATATAC TATGGGCAAC TATAAAGTTT 9900
 GAAAAGTGAA ATAAGGAGAA TAAGATGCCA GTAAATGAAT ATGGTCAAAT GATGGGGAG 9960
 TCAATGGAAG CTTATACTCC AGGTGAATPG CCTTCTTTTG ATTTCTTAGA AGGGCGTTAT 10020
 GCTAGGATAG AGGCTCTTTC AGTGGAAAAG CATGCGGAGG ATTTATTAGC TGTTTATGGC 10080
 CCTGATACGC CTCGGGAGAT GTGGACCTAC CTCTTTCAGG AGTCAGTAGC AGACATGGAG 10140
 GAACTGGTCA GCCTTTTAAA TCAGATGTTG GCTCGTAAGG ACCGTTTTTA TTATGCAATC 10200
 ATAGACAAGG CAACTGGTAA GGCTTTGGGA ACTTTTTCCC TCATGCGAAT TGATCAGAAT 10260
 AACCGAGTAA TAGAAGTGGG AGCTGTCACT TTTTCTCCAG AGCTCAGGGG GACACGGATA 10320
 GGAACAGAAG CCCAGTATCT CTTGGCTTGC TATGTCTTTG AGGAGCTTAA CTATCGTCGC 10380
 TATGAGTGGA AATGCGATGC TCTTAACCTG CCATCCAGAC GAGCAGCGGA ACGTTTGGGA 10440
 TTTATTTATG AAGGAACCTT CCGTCAGGCA GTGGTTTATA AGGGGCGTAC AAGAGATACG 10500
 GATTGGTTGT CTATGATGA TAAGGACTGG CCTCAAGTCA AAGCTCGATT GGAATATGG 10560
 TTGCGTCCTG AAAACTTTGA TAAAAATGGA CGACAGCACA AGAGCTTGAG AGAACTTTAA 10620
 GAGGTGTTGA GATGATTACT ATTAAAAAGC AAGAAATTGT CAAGCTAGAG GATGTTTTGC 10680
 ATCTCTATCA GGCTGTCGGT TGACAAAAC ATACCCATCA AACAGAGATG CTGGAGCAGG 10740
 CCTTATCTCA TTCATTAGTA ATTTATCTGG CACTTGATGG TGATGCTGTG GTGGGCTTGA 10800
 TTCGTTTGGT TGGAGATGGT TTTTCATCAG TTTTGTACA GGATTTGATT GTTTTGCCTA 10860
 GCTATCAGCG TCAAGGGATT GGTAGCTCCT TGATGAAAGA GGCTTTAGGA AATTTTAAAG 10920
 AGGCCTATCA AGTCCAGCTG GCGACAGAAG AGACAGAAAA AAACGTGGGA TTTTATCGTT 10980
 CTATGGGCTT TGAATCTTA TCCACCTATG ACTGTACAGG AATGATTTGG ATAAACAGAG 11040
 AAAAATAAAA AAACCTGTTT GTTCTTAAGC AAAGTTTAAAG GATGGTCTAG TATCATATAG 11100
 TCATTAATAA AAGACCTCCT AACTTTATTT AATAAAATCC TAAACTTTTT TCATCACAAAT 11160
 CTCCTAATGA AGCCACCCAA TCAGGTGGCT TTTTGTGGT ACGACGGGCA TGTCGTATAT 11220
 CTGAGGTGTA AGTCCCTCAGC CTGACTATCG TGAGGTAGCA GGGAGAGGAA GGGATAGCGA 11280
 AATCGTGGCT CTACGAACAG GAACGTGATA GTAAGGCCGA TATAGCGGAT AAGGAGGCTT 11340
 CAAACTCTAA AGTCCAAAAA GGTAGTCGTA ACCTATATGT GTAAATCACG AGAGTAATTG 11400
 AATTCGGACT AAGGTTTGTG TGAAAAAGAT AAATCTTCT AGAGTCTAAA GACTCTGCGT 11460
 CAGATTTCTT ATTTTCACTG TAACCTTTTA ACGTCTCAT ATCTTGATA AACGAGGAAA 11520
 GATGTACGAC TTATCCCCTG AGGTTTCATG AGCGCTGAAA GCGTAGTAAC AACGAATCAT 11580
 GAGAAGTCAG CCGAGCCCAT AGTAGTGAGG AAACCTCCGT AATGGAAGTG GAGCGAAGGG 11640

1101

GTGAATACTC AACAGTCTG GGGAGAGACT GTTTGAGGTC TGTCGCTAGA AAGAGAAAAC 11700
 GACAGATCGA AGTAATCCTA CTTCACTTGT GTCTGTAAAA TGAGTGGTCT GATAGAACTG 11760
 GACTTTGAGG 11770

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAAACTA CTTTCTTAGT ATAACACTTT CAGAATCATT GTCAATAGAA ATGACTTGAT 60
 TTTTCAATT TTTCAAGCT ATTCCAAGG GTTGTAATAAT CGTCCCTGAT TCTGCAAGAT 120
 AAGTAGTAAA CTAACTACTA AAAACAAGGT TGCCAAGAGC AAGGTAATAT AGTCTCCTTT 180
 TTTCAAGGCC TGATAACTAT ACCATGTGCG TTTTCTCTCT TCCCAAAGC GGCGAACTCC 240
 ATGGCAGTCG CAATGGTATC AATGCGTTC AGCGAGCTAA AAATCAAGGG CGTAATAATG 300
 AGCAGATTGC CTTTGATTTC TTGCATAAGA GAAGCTTCT TGGATAATTC CATCCCACGC 360
 GCCTCCTGAG ACATCTTGAT AGTAAAGAAT TCTTCTGCA AATCTGGAAT ATAGCGCAAG 420
 GTCAGGCTGA CAGAATAAGC AATCTTATAG GGCACACCAA TTTGATTAA ACTGGAAGCA 480
 AACTGACTAG GATGGGTGTT CATCAAAAAG ATAATAGCCA GAGGAATGGT GCAAAGATAC 540
 TTAATGGCCA AATTAGCAG ATAAAAGAGC TCCTGGCTGG TTAGAGTGTA GACACCGATT 600
 CCCTGCCAAA TCACACTTCT CTCTCCATAA AGTCCAACCC CATACTCGGG AGAAAAGAGA 660
 TAGACCATCA AAACGTTTAA AACGGCAAAT ATCGTCGCAA AAACGGCTAC AAAGGAAACA 720
 TCTTTAAAGC GAATTTCTGA TAAATAGAGG AGAAAGACTG AAAAGATGGC AATCAGCAAG 780
 AGCATTCTGG TATCATAGCT AATCATGGCC GCCAATGATA CCAGAATGAA AAAGAGAAGT 840
 TTCCCAGCTC CTGACAAGCG ATGAATCACA GTATCTCTAT GCTGGTAACC GATTAATTTA 900
 GCTTGCATCC CTCTCTCCTT TCTTTGTAAG ATGCCGTTAA ATCCAGTGGA TCCACATCTA 960
 GTTCTTAGC CAAGTTAAAG ATGAGGTTT CTTTLAGATT GGCTTTTACT AACAGCTCAG 1020
 GATCGCTCAA CAGACTGGCT GGAACAGTAT CGGCAATCAA TTCTCCATCC ACCATGACAA 1080
 GGACCCGGTC TGAATAATCC AGCATCAATT GCATATCATG GGTAATCATG ACAATGGTAT 1140
 GCCCTTTTTC ATGTAACCTC TCGAGAAATT CCATAATCTC AGTATAGTTC TTCTGATCTT 1200

1102

GACCTGCAGT	CGGTTTCATCT	AGGAGAATAA	TFTCAGCTCC	TAAGACCAA	ATTGAAGCAA	1260
TGGTGACACG	TTTTTCTGA	CCAAATGACA	GGGCAGAAAT	AGGCCAATTA	CGGAATTCAT	1320
AAAGTCCACA	GATTTTCAAG	GTTTCATATA	CTCTCGTTTC	AATTTCTTC	TCATCCACAC	1380
CTCGCAAACG	GAGCCCTAGA	GCCACCTCAT	CAAAAATCAT	ATTGGTTGAA	ATCATTTGAT	1440
TAGGATTTTG	TAGCACATAT	CCTACTCGTT	CCGCCCGCTC	TGCAACAGAA	TCGCCTTTTA	1500
TATCCTGTTT	TTCCCAAAGA	TAGCGTCCTT	CCGTCTGAAT	AAAGCTACTT	ATAGCCTTGG	1560
CTAGAGTTGA	TTTCCCTGCT	CCATTTTTC	CGACAATAGC	AATCTTTCA	CCCTTTTAA	1620
TATCTAAATG	TAGGGATTTT	AAAATCGGTC	TATCATCATA	AGAAAAGAT	ACTTCCTCTA	1680
GTCTAAAGAG	TGACTGCAAT	GCTGGGGTTT	CTTTTGCCAG	TTCATTCTGC	AACTGAACCT	1740
GACCTTTTGA	GATAGACAAG	TTATCCAGAT	TCGCTAATTG	TTCTTCCTTG	ACTAAGTCCA	1800
CACCTAATTG	ACGGAGAGTC	GTTAGATAAA	GGGGTTCTCG	AATTCCATTT	TGAGTCAATA	1860
AATCAGTCGC	AAGCAACTGG	TCAGGGCTCC	CATTA AAAAG	GATACGACCA	TCGTTTATCA	1920
AGACAATCCG	ATCCACAGGG	CGATGCAGAA	CGTCCTCAA	ACGGTGCTCG	ATAATAAGAG	1980
TCGTCGTCCT	CTCTTCCTTA	TGAATCTGGT	CAATCAATTC	GATAATATCC	TGACCTGACT	2040
TGGGATCTAG	ATTGGCGAGT	GGCTCATCAA	ACAAGAGAAT	CGGACTTTCA	TCAATCAAGA	2100
CACCAGCCAG	ACTGACTCGC	TGCTTTTGTC	CACCTGACAA	ATCCTGAGGA	CGCTGATCCA	2160
GTAAGGAAG	AAGGTCCAGC	TTTTCAGCCC	ATTTATAAAC	ACGACCTTTC	ATCTCATCTA	2220
GGGCTGTCAC	ATCATTTTCC	AGAGCAAACG	CCAAATCTTC	TGCCACAGAC	AAGCCAATAA	2280
ACTGCCCATC	TGTATCCTGC	AAAACGTGC	TAACCAGATG	AGACTTATCA	TAGATGCTCA	2340
TATCAAAGGC	TACTTGACCC	TTTATCAAAA	ATTCTCCATA	TGTCTGACCC	TTGTAAATAT	2400
TGGGAATAAT	CCCATTCAAA	CACTGACCCA	AGGTAGATTT	ACCTGACCCA	GATGGTCCAA	2460
CAATTAAGAC	TTTCTCTCCC	TTGTAAATGG	TCAAGTCTAT	CCCTTGCAAG	GTCGGTTCTT	2520
GTTGTGTTTC	ATACCGGAAA	GAGAAATCCT	TCCACTCAAT	TaTAGCTTCT	TTCATCTIAC	2580
TCTCTTCATT	CGCTTCTTAG	ACTTCTATTT	TATCATAAAT	CAAGCCCTTC	TTGCAGTCTC	2640
TCCTCTTAAA	ATCTTAGCGC	CAAAAAGATT	CCTATCCTAG	CTTACTTGCC	TAAC TAATCT	2700
ATAAACATCG	AAAAAGACTA	GTTGCCCAGC	CTTCCCATC	ATTTTATACT	CTTCGAAAAT	2760
CTCTTCAAAC	CACGTCAGcT	TCGCCTTGCC	GTAGGTATGG	TTACTGACTt	CGTCAGTTTC	2820
ATCTACAACC	TCAAAACCAT	GTTTTGAGCc	TGCTTCGTCA	GTTCTATCCA	CAATCTCAAA	2880
ACACTGTTTT	GAGCAACtGC	GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	2940
TAGTCCTTTT	TCAAAC TCC	TGCACGAGTT	TGGGTTCCTG	CATAGGCAAG	TAAGAGAAGA	3000

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GTTCCTGCAA TAGCTACAGA TACACCATTG GCAATTCCTG CAACAATCCC TTGTGCAAAT 3060
 ACTTTTTCTG CCGCTTCTTG ATAAATCACA ACATCTCCAA GTGGTGCCAA GACACCCCAA 3120
 ACAAGGGCAT TTGCAAGTAG TTGAATGAGA TTAATAATAA GAATATCTTT CCAGTCAAAA 3180
 ACACCATTGA TCACGCGAAC GACTTTCTA AAAAGTCCCA CAACTAAACC AAAGAGTCCG 3240
 CTAGCGATAA TCCAAGTCCA CCATAGACCA TAACCAACAA GAGAGTCCTT GATTGCATGA 3300
 CCAATCAACC CGACAAGCAA ACCGATAATC GGTCCAAAA TAATAGAAAG TAGCGCTTGT 3360
 ACCGCATACT GAAGCTGGAT GCTTGTATTT GGAACAGGGG TTGGAATGTT GATCATCCCG 3420
 ATGACGACAA AGAGGGCAGC GCCAATTCG ACAGCAACAA CTGTTTAAT TGTAAATTG 3480
 ATTTCCATAC TATTCTCCTA TTTTATCCTT CTATTTCTT TATTTCAATG GTCCAAGATG 3540
 AACCGACACC TACATTATAG GCCTTGCAA AGGAACCTTG GTTGATAGCC AAACCTAAAC 3600
 GATAGAGAGA GTTGATGTAA AGGATGGGTT GCCCAATTCT CACATCTGCA AATGATTTGC 3660
 CATAGACAACT CTGATTTTGA TAGACCAGCA TATCAGCATG ATAGATGGTC ACTTCAAAAC 3720
 GATCACCAA TCTGGTTC AGCTTGTAAT ATCTTCCCG TGTGATAGAG GTCCAAAGCG 3780
 AACCGAAACG CACATCCAGA ATATCAATGG CTCCCTCAC CAGATGATCT TCTATGATGG 3840
 TCGCTACGAC TGGGAGCTCT ACAATCTGTT CCACACTGAG CTCTGGCCCT ACTTCCTCAA 3900
 AAGTAATGTG ACCACTGGCC AGTTTAGCAC CAGTATAGGC ATAGACATCA CGACCGTGA 3960
 AGGTATAAGA ATGCTCTGTG TTTTGACGCC TATTGGCCAC CTCAGAAATC TCACGAATGG 4020
 CTACAATGCC AACGTGTTT TTGATAAAGG AAAGCGTCCC ATTATCTGGC GTGACAATGT 4080
 ATTGATTTTT TGCACTCTG GCAACTACAC TCTTACGTTT CGAACCGACA CCTGGATCGA 4140
 CAACCGATAC AAACGTCGTT CCCTCAGGCC AGTAATCCAC CGTCT 4185

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2069 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TGATAGAGTT AAAGCCGCTG AGTCATTCAA TCCATCTCCA ACCATCAAAA TAGTGTGACC 60
 TGCTTTCTGC AGTTTCTCTA CTAACCTCAA TTTCCCATCA GGTTCAGT CTGTATAGAC 120
 CTGATCAAAG GGCAAATCTT TACTAATTC CTCTGTCCTA ATCAAGGTGT CTCCTGTGTC 180

1104

CAGAATCAAT TTTT ^y CCCCCT GTGCCTTAAG TTTATCCAAG GCTGTTTTTG CTTCTTTTCT	240
CAAAGGAGTA TGAATGCAGA ACATTCCAAT CAATTCATTT TGATAAGCCA AGAATAAGAG	300
ATTGTAGTGA CTCTTGACT CTTCAATTAA AGCATTTTGT TCTGAACTGA TATGAATCTG	360
CTCATCCTGC ATCAAGACAT AATTCCCAAT AAGAACTGGT TGGCCATCTA TATGAGATTT	420
GATCCCCCTG CTTGCGATAT ATTGGAGTTT CCCATGCATT TCCTCATGTT CAATTC CCTC	480
TATCTCAGCT TGCTTGACGA TGGCATTAGC AATAGGATGA TAAATGTGTT CCTCAAGACA	540
GGCACTGATT CTGAGAATAT CTTCCCTCACT ATAGTCTCCA AAAGGTAACA CCTTTTCAAC	600
TATAGGATAA CTAGTTGTGA TTGTTCCGT CTTATCAAAC AAGAAAGTAT CAACTTCCAG	660
ATATTTCTCC AGAACATCTC CATCCTTAAT CACCATTTCA CGGTTCAACC CTTCCTTGAT	720
AACTGTCAA TAAGCTACAG GAGTAGAGAT TTTCAAAGCG CAGGAGAAAT CGACCAATAG	780
GAAAGAAATA GCCTTAGAAA AAGAACCTGT CAATAGGTAA GTCAGCCCAG CCCCCAAGAA	840
ATTATATTTG ACGACTTTAT CCGCCATCTT GATGAAATAG CGTTGTTTCG TTTTCTTGTT	900
TTCTTCAGAT TTCTTCATCA ACTCAATCAG CTGTAAAATA CGGCTGTTCA TCTGATTATC	960
TGTTACACGA ATGCGTAACT CTCCAGTTTC TAATACTGTA TTTGCACAAA CCAAATCAGA	1020
CTCTCTTTTT TCAACTGGAA AACTCTCTCC TGTC AAGGAA CTTTCGTTGA CCATACCTAA	1080
ACCTGAAACT ACTTGTCCAT CAAACAGAAT TTCATTTCCCT TGAGATAAGA TCAAGACATC	1140
TCCTATTTGA ACATCGGAAC TCTTGATACT AACAACCGTA TCGCCCTGTA CTAGGAATAC	1200
ATCGCTCTCT TTTGCAAGAA GACTCTGTTC TAAATCTGTT GCAGTTTTTT TCAAGGACCA	1260
CTGATCTAAA TGATTC CCA AATCAAGCAT AAACATGATA TTGCTAGCTG TCTTGGATTG	1320
GTTCATAAAC AAAGACAATA AAATAGCCGA ACAGTCCAAG ACTTCCATCG TTAGT ^y CCTT	1380
ACGCGCTAGT GTTTGATAGG CTTCTCTAAT ATAACCCAAA GCCTGATAAC AAGTCCATAT	1440
ATAGCGAATA GGATACGGCA CAAAAC TACG AAAAAGTACA CGCTTAACCG CTGCACCTGA	1500
AACAATAGAA TAAGCACTCT CTTCTCTACG AATGGGAAGA GTCATCAACT CAGAACTTT	1560
CCCTTTATCA ATTCTTTTAA AAAAGGCTTC TGCATTATCT AATACAGAAA AGCCTTCTTT	1620
TATGCGTAGA GTAAAGTGCT GTTGATCCAT GTAAAAC TGG ATAGACTCAA TCCCCTTTTC	1680
ATCTCTCGCC AAGGAACGAA GATAGTCTTG AATATCCAAG GTAAGTGAAA AAGAAGATGA	1740
TAGTCGGATA TGTGGTATC CTCTATGTAG CACTTTAAAA GACATATAT TACCTATAA	1800
GGCTATCTAA TTGCTCTTCT TTTTCTCTT GCTCGTACAA ATATTTGGCA TCTTGCAAGA	1860
CATCGTCTCC ATGTTGCTTC ACAACAGAAA CAGATGCATC TAGCTCGTCT TTCAACTTGT	1920
AAGCCTTAGC CAAAGCTTTA GAATAACCTT TTTTAGCTTC CTTACTTGCT AAGATTTTCA	1980

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AACCAAGGGT ACCAAATGCG ACACCACCCA AAAATAATGA AGATTTTTTC GCAACTTTTG 2040
 CAACGGTTAA TACTTCTTTT AACATAGGG 2069

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4597 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AAATCTTGCG CAATAAAGCT CATCTCCATC TCCCGATTGA AACAGTCACT CCCC GGACTG 60
 TTCAACGTC CCAAGACATA ATCTTAGGCA GATTTCTAAA ATTACTCA AAGTGGAAAGT 120
 CATTGAGCTT TCGAATGACA GTTGAAGTTG AAATGGCCAG CTGATGGGCA ATATCGGTCA 180
 TAGAAATCTT TCAATTAAC TTTTGCGCAA TCTTTTGTTT GATAATACGA GGAATTTGGT 240
 GATTTTTCTT GACGATAGAA GTTTCAGCGA CCATCATTTT CAAGCAATGA TAGCACTTAA 300
 AACGACGTTT TCTAAGGAGA ATTCTAGTAG GCATACCAGT CGTTTCAAGG TAAGGAATTT 360
 TATAGGGTCT TTAATGTCTA GTAATTTTGT GATAAAATGT AATTGTTCCA TATGATTCTT 420
 TCTAATGAGT TGTTTTGTGCG CTTTTTCATTA TAGATCTTAT GGGACTTTTT TTCTACCCAA 480
 AATAGGCTCC ATAATATCCA TAGGGAATTT ACCCACTACA AATATTATAG AGCCCAAAGT 540
 TTTAGGTCGC TTGATAATAT GCGTTTTTTG AATTTTATAG ACTGCTCGTT TAAACTCTAT 600
 TFACTTCGTA CCTTCTGGAG CGAGACGGAA TATTAGTCAC ATACAAAATG AGTACTATTA 660
 GGATTTTATT TTCATGTACA ATTTTCAGCCA GTCTTGTTAT AATCAGCCTA TAGGAATCAA 720
 GGAGGTGACT CTTATGGCTG TTTTGTGTC TTTGGATGGA ATTGTGGTAG AAGTCCTTGA 780
 TGTCTTTTCT TCTTTTAATG GGGATAGTGA GTTTTCTTG TGTATAGCAT TTTGAATCTG 840
 GAATAGGACG CCATGACTGC TAAAAGATTT CTATAAATTA ATTTGATTTT CCTAATCAAT 900
 TTGTTTCATAT CTTATTTTCAT TCCACTATAA ACGTCTTAAA GACAAGAGTC AGTTTGTAT 960
 GGAACGCTCT CAGTTCGAGG AGATGTTCCA ACTTCAAAGT AGTCGCTTGA CGACGCAAGA 1020
 AAAATTACAA TTGTTTACCT CTGTGTTTGC TGGCCGTTAT GATGTTTATG CTAAGAATTT 1080
 TATCAATGAA CAAGGAAAA TTCAGTATTT TCCTTCCTAT GATTATGGTT GGAAGCAGTT 1140
 GCCACCTGAA AAACGGAGTT TCCAGACATT GACGAACTCC GTTTTGAAAT CTCATTTTCG 1200
 TGGGGAGGCA GCTATCGGTA TCTTTCCTAT GCACTTAGAT GATAGCTGTT ATTTTTTGGT 1260

ACTGGATTTG	GATGAAGGAG	ATTGGAAAAGA	AGCTGGTTTA	ACCATTCGAA	GAATAGCCAG	1320
GGAACGCCAG	ATGGAAGCCC	ATTTAGAGAT	TTCTCGTTCG	GGTCACGGAC	TCCATATTTG	1380
GTTCTTCTTT	GAGGAAGCGA	TTCCGAGTCG	AGAGGCTCGC	TTGTTTGAA	AGAAACTGAT	1440
AGAACTGGCA	ATGCAGGAAA	GTATGCAACT	GTCCTTTGAT	TCTTTTGATC	GCATGTTTCC	1500
AAATCAGGAT	GTCCCTCCTA	AGGGGGGATT	TGGAAATTTG	ATTGCCTTGC	CTTTTCAAGG	1560
AGAAGCTTAC	CATCAAGGGC	GAACGGTCTT	TGTGGATGAA	CAGTTTCAGC	CTTATGAAGA	1620
CCAATGGAGG	TATCTACAAG	AAATTCAGAG	GATTTCAACT	GCTAAAGTGG	CACTGTTAAT	1680
CCAAGAGGAG	TTAGGCAAGC	AAGAATTGGA	TAAGGAGTTG	AAGGTCGTTT	TATCCAATAT	1740
GATCCAACTT	GAAAAATCGT	CTGTGACATC	CAAGGCACTT	TTTTCTTGAA	AAATATGGCT	1800
TCCTTTTCTA	ATCCCGAATT	TTATAGTAGA	TTGAAACTAG	AATAGTACAC	CTCTGCTTCT	1860
AAAACATTGT	TAGAAATCGA	TTTGACTTTC	CTGATCGATT	TGTCCTGTTA	TTATTTCAAT	1920
TTACTATATT	TAAAGCAGGC	TATGCGACAG	CCAACCTATC	AAATTCCTGA	GAGAATGTAT	1980
TTATTTGGAG	AATCCGATCA	TTATTTATGG	TTGCCAAGAG	GTTTGCTGTA	TCCATTGCAA	2040
GATAAATTTA	AGCAGGTATC	TGTGGAAGAT	AGGAGAAAGG	TACAAAGGTC	TATTAGCGTG	2100
GAATTTAAGG	GAGAACTCAC	TTTTGAGCAA	GAGTTAGCCC	TGTCAGATAT	GACTTCTAAA	2160
GAAAATGGTT	TACTTCATGC	GGAGACTGGT	TTTGGGAAGA	CCGTTT TAGG	TGCTGCTCTT	2220
ATCTCTGAAC	GGAAAACAAA	AACAATTATT	CTAGTCCATA	ATAAGCAACT	CTTAGACCAA	2280
TGGCTAGATC	GCTTAAACTG	CTTTT GACT	TTCGAAGAGG	AGGAGGCTAT	CCGTTATACG	2340
GCATCAGGTC	GTGAAAAGGT	AATCGGCTAT	GTTGGGCAGT	ACGGTGGGAC	TAAGAAATGG	2400
CTGAGTAAAC	TGGTTGATGT	CGTTATGATT	CAATCTCTAT	TTAAGTTGGA	AAATAGTCAA	2460
AGTCTTTTGG	ATGAGTATGA	GATGATGATT	GTGGATGAGT	GTCATCATGT	CTCTGCCTTG	2520
ATGTTTGAAA	AAGTTGTTGC	TCAGTTTAGA	GGGAAGTATC	TTTACGGTTT	GACGGCTACG	2580
CCTGAGCGTA	AGAATGGTCA	TGAGCCTATT	GTTTTTCAGA	GAATTGGTGA	GATACTCCAT	2640
ACTGCTGATA	AGAGGGAAAC	GGATTTTAAA	CGGCAATTGC	AATTAAGATT	CACTTCTTTT	2700
GGTCATTTGG	AAATTGAAAA	GACCAAAGCA	AGTAATTTTA	TACAGCTTAG	TGATTGGATT	2760
GCTACTGACT	CAGTGAGGAA	TCAGATGATT	CTCAAGGATA	TTCTAGCCCA	AGTGGCAGAA	2820
GGACGGAATA	TCTTGTTTTT	AGTTAATCGA	ATTCAACAGA	TAGATGTCTT	TGAAAAATTA	2880
TTGAAAAGAGA	AAGAGGTTGA	TGACTGTTAC	ATTATTAGCG	GAAAAACCAA	AGTCCGAGAG	2940
AGAACGAGTT	TACTGGAGAC	GTTAGAACAG	TTAGATAAAG	GGTTTGT TTT	GTTGTCTACT	3000
GGAAAATACA	TTGGCGAAGG	TTTTGACTTA	CCTCAGTTGG	ACACGCTTAT	CTTGGCAGCA	3060

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CCCTTTTCTT GGAAAAATAA TTTGATTCAG TATGCAGGTC GGATTCATAG AACTACAAG 3120
 GATAAGTCTT TGGTGCCTAT TTTCGATTAT GTGGATATTC ATGTTCCCTTA TTTAGAAAAG 3180
 ATGTTTCAGA AACGACAAGT AGCTTATCGA AAGATGGATT ATCGTGTTCAT CGAGGGTGAG 3240
 GAGAAACAAT TCGTTTATGT TGATAGTAGA TATGAGAAGG TGTTGAGAGA GGACTTAGCA 3300
 GGGGAAAGAC AGGAATGTCT GCTTATTTTA CCTTATGTGC ACCAGACAAA ACTGATGAAT 3360
 TTTCTAAAAG AATTTAGGAT TAGTCAAATF GAGATATGTA TACCAGAGAC GGTGCAAAAT 3420
 AAAGCATGGC TAGACCAGTT GAAGAGCCAG AAAATTAAG TGTCTTTTAC TCAATCAAAA 3480
 ATAGTAACGC CTATTCTTTT GGTGAATAAG ACTATTGTTT GGATGGTGC AATGCCATTA 3540
 TTAGGGAAGG TAGATGAGAT GACCATATTA CGTTTGGAAAT CAGCTAGTAT AGTTTCTGAA 3600
 CTAGTGGCAG GTTTCAGATA GAGAAAATTT TTA AAAATTT CTATGTATGA TTTTCATTTT 3660
 TTTAGTGAGA CTGTTGCCAT TATCACATTC GAATCACACA AAATAAAAAA ATTTTATAAA 3720
 GTACTTGACA AATAGATTGA AATATCATAA AATAAAAACG GTTACAGAGT TATTAATTAT 3780
 TTAAGCTTCA TGTCAACATT AAAAATTGAA ATAAAAGGAT GTTATCACTA ATACAAGTGA 3840
 GCAGGAACCT ATTTAATCAC ATCAGAAGAA GTTCTTGAT GTTTTAAAGT AGGTTCTTTT 3900
 TATTTTAAAA GGGAAATTTT ATGATCATAA AACGAATACT AAACCACAAT GCCGTAATTG 3960
 CGCAAAGTAA AAAAGATATC GATATTCTTC TTTTGGAAAG GGAATAGCT TTTGGAAGAA 4020
 AACTGGAGA TAAAGTAAAT CCAATTGATA TTGAGAAAAG TTTTCTTC AAAAAAGAG 4080
 ATAATATGAC CCGTTTTACA GAGATGTTTA TTAACGTTCC TTTGGAGTTG GTGTACATCA 4140
 CCGAAAAAAT AATTAACCTA GGTAAAATAA CATTTGGTAA TAATTTTGAT GAAATTATCT 4200
 ATATTAATTT AACGGATCAT ATTTCTTCGA GCATAGAACG TTATAAAGAA GGGATTATTA 4260
 TTTGCAATCC CCTACGCTGG GAAATATCGA AATATTATAA AGAAGAATTT GAACTTGGGA 4320
 AAAGGGCTTT ACAAATAATA AAAAAAGAGT TAGGTATTGA ACTTCCAATT GACGAAGCTG 4380
 CATTCATAGC GCTACATTTT GTTAATGCTA ATTTAGAAAA TAATTTTCAA GAGTCGTATA 4440
 AAATCACTGA AATAATTATG GGAATTGAGA AAATCATTCA AGATTTCTAT TGFACTGAGT 4500
 TTAACCAAGA TTCTATTGAT TATTATAGAT TCATAACTCA TATGAAATTA TTTGCCCATC 4560
 GCTTGGTTGA GAATACAAC TATTGTGACG ATGATGA 4597

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3984 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

CGGCTTATTT	ACTACTTGTT	CCATCATATA	TGGAATATGC	ATGAAACCTG	CTCTCATATT	60
AGGGAATTTT	TTATCCACTA	AATAAGAGC	TTGGTACATC	AAATGATTGC	AAACAAAGGT	120
TCCTGCACTA	TTGGATACAA	CTGCCGGAAG	TCCCTGTTTT	TTGATAGCTT	GTACCATCGC	180
TTTGATAGGT	AAACTACTAA	AATAGGCCGA	TGCTCCATCA	ATACGAATCG	GTGTATCAAT	240
TGGTTGATTG	CCTTCGTTAT	CAGGTATGCG	AGCATCATCT	TGATTAATAG	CCACTCGTTC	300
AGGTGTTAAG	CCGGTCCTGC	CGCCTGCTTG	TCCAATACAA	AGTACAGCAT	CTGGTTGATA	360
TCGTAATATT	TCTGCCTCTA	AAACTTCTGA	CGACTTATAA	AAAACCGTTG	GAATTTCTAC	420
CCAGCGAACT	TCAGCCCCAT	TAATCTCAGA	TGGTAATAAT	TTTACAGCCT	CCAAAGCTGG	480
ATTAATCTTT	TCACCTCCAA	AAGGATFAAA	ACCTGTAACC	AATATTTTCA	TTTTATTTTC	540
CTTTACTAAA	ATGCGAGAAA	GTACATTAAG	AATATGTGAA	TAACAATCAT	TACTAGAGCA	600
ACACCTGCTT	GAGCCTTTAT	AACGCCATTC	TGATCTTTCA	TATCCATCAA	TGCTGCTGGT	660
AGAGCGTTAA	AATTAGCAGC	CATTGGGGTC	AATAAGGTCC	CACAATAACC	TGCTGTATCG	720
GCAAGAGCAC	CAGCCACAAT	TGGATTAGCT	CCCAGAGCAA	ATACAAAGGG	AACTCCAACA	780
CCTGCTGTAA	TAACGGTGAA	TGCTGCAAAA	GCATTTCCCA	TAATCATTTG	GAATAGAACC	840
ATTCCAAGAA	CATAGGCCAA	AACTCCTATA	AAGCGACTAT	CTGAAGGAAC	AATACCGCTA	900
ATCAGATGAG	AGATAACATC	ACCAACACCT	GCTACAGTAA	AAATAGCCCC	CAAAGCCCCT	960
AATAATTGAG	GAACAATCCC	ACTTGTGAA	ACTTGCTGAG	TCATTCGATT	ATTTTCTGAT	1020
AACAGACTCT	TAGGGTGACT	ATTGGTAATC	ACAAGAACAG	AAATTGTAGC	AAACAAGGCG	1080
GCAAGGCTAA	TCGAAATCTT	GCTAAATTCT	GGAATCATTT	GCGCTAAGAC	CAACGCAAGT	1140
ATTGCCATCA	GCATAACTGG	AATAAAAAAT	TTATTTTTC	ACCTGTTAGA	TTCAATATTG	1200
GCTTTCATTT	CATCTAAGGA	TGGCAAGGTT	CCGATACGGA	CTTGCTTAAA	CAATGTTAAC	1260
AGCGATAATA	GGATTACAAT	AATACCAATA	CTCATATTTG	GCATATAGGA	ACCACCTATA	1320
AACGTAATAG	ACAATAGAGT	CCAAAATGCA	GATGTCCCAA	GTCGAACTGG	GTTTGTTTTA	1380
TCTTTATAAC	TACAATAGGC	TGTATGGAGA	AATTGACAAC	CAATCACAAT	ATAGGTCAAC	1440
TCTAATAGTT	GCTTTGCCAA	CTCTGTCATT	TTTGTCTCC	TCCCCTAGTC	TTTTTTGATA	1500
TCAATTTTTT	ATCAAATAAA	TAATTATAAA	TCCCCACTAC	AATAAGTGTT	ATAACAGCAA	1560
CAATAATAGA	TGTAGAAGCA	ATCCCTGCAT	AATTGCTTTC	ATAGCCTAAC	TGATCTAATG	1620

1109

TTCCCCCTAT	CAAGAGGACT	CCCCCAGCAC	CTACAAACGT	ATTTTGAGCA	AAGAAATTTT	1680
CAAAATTTTC	ATTCGCAGCC	GCACGCGCTT	TTATTGTCTC	ATCTTCAACC	TCTGTTAACT	1740
TTCTACCTAA	TTGAGACTCT	GCAGCTGCTT	CTCCCATAGG	TTGAACCAA	GGTCTGACAA	1800
ACTGAGGGTG	TCCTCCTAGA	CGAATTGAAA	AGAAACCAGC	TAACCTCTCGA	ATAAAGAAAT	1860
AAACTGTATA	GAAGTTTCCA	ACTGTCAGAC	CTTTAATCTT	TCGAATCAA	TCGATTGATC	1920
GTTGCTTGAG	TCCAAAGGTT	TCTGACAGCC	CCACAAGAGG	CAAGGTAACC	ATAAAAAATCG	1980
TGAGCACTCG	CTGATTGCTA	AATTCTTTTT	CCAAAATCTC	CAAAAATCA	ACGAGAGAAA	2040
CACCTGAAAC	TAAAGCTGTA	ACCAAACCAG	CTAAGACTAC	TGTTGCAATT	GTATCAAATT	2100
TTAAAATAAA	ACCCACAACA	ATGATTGCTA	TTCCATTATA	TCTAATCCAC	TCCATATCAA	2160
ACTCCTTTAT	ATTCAAAATG	ACAGTATTTT	TAAAATTTTA	TCAAGATCAA	TACCATTTCCT	2220
TATTTAATGT	GTTTTTCTAG	TTCTTTTTGG	TATTTGCTAT	TGGATTCCAA	TTTTTCTTTT	2280
TGCCATTTTT	TAAAAACCTC	GTTATATTCT	TTTGTGTGTA	CAATATCTTT	TTGCAATTTT	2340
ATTCCTTTAA	AGATATATGG	ATCCCCCTTA	ATACCAACTT	GTGAGTATGG	TTTTGAGAAT	2400
GGTACTACGT	TACTTACAAC	TGGAGAACCA	CCAGATGAAG	CTGTTGGCAT	CAATAATGAA	2460
CTATCTGTCTG	ACCAAGCTTG	AGCTTTGGCA	TATTTTTCAT	ATCTTTTCTC	TAGGTCAGTG	2520
GTCTCAGAAA	CAGCATCTTC	TAACAATTTT	TTATATTTAT	CCAAACCAGG	TTAGCTACA	2580
ACATCCTTAT	CTTTTCCTTT	CGTAATACCA	AGGTGTTTCA	TGGCAGAACC	AGATTTTGGA	2640
TCTATAATAT	TCAAGTGAGA	CGCTGGATCT	TGATAGCTTG	GAGCCCATCC	TGTAAGTTC	2700
AAATCATAGT	CTTTTTGAGA	AGGAGCAACA	TTGCCGTATT	TATCATTTTC	CATCAAACCA	2760
TCAATAACAT	TTCCAATAAC	GTCTGTCCTC	GATGTTGCGAG	TCGCTATACT	GTAGCCCAAT	2820
GATGCTGGAT	CTACTGCATA	GACATAAGAA	AATGTTGTCG	GTGCATCTGC	TTCTTTATCA	2880
GTTTTTCCAC	AAGCCACTAA	AATAGCTGAC	GTGCTCAGGA	CCACTCCTGC	TGTTAAGAGC	2940
CACTTTTTCT	ATTTTCATAA	GAATCTCCTT	TGGTTTATTT	TAATCTACTT	TTACAATCCA	3000
ACCTTCTGGC	GCTTCAATAT	CGCCAAACTG	AATACCCGTC	AATTCATTAT	ATAATTTACG	3060
CGTCACAGGA	CCTACTTCTG	TTTCACTATA	GAATACATGG	AAATCATCAC	CATGTTGAAT	3120
ACCTCCAATT	GGAGAAATAA	CCGCTGCTGT	ACCACAGGCA	CCTGCCTCTA	CAAAACGGTC	3180
AAGATTATCA	ATTGGAACAT	CACCCTCAAT	AGGAGTTAAT	CCCAAGCGAT	GTTCTGCCAA	3240
ATAAAGCAAG	GAATACTTGG	TAATAGATGG	CAAGATAGAT	GGACTCAATG	GTGTTACAAA	3300
TTCATATATCA	GCTGTAATTC	CAAAGAAGTT	AGCTGATCCG	ACTTCTTCAA	TCTTTGTATG	3360

1110

AGTTGATGGG TCCAGATAGA TAACATCTGA GAAATGACGT GACTTGGCCA TTTTFCCTGG	3420
TAAGAGACTT GCAGCATAGT TTCCACCAAC CTTAGCCGCA CCTGTACCAT TTGGTGCTGC	3480
ACGGTCGTAC TCATCCTGAA TCAAGAAGTT GGTGGGACC AAACCACCTT TAAAGTAATT	3540
TCCAACGGC ATAGCAAAGA TGGTGAATAA GTACTCTTCT GCCGGTTTTA CCCCATAAT	3600
ATCTCCGACA CCAATCAAAA GAGGGCGAAG ATATAAGGTT CCACCTGTTC CGTATGGTGG	3660
TACGTATPCT TCATTCGCAC GGACAACTGC TTTACAAGCT TCTACAAACA TGTCTGCTCG	3720
AACTTGTGGC ATCAAGAGAC GGTCACATGT ACGTTGCAGA CGTTTAGCAT TTTATCAGG	3780
ACGGAACAGT TGAACACTGC CATCCTTAGT ACGATAAGCT TTCAAACCTT CAAATGCTTG	3840
TTGTCCATAG TGAAGACTTG GAGAAGACTC TGAATATGC AAAGTTGCAT CCTCTGTAAG	3900
CTCTCCTTGA TCCATTGTC CATTTTTGAA ATGAGCAAGA TAGCGATAAG GTAATTTTAT	3960
ATAGGAAAAA CCGAGGTTTT CCGG	3984

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TATCTAATTA TTGGTTTTTA TCGCTGACCT TGGCTATTGT TGGGGTTGTT TTACCCTTGT	60
TGCCTACAAC ACCTTTCCTT TTGTGTCTA TTGCTTGTTC CTCCAGAAGT TCCAAGCGAT	120
TCGAAGATTG GCTTTATCAT ACCAAGCTCT ATCAAGCATA TGTAGCTGAT TTTCGTGAGA	180
CCAAGTCTAT TGC CGGTGAA CGAAAGAAAA AAATCATCGT CTCTATCTAC GTCTTGATGG	240
GAATTTCTAT TTATTTTGCA CCTCTTTTAC CAGTCAAAAT CGGTCTGGGT GCTTTGACCA	300
TCTTTATTAC TTATTATCTC TTCAAGGTCA TTCCAGACAA AGAATAGTTA AAACAGTACT	360
TATTTGCCTT GATAAAATG AAAGCATATT CATAACAATA TGATATAATA AAATTGAAGT	420
AATATTCAAG GAGAATCAAA TGATTTACGA ATTTTGTGCT GAAAATGTGA CTTTACTTGA	480
AAAAGCGATG CAGGCTGGAG CTCGTCGGAT TGAACCTCTG GATAATCTAG CAGTTGGTGG	540
GACAACACCC AGCTATGGAG TGACTAAGGC AGCGGTTGAA CTGGCAGCTA ACTACGATAC	600
AACCATCATG ACCATGATTC GGCCACGTGG TGGTGACTTT GTCTATAATG ACCTAGAAAT	660
TGCTATCATG CTAGAAGACA TTCGTTTGAC TGCTCAGGCT GGAAGTCAAG GGGTTGTATT	720
TGGAGCTTTA ACTGCTGATA AAAAGTTGGA TAAGCCTAAT CTGGAAAAGT TAATTGCTGC	780

1111

ATCAAAAGGA	ATGGAAATTG	TCTTTCACAT	GGCCTTTGAT	GAAC TAAGTG	ATGAAGATCA	840
AGCGGAAGCT	ATTGACTGGC	TCAGTCAAGC	CGGTGTCACT	CGTATCCTAA	CTCGTGCTGG	900
TGTGTCTGGC	GACTCCTTAG	AAAAACGTTT	TGTTCACTAT	CACAGAATTT	TGGAGTACGC	960
TAAAGGTAAA	ATTGAAATTC	TACCAGGTGG	GGGGATTGAC	CTTGAAAACC	GTCAAACCTT	1020
TATCGACCAG	GTGGGGGTAA	CACAATTGCA	TGGTACTAAG	GTTGTTTTTT	AAAAAATAGA	1080
AAGGAACTGC	TAGCTTTGGG	TAGCAGTTTT	CACTTATGTT	TGAAATTTTT	AAATCCTATC	1140
AATTTAATCA	AGAAAAGGCT	CATGATPATG	GTTTTATAGA	AAATAGCGAA	GTCTGGACAT	1200
ATAGTTGCCA	GATTTTGCAA	GGTGACTTTG	TCATGACTGT	GTCCATCACT	GCTGATAATG	1260
TGAACTTTCA	AGTCTTTGAC	CAAGAGACTG	GTGACCTCTA	TCCTCACGTT	TATATGGAAA	1320
GCATGAGGGG	AAGTTTTGTC	GGAAATGTCC	GTGAGGCTTG	TCTGGAGATT	CTTTACCAGA	1380
TTCGGAACCC	TTGTTTTGAT	GTGCAAGATT	TTATCTGTCA	TCAGACTAAG	CGTATCATGA	1440
CTCAAGTTCA	GGAAAAGTAT	GGAAACCAGT	TGGAGTATCT	GTGGGAAAAA	TCGCCTGATA	1500
CAGCTGTATT	GCGCCATGAA	GGCAATCAAA	AGTGGTATGC	CGTCTTGATG	AAAATCTCTT	1560
GGAATAAGCT	GGAAAAGGGC	AGAGAAGGAC	AAGTGAAGC	AGTCAACCTC	AAGCATGACC	1620
AAGTAGCTAA	TTTGCTTTCA	CAAAAGGGGA	TTTATCCAGC	CTTCCATATG	AGCAAGCGCT	1680
ACTGGATTAG	TGTGTCCTT	GATGATACTT	TATCAGATGA	AGAAGTACTG	GAATTGATAG	1740
AAAAAAGTTG	GAAC TTAACC	TCTAAAAAAT	GAAATATTTT	AATAATTTTC	ATGAACTTTC	1800
AATTAGCTAA	ATATTCTTTA	CTGAAGAGAT	TTTTAGAAAA	TATAGGATTT	ACCACACTAG	1860
AGGAATATGG	TGCCATCTTC	AAATACCTGA	TTGAGAATGT	CAAGACGGAT	CGTCAGATCA	1920
TCTATTCGCC	TCACTGTCAT	GATGACCTCG	GAATGGCAGT	GGCAAATAGC	CTTGCTGCTG	1980
TCAAGAATGG	TGCAGGACGT	GTTGAAGGGA	CTATCAATGG	TATTAGGGAG	CGAGCTGAAA	2040
ATGCTGCTTT	GGAAGAAATT	GCAGTGGCTC	TCAATATTCG	CCAAGATTAC	TACCAAGTAG	2100
AAACCAGTAT	TGTCCTAAAT	GAGACCATCA	ATACGTCAGA	AATGGTTTCT	CGCTTCTCTG	2160
GTATTCAGT	TCCTAAAAAC	AAAGCCGTCG	TTGGTGGCAA	TACCTTCTCC	CACGAATCTG	2220
GTATTCACCA	AGATGGAGTC	CTTAAAAATC	CTCTCACTTA	TGAGATCATC	ACACCTGAAT	2280
TGGTTGGTGT	TAAGATTCTG	CTTGAAAAAT	TATCTGGTCG	CCATGCTTTT	GTTGAGAAAC	2340
TGAGAGAATT	GGCCCTAGAT	TTTACAGAAG	AGGATATCAA	ACCACTCTTT	GCTAAGTTCA	2400
AGGCACTGGT	CGATAAGAAG	CAAGAAATCA	CAGATGCAGA	TATTCGAGCT	TTGGTAGCTG	2460
GAACCATGGT	TGAAAATCCA	GAAGGCTTCC	ACTTTGATGA	TTTACAACCT	CAAACCTCATG	2520

1112

CAGATAATGA	CATTGAAGCG	CTCGTTAGCC	TAGCCAATAT	GGATGGTGAG	AAAGTCGAAT	2580
TTAATGCGAC	AGGGCAAGGT	TCCGTTGAAG	CAATCTTTAA	TGCTATCGAT	AAGTTCTTTA	2640
ACCAATCTGT	TCGTTTGGTG	TCCTACACTA	TCGATGCGGT	AACAGATGGA	ATCGATACCC	2700
AGGATCGGGT	TTTGGTCACT	GTTGAAAACA	GAGATACAGA	AACCATCTTT	AATGCAGCAG	2760
GGCTTGATTT	TGATGTGTG	AAGGCTTCTG	CTATTGTCTA	TATAAACGCT	AATACCTTTG	2820
TTCAAAAAGA	GAATGCAGGT	GAGATGGGAC	GCAGTGTTC	TTACCACGAT	ATGCCTAGTG	2880
TGTAAAGGAG	AAGGCTATGG	CAAAGAAAAT	AGTAGTCTTA	GCAGGAGACG	GAATTGGCCC	2940
AGAAATCATG	GAGGTTGGTT	TAGAAGTTCT	GGAGGCTCTA	GCTGAAAAAA	CAGGTTTTGA	3000
CTATGAGATT	GACAGACGAC	CGTTCGGAGG	TGCAGATATT	GATGCAGCAT	GACCTCCCTT	3060
ACCTGATGAA	ACCCTTAAGG	CAAGTAGGGA	AGCAGATGCT	ATCCTACTAG	TAGCTATCGG	3120
TAGTCCTCAG	TATGATGGAG	CAGTGGTTCG	CCCTGAACAA	GGCCTGATGG	CTCTCCGTAA	3180
GGAACCTCAAT	CTTTACGCTA	ATATTTCGTCC	TGTAAAAATC	TTTGACAGTC	TCAAGCATTT	3240
GTCACCCTC	AAACTGGAAC	GAATTGCTGG	TGTAGACTTT	GTCGTGGTGC	GTGAATTGAC	3300
AGGCGGGATT	TACTTTGGAT	ATCATATCT	TGAAGAGCGC	AATGCGCGTG	ATATCAACGA	3360
CTATAGCTAT	GAGGAAGTGG	AGCGGATTAT	TCGCAAAGCC	TTTGAAATG	CAAGAAATCG	3420
CAGAAAAATC	GTTACTAGTA	TCGATAAGCA	AAATGTTCTA	GCGACCTCAA	AACTCTGGCG	3480
GAAAGTAGCT	GAGGAAGTCG	CACAGGATTT	CCCAGATGTA	ACCTTGGAAC	ATCAGCTGGT	3540
AGACTCAGCT	GCTATGCTTA	TGATTACCAA	TCCTGCTAAG	TTTGATGTTA	TTGTAACGGA	3600
GAATCTTTTT	GGAGATATTT	TATCTGATGA	ATCAAGCGTC	TTATCTGGTA	CACTTGGGGT	3660
TATGCCATCA	GCCAGTCATT	CTGAAAATGG	ACCAAGTCTC	TATGAACCTA	TTCACGGTTC	3720
AGCACCTGAT	ATTGCAGGTC	AAGGAATGTC	CAATCCTATT	TCCATGATTT	TATCAGTTTC	3780
CATGATGTTG	AGAGATAGTT	TCGGACGTTA	TGAGGATGCA	GAGCGTATCA	AACGTGCTGT	3840
TGAGACAAGT	CTGGCGGCAG	GAATTTTAAC	GAGAGATATA	GGAGGTCAGG	CTTCAACAAA	3900
GGAAATGACG	GAAGCTATTA	TTGCAAGGTT	ATGAAGTTAG	ACGAAAAAAT	TACTCTAGTC	3960
CTTTTGATTT	GGAATGTCAT	CATTTTCTTG	ATTTATGGTA	TTGACAAATC	TAAGGCAAGG	4020
AGAAGAGTTT	GGCGCATCCC	TGAGAAAATC	TTACTTATTT	TAGCCTTIAC	TTTTGGTGGT	4080
TTTGGTGCCT	GGCTAGCAGG	AATCATCTTT	CACCACAAGA	CTCGAAAATG	GTACTTTAAA	4140
ATAGTTTGGT	TTCTTGGGAT	GGTGACCACA	CTAGTAGCCT	TATATTTTAT	TTGGAGGTAA	4200
TGGATGGCAG	GGTCTTCGAG	GGAATACGCT	GCTTGGGCTC	TAGCGGACTA	TGGTTTTAAG	4260
GTCGTGATTG	CAGGATCTTT	CGGTGACATT	CATTACAATA	ATGAACCTAA	TAATGGCATG	4320

1113

TTGCCAATCG	TTCAGCCTAG	AGAGGTTAGA	GAGAACTAG	CCCAGCTAAA	ACCAACCGAC	4380
CAGGTAAC TG	TGGACTTGGA	ACAACAAAAA	ATCATCTCAC	CAGTTGAAGA	ATTCACCTTC	4440
GAGATAGATA	GCGAGTGGAA	ACATAAACTC	CTAAATAGTT	TGGATGATAT	CGGTATTACC	4500
TTGCAGTATG	AAGAGTTGAT	TGCTGCTTAT	GAAAAACAAC	GACCAGCCTA	CTGGCAGGAT	4560
TAGAAAAAAT	AGAAAAGGAG	ATATAGTAAA	CTGAAATAAG	ATGTAAACAA	ATGAATTGGA	4620
GCTTAACATC	CATTTCCAGC	AATTTTITAG	AAACTACAGT	GGACTATTCT	GGATTCAACA	4680
CATTATAAAA	TTATGACAAA	ACACATTAC	AAGAAGGCTA	CGACATTTTA	AAAGGTGAGG	4740
GCGGATGTAT	CGTTTGCCCT	ACTAAAGTTG	GTTACATTAT	CATGACCAGT	GACAAGGCAG	4800
GACTTGAGCG	TAAGTTCGCA	GCCAAAGAAC	GTAAGCGTAA	CAAACCAGGT	GTTGTTCTCT	4860
GCGGTAGCAT	GGATGAACTT	TGCGCTTTAG	CGCAACTCAA	CCCAGAAATT	GAAGCATTCT	4920
ACTAAAAACA	TTGGGATGAA	GATATTCTTC	TTGGTTGTAT	CCTTCCTTGG	AAACCAGAAG	4980
CCTTTGAAAA	ACTCAAAGCA	TACGGGGATG	GCCGTGAAGA	ACTTATTA	GATGTACGTG	5040
GTAAGTAGCTG	TTTTGTATC	AAGTTTGAA	AAGCAGGTGA	ACAATGGCT	GCCAAGCTTT	5100
GGGAAGAAGG	TAAAATGGTC	TACGCCTCAT	CTGCTTCAAT	GACAAAACGA	TTGAAACTCG	5160
CTATGAGCAA	GGTGTAAATG	TGTCTATGGT	CGATAAGGAC	GGCAAAC TCA	TCCCAGAACA	5220
AGGAGGAGCA	CGTTCAACTT	CACCAGCTCC	AGTTGTGATC	CGTAAAGGGC	TTGACATTGA	5280
TAAAATCATG	ATGCACCTGT	CAGATACTTT	TAAC TCA TGG	GACTACCGTC	AGGTGAGTA	5340
TTATTAGGAT	AGAGAAGAAG	TCTAGTGTTA	TGAGATATTA	AAGCTCCTAA	CACTGGGCTT	5400
TTGTTTAGAA	TTTCTTTTCT	TTTTCTATAG	GATATGGTAT	TCTATGTAGA	AAATATATGT	5460
TAATAAGTAA	TGCCAATATT	TAAACATCAT	TAGTAAAAGG	AGTTAGATTG	ATGAATAAAA	5520
GAAAAGTTAG	TTTAGAAGAT	TTTTATAAAT	GGTATAGTCT	AAATAAAGAA	GAGTTATTAA	5580
ATAAGGCAAC	TGTTGGTGAA	AAGTTAATG	ATAAAT TAAA	AGAAGAGTTT	CTCCAGGAAT	5640
GGCCTTTGGA	TAGGATTTTA	ACAATGTCAA	TCGATGAATA	TGTAATAGGA	AAGGGACAGC	5700
AAAATAAGTC	TTTATGCTAC	GCTCTTGAGA	AGGGAAAATA	CAAAAATCTA	TTTCTTGGA	5760
TTTCTGGTGG	CTCAGCTTCA	AAATTTGGTA	TTTATTGGA	TAAAAAACA	AACAAATATA	5820
AAGATCAAGC	TAATAATGAG	ATTT CAGAGT	TGGATCAGCG	ATTTTCAAAA	TTAAAATCAG	5880
ATTTGTATGA	AATTATCAAA	GAAGGTATTC	GTTTTAACTT	TGAAAATCCT	ATTTT T GATA	5940
TGAAAAGATC	AACAAATGAA	TTTATGGTC	GTTCTGCTAT	GGTGACAAA	TFACTTTGTA	6000
TCTATACTGA	GGGAGATCCT	TTCTTTGGTG	TAAATAT TAA	TAGTCAGAAA	GAATTTT GGA	6060

1114

ACCACTTTGT	TTCTCAGACA	AATCAAGGTG	GACCTTATCT	GCAAAATCAT	AAAATAATTG	6120
AACTGGTGTC	CAAAACTTAT	CCTGAGTTGG	AGCCATCGAA	ATTAGGAACT	ATGCTTTTTG	6180
AGTATTCTAA	GCTTTTTATG	GAAAATAAGG	AAGACAATAG	TACAATGGAT	TCATCAAACA	6240
ATTTTCGTCA	TCAATTAACT	CAATCTCTAT	TAAAGTCTCC	AAACCTCATC	CTCCGCGGTG	6300
CTCCTGGCAC	GGGAAAAACT	TATCTTGCTA	AAGAAATGTC	TAAAGAATTA	ACGGATGGCA	6360
ACGAAGATCA	AATCGGATTT	GTACAATTTT	ACCCATCATA	TGATTATACG	GATTTTGTAG	6420
AAGGTTTAAG	ACCAGTATCA	AATGGGGATG	GAGCTATTGA	GTTTAGGCTA	CAGGACGGTA	6480
TTTTTAAAGA	TTTTTGTCTAG	AAAGCAAAAG	AAACCCAATT	GATTGGAGGA	CAAGATAAAT	6540
TTGATGAGGC	TTGGGATTCT	TACTTAGAAT	ATATAAATGT	TGCTGAAGAA	AAAGAATATA	6600
TAACAAAAAC	ATCTTACTTA	TCTGTTAATA	GTAGACAAAA	TTTGTCTAGTA	AATTATGATA	6660
GTGGTGTTC	AGGATGGTCA	CTACCTAGCA	AATATGTTTA	CGAGTTGTAT	AAAGATAAAA	6720
ATTATAATAA	GCAAGAATAC	TACAAAAGTG	GTGAAAAAAC	TGTCCTAGAA	ACATTGAGAA	6780
AGAGATTTGG	TTTGAAAGAC	TATGTTTCCC	CAACAGAAAT	TGATACTGAT	AAGAATTTTG	6840
TCTTCATCAT	CGATGAGATC	AATCGTGGGG	AGATTTCTAA	GATTTTTGGC	GAACCTTTTT	6900
TCTCTATCGA	CCCCGGCTAT	CGTGGTGAAA	AAGGAAGTGT	TTCTACCCAA	TATGCAAATC	6960
TACACGAAAC	TGATGAAAAG	TTCTATATCC	CCGAAAATGT	TTACATCATC	GGAACATATGA	7020
ATGATATTGA	TCGTTTCAGTG	GATACCTTTG	ATTTTGTCTAT	GCGTCGTCGT	TTTCGTTTTG	7080
TTGAAGTTAC	TGTCGAGGGT	CAAGCTGGCA	TGTTGGATAA	AGAGTTGAAT	ATCCATGCAG	7140
AAGAAGCAAA	AATTCGTCTA	AGAAACTTGA	ACGCTGCTAT	CGAAAATATT	CAGGAATTAA	7200
ACAGTCATTA	TCATATTGGA	CCAAGTTATT	TTCTTAAGTT	GAAGGATGTA	GATTTTACT	7260
ATGAATTACT	CTGGTCTGAT	TATATTAAGC	CTCTCCTAGA	AGACTACTTG	CGAGGTTCTT	7320
ATGATGAGGT	TGAAACTTTG	GAAACTTTGA	AAAAGCATT	TGATCTGACA	AATAATGAGC	7380
AAAAAGATCA	GGCAGTAGCT	GATGACAATG	AAGGCGATGA	AAACGATGAT	GCGGATTAAT	7440
GATAATCAAC	ACAAGATTAT	TAAAGAAAAA	TTTGTGAAG	AATATCCTAA	ACTAAGCAAT	7500
CCTCTTTTAG	ACAGAACCTT	GGAAAGTCTA	TCCCAAGATG	AACGTATTTT	CATTTTCCA	7560
AATGATTWGA	CTCATACTCC	TGATTTGGAT	AAGGACCAA	AGATTTTGA	AACAGTCAAT	7620
CAGAAAATCA	AGACAGGGAA	CGTGATTGGT	TTTCTTGGAT	ATGGTCAGGA	AAGATTAACG	7680
ATTTCTCAC	GATTTTCTGA	TGAGAGTAAT	GACCACTTT	TGCATTATCT	CTTAAACAAG	7740
GTTCTTCATA	TCAATCTCAC	TAGTTTAGAT	GTTGCTTTGT	CTCGTGAAGA	GAGGCTTTAT	7800
CAACTTTTGG	TGTATCTCTT	TCCCAAGTAT	CTACAAGCTG	CTATTCGAAA	AGGTCTTTAT	7860

1115

AAGGAATATC ATCGATTTTC TCATAACGAC AGTCATGTTA AGGGAGTGAT TGATGTAAGA	7920
AACCATCTCA AGAAAAATCT TCCTTTCACG GGAAATATTG CCTACGCAAC GAGAGAGTTC	7980
ACCTATGATA ATCCCCCAT GCAGTTGGTC CGTCACACTA TTGAATACAT TAAGAATCAG	8040
AAAAGCATTG GTCAAGGGGT ACTAGATAAT CTCTCAACTA GTCGTGAAAA CGTATCTGAA	8100
ATCGTGCGTG TAACGCCCTC TTATAAACTA GCTGATCGTG CTAAGATTAT TCGGGGAAAT	8160
CAATCTAAAC CTATACGTCA TGCATACTTT CACGAGTACA GAAACTTACA AGAACTTTGT	8220
CTGATGATCC TAAACCAAGA AAAGCACGGT TTAGGGTATC AAGATCAAAA AATCTATGGT	8280
ATTCTCTTTG ATGTTGCCTG GCTTTGGGAA GAGTATGTTT ACACCTTGTT GCCAAAAGGT	8340
TTTGTACATC CCAGAAATAA GGATAAGACG GATGGAATTT CAGTATTTTC TGTGGGAAA	8400
CGAAAAGTAT ATCCAGATTT TTATGACAGA GAACGAAAGA TTGTTCTAGA TGCAAAATAT	8460
AAAAAAGTGG AATTGACTGA AAAAGGAATC AACCGTGAGG ACTTATPCCA GCTGATTTCC	8520
TATTCTTATA TTTTAAAAGC TGAGAAGGCT GGACTGATTT TTCCTAGTAT GGAGCAGTCA	8580
GTAATAAGTG AAATAGGAAA AGTAGCTGGC TATGGAGCTC AATTGAAGAA GTGGTCTATT	8640
CGAATCCCTC AGAATGCCTC ATTCTATAGT ACATTTTGTA AAATGATGGA AAATTCAGAA	8700
GAG	8703

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

CATCACCAGT TTTAGATGGC TTTAACAGTG AAATATTGTC TTTTAATCTT TCTTGTTTCG	60
CTAATTTAGA ACAAGTACAA ACAATGTTGG AACAGGCATT CAAAGAGAAG CACTACGAGA	120
ATACGATTCT CCATAGTGAC CAAGGCTGGC AATATCAACA CGATTCTTAT CATCGGTTCC	180
TAGAGAGTAA GGAATTCAA GCATCCATGT CACGTAAGGG CAACAGCCAA GACAACGGTA	240
GGATGGAATC TTTCTTTGGC ATTTTAAAAT CCGAATGTT TTATGGCTAT GAGAAAACAT	300
TTAAATCACT TAACCAATTG GAACAAGCCA TTATAGACTA TATTGATTAT TACAACAATA	360
AGAAAATTAA GATAAACTA AAAGGACTTA GTCCTGTGCA GTACAGAACT AAATCCTTTG	420
GATAAATTAT TTGTCTAACT GTTTGGGGGC AGTACACAAG AAAGCGCTTT AAAACCAGTA	480

1116

GACCTTTTCA	TAAGGTTTCG	TTGATGTACC	AAGATGAGGC	TGGTTTCGGT	AGAATCAGTA	540
AACTGGGATC	TTGTTGGTCT	CCAATAGGAG	TAGGTCCACA	TGTCATAGT	CACTATATAC	600
GAGAATTTTCG	CTATTGTTAT	GGAGCTGTTG	ATGCCCATAC	AGGCGAATCA	TTTTTCTTAA	660
TAGCTGGTGG	ATGTAATACT	GAGTGGATGA	ACGCCTTTTT	AGAAGAGCTT	TCACAAGCTT	720
ATCCAGATGA	TTATCTTTTA	CTCGTTATGG	ACAATGCTAT	ATGGCATAAA	TCAAGTACCT	780
TAAAGATTCC	GACTAATATT	GGTTTTACCT	TTATTCTCTC	ATACACACCA	GAGATGAACC	840
CATTGAACAA	GTGTGGAAAG	AGATTCGTAA	ACGTGGATTT	AAGAATAAAG	CCTTTCGAAC	900
TTTGGAAGAT	GTCATGAATC	AACTCCAAGA	TGTCATACAA	GGATTGGAGA	AGGAGGTGAT	960
AAAGTCCATC	GTTAATCGGA	GATGGACTAG	AATGCTTTTT	GAAAACAGAT	GAGTATAAAA	1020
TTGAATTGCT	TATAAAAAAG	CTCCATACAC	TGGATGTGTA	TAGAGCAATG	GGGCTTTATT	1080
TGATATAGAG	TTCTTGGTTT	TTTAGGACAA	TTTCTCGGAT	ACTTGCAAAC	TTTTTAAGTT	1140
TTTTGATTTT	TTCTGGATGA	GTGACGAGAG	TGATAACATA	ACCTTCCTTG	CCCATACGAC	1200
CAGTACGGCC	AGCACGGTGT	GTGTAGGTTT	CGCTATCTCT	AGGAATATCA	AAGTTTACGA	1260
CACATTCTAG	GCTATCGATA	TCAATTCCAC	GAGCCAAAAG	GTCAGTTGCA	AGAAGCAGGG	1320
TTAGTTGGTT	ATCTTTAAAC	TTTTCTAAGA	TGATTTTTCT	AAATTTAACA	TTAACATCAC	1380
TAGCGAGGGA	AACAGCCAAT	ATATCACGAT	ACTGTAGTTT	TTCTTCGGCA	TTCCCAAGGT	1440
CTGACAGGCT	ATTGAAGAAG	ACTAGACCAC	GGAAATCCTC	TACATGAGCC	AGTTTTCGTA	1500
GCATATCCAC	TCGATGACGT	TGGTCTACCT	GCATGTAGAA	ATGCTGGATA	TTGTCCAATT	1560
TTTGATCAGA	GAGATCAATA	GTGCGTGTAT	TCGGCACAAT	CTTTTCTTGG	TCAAACCTGG	1620
TCGTGGCACT	CATGTAGACC	AGTTGGTGGT	CACGAGGTGC	GTAGTGAGTG	ATTTTTTCTA	1680
CAAAGTGAAT	CTGAGAATCA	TCTAGTAATT	GGTCAAATTC	ATCCAGGATG	ATGGTTTCCA	1740
CATTTCATCAT	CTTGATTTTT	TTAAGTTTAA	TGAGTTCAAA	GATACGGCCA	GGAGTTCCAA	1800
TCAGAATTTT	TGGCCCTTTT	TTAAGACGTT	CAATTTGTCG	TTTCTGACTT	GAACCTGAAA	1860
GGAAGAGTTG	AGCAGTCAAT	CCGATAGCTT	CTGCCACGTT	TTTACATACA	TCAAAAATCT	1920
GTCCAGCAAG	TTCCGTATTT	GGTGTAGAA	TCAAGAGTTG	TTGGGCTTTT	TTCTTTTGTA	1980
GTCTGAGAAG	ACTTGGTAGG	AGATACGCTA	GGGTCTTACC	AGTTCCGGTT	TGGCTCACTC	2040
CTAGGAGGTT	TTCTCCAGCA	AGAAGGGGCT	CAAATAGTTG	AGTTTGAATG	GGGGTGAATT	2100
CTTGGAACCC	GAGTTGGTCA	CTCAGTTCTT	GCCATTCAGT	CGGTAGTTTG	GTTTTCATTT	2160
TTCTGCCTCA	AATCTAATGC	CAGCAGTCTG	GCGCATGGTA	TATAGTAGCT	CATGAACAGA	2220
GCCTGCATCA	TACAGCCAAG	TTTGGTAGAG	ATTCAGATCT	GGTTGCTGGA	TCATGTGTGC	2280

1117

AAATGCAGCG	ACTTCCTCAG	TCATCGTATG	AGGAGCCTGT	TGGATAGGAA	GCTGGACTTG	2340
ATTTCCCTTG	TGGTCGGTAA	AAATAGCTGA	GCGAATATGC	TCAATCGTGT	TGAGAGTCAA	2400
GGTTCATCT	GTTGTATAAA	TCTCGCAAGG	AAGATGGAA	GTGATGTTTT	TTCCAGCCTT	2460
GATGTGAACT	TGATAGTCTG	GGTAGAAGAG	GATACCATCT	CCATTTAGGT	CAATGCTATT	2520
GTCAAGCTGT	TGAGCATGGT	AAGTCGCGTC	ATTGGCTTTT	CCAAAAAGAC	GAACAGCAGC	2580
ATAGAGGGGA	TAAATCCCCA	AATCCATGAG	GGCTCCACCA	GCAAAACGGT	CTGAAAAGAC	2640
ATTTGGTGTT	TGTCCAGCCA	ACAAGTCAGG	CATCTTGGAA	GAGTATTTGG	CATAGTTGAA	2700
ATCTGCTCCT	AACACTTGCT	TATCTGCTAA	AAAGTTTTTG	ATAGTAGTAA	AGGCTTTCTC	2760
GTGGTAATTA	CGAGCTGCTT	CAAAGATAAA	ACAGTTATTT	TTTTCAGCTG	TTTGAATCAA	2820
ATCAAACCAT	TCTTGTGGTT	GAGAGACAGC	TGGCTTTTCG	AGAATAACAT	GTTTACCAGC	2880
AGACAAGGCA	GCTTTTGCCT	GAGCAAAATG	TAAGGAGTTT	GGACTGGCGA	TATAGACTAA	2940
ATCAAAGAA	GATTTGAAGA	AGACTTCTAA	TTGATCGAAT	AGTTGGATAT	TCTGATAGCG	3000
AGAAGCAAAG	GTTGCTGCAG	TTTCTAGTTT	TCTAGAATAG	ATTGCGACCA	GTTGGTATTC	3060
TCCACTGGTA	TGGCTGCTT	CTATGAAATG	ATGCTGATA	GCGCCAGTTC	CGATGACACC	3120
TAATTTTAGC	ATAAATACTC	CTTTCCGAT	TTTAAATCCT	TCTTTCATTA	TAACATAGAT	3180
AGACGGGACT	ATCCAACAGA	GAGGAGAAAA	TTTCAAATAA	GCTATTAGCT	TTCTTTTCCG	3240
AATAAATAGA	TAGAAGCATA	GAATCTAGCA	AACCTAGATT	TAAAAATGTG	CTATAATAGA	3300
AGGAGGAAAA	GGAGGATTCT	CAGACATCTA	GGTATCAGCC	CAACTAATGA	TTTGTCAATT	3360
TATCCGCGAT	ATGCTGGACT	TGCCAGCAAA	AAATGTGACG	ATTTTGGAGG	GAAGTAACAT	3420
TCACGTCTTG	CCTTCCATGC	CCTACTCAGC	GTAAGATTC	TATACTAGTA	TAGACGTCTT	3480
GGCGGAGTTA	GATAATGGAA	TCCAAGTTAT	CATCGAAATT	CAGGTTTCATC	ATCAGAATTT	3540
TTTCATCAAT	CGCCTATGGC	CTTATCTGTG	CAGTCAGGTT	AATCAAACC	TAGAAAAAAT	3600
TCGCCAACGT	GAAGGTGATA	CCCACCAGAG	CTACAAACAA	ATCGCACTAG	TATACGCTAT	3660
CGCAATTGTC	GATAGTAATT	ACTTCTCAGA	TGACCTAGCT	TTTCATAGTT	TTATAGTAAA	3720
ATGAAATGAG	AACAGGACAA	ATCGATCAGG	ACAGTCAAAT	CGATTTCTAA	CAATGTTTTA	3780
GAAGTATAGG	TCTACTATTC	TAGCTTCAAT	CTACTAGAAA	TTCCATAGAT	AGAAAACACTAC	3840
ATAATCTCTA	CAGATACGGA	TGTTGGAGTT	GATGTAAGAT	GCTTTGGCTT	GCTAGAGGAA	3900
TTGTGGATG	CCAAATTGTA	TCATTGAAAT	TATTGCTCAA	ATTTGTTATG	ATATAAATAT	3960
GAATAAAAGT	AGACTAGGAC	GTGGCAGACA	CGGAAAACG	AGACATGTAT	TATTTGGCTTT	4020

1118

GATTGGTATT TTAGCAATTT CTATTTGCCT ATTAGGCGGA TTTATTGCTT TTAAGATCTA	4080
CCAGCAAAAA AGTTTTGAGC AAAAGATTGA ATCGCTCAA AAAGAGAAAG ATGATCAATT	4140
GAGTGAGGGA AATCAGAAGG AGCATTTCG TCAGGGGCAA GCCGAAGTGA TTGCCTATTA	4200
TCCTCTCCAA GGGGAGAAAG TGATTTCCCTC TGTTAGGGAG CTGATAAATC AAGATGTAA	4260
GGACAAGCTA GAAAGTAAGG ACAATCTTGT TTTCTACTAT ACAGAGCAAG AAGAGTCAGG	4320
TTTAAAGGGA GTCGTTAATC GTAATGTGAC CAAACAAATC TATGATTTAG TTGCTTTTAA	4380
GATTGAAGAG ACTGAAAAGA CCAGTCTAGG AAAGGTTAC TTAACAGAAG ATGGGCAACC	4440
TTTTTACTT GACCAACTGT TTTCAGATGC TAGTAAGGCT AAGGAACAGC TGATAAAAGA	4500
GTTGACCTCC TTCATAGAGG ATAAAAAAT AGAGCAAGAC CAGAGTGAGC AGATTGTAAA	4560
AAACTTCTCT GACCAAGACT TGTCTGCATG GAATTTTGAT TACAAGGATA GTCAGATTAT	4620
CCTTTATCCA AGTCTGTGG TTGAAAATTT AGAAGAGATA GCCTTGCCAG TATCTGCTTT	4680
CTTTGATGTT ATCCAATCTT CGTACTTACT CGAAAAAGAT GCGGCCTTGT ACCAATCTTA	4740
CTTTGATAAG AAACATCAA AAGTTGTCGC TCTAACCTTT GATGATGGTC CAAATCCAGC	4800
AACGACCCCG CAGGTATTAG AGACCCTAGC TAAATATGAT ATTACAAGCG GGGT	4854

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2186 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TAAACAGGTG TTAGGTGCTC TAACTATTA AAATCTAAG GAAATAAGGC TACTTTTTCT	60
GGGTCTTGTT CATAGTAGGT GTGGTTCTTT TTTTCGAGTG TAGCCCATAG CTTTGAGCGC	120
ATAGTGGATG GTAGTTGGAT GACAGCCAAA TTCAGAAGCT ATTTAGTCA AATAAGCAAC	180
TGGATTGTCA GTAAGATAGT TTTTAAGTCT ATCTCTATCA ACTTTTCTTG GTTTTGTTC	240
TTTTACTTGG TGGTTTAGCT CTCCTGTTTT CTCTTTTACG TTTAACCAGC CATAAATGGT	300
ATTACGTGAG ATTTGGAAAA CGTGTGATGC TTCTGTTATA CTACCTGTTG GCTCACAATA	360
AGAGAGAACT TTTTACGAA AATCTATTGA ATATGCCATA AGAAGATTAT ACCACATGT	420
GTAATTTTT TGGTTCATTT TACTATATTT CTTAACACTT AGAAATAATA AAACAAATTA	480
AATATTATTT CTTAATATTT GAAAATAACA TCTATTTGTA TTATACTATC TTTGAGGTAA	540
CTATTATGAA CTATATCAA AGACCACATT ATTTAGATTT TTTAAGAAAA CATCGTGACC	600

1119

GACCAATCAT CAAAGTTGTG AGTGGAGTTA GACGAGCTGG TAAATCTGTG CTTTTTCAAC 660
 TCTATAAAGA GGAGTTACTA GCAACTGGGG TAGACGAGGA TCAGATTATA TTCATCAATT 720
 TCGAAGATTT GAGTTACTAT GATCTGCGAC ATTTTCAAAC ATTATTCGCT TATATAAAG 780
 ATCAATTAGT TAGCAAGAAA ACATACTATA TCTTTTTAGA TGAAATTCAA TATGTTGAAA 840
 AATTTGAACT GGTAGCAGAT AGTCTATTCA TCTTAGCAAA TGTAGACCTC TATTTGACTG 900
 GATCTAACGC CTACTTTATG AGTAGCCAAT TAGCAACAAA CTTGACTGGT CGGTATGTTG 960
 AGATAGAGGT TCTTCCTTTG TCATTTGAAG AATATCTATC AGGTCAATCT CTCACAGAGA 1020
 ATCTGAATAC AACAGAAAT TTTAACAATT ATCTCTTTAG TGCTTCCCT TACTTATTGC 1080
 AAACATCATC TTACGATGAA AAAATTGACT ATCTCAGAGG AATATATAAC TCCATACTGT 1140
 TAAATGATAT TGTCACTAGA TTGGGAAAAC CAAATCCTAC TATTATTGAG CGCATTGTCC 1200
 GAACCCTTCT CAGTAGTACA GGTAGCTTAA TATCAACAAA TAAGATTCGC AATACCCTAG 1260
 TCAGCCAAA TGTTCATA TCCATAATA CTTTGAAAA TTATTTGACA ACTTTGACAG 1320
 ATAGTTTACT TTTTATTCC GTTCCACGTT TTGATGTAAA AGGTAGAGCA TTATTGCAAC 1380
 GTTTAGAAAA ATATTATCCC GTTGATTAG GTTTACGACA TCTCTTATTA CCAGACCAGA 1440
 AAGAAGACAT TAGGCATATC TTGAAAAATA TGTATATTT GGAATTGAGA CGTAGATATT 1500
 CACAAGTATA TGTGGTAAT TTAGATAAGT ATGAGGTTGA TTTTGTGTT GTAACGTAC 1560
 TTGGCCACTA CGCTTATTAT CAGGTCAGTG AAACAACACT TGCTCCAGAA AACTAGAAA 1620
 GAGAAGTTAG ACCACTAGAA GCCATTAAAG ATCAATCCC TAAATATCTA TTAACAATGG 1680
 ATACGATCA GCCAACAGCC AATTACAATG GAATCGAGAA GAAAAGCATT ATAGATTGGT 1740
 TACTAGAAA ATAGATAAAT ATAAATCATA CAGCTAATTA GATTGCAAC AGTCTGTTAT 1800
 CAATGATTCT ACCCAAATCC TAACAAGATA TAGTGAATTT CGAATACGCT ATATAATACG 1860
 GACACTGAA AATAGAAATT GGGGATGAAA GGGGATCTAT AATTTCTGGA AGTACTATCA 1920
 AAAATTAATA TCATAGTCTT ATTAGAGAAT AGCATCACC ACTTTCTCAA ATAAGATTAA 1980
 ATTGTAAGT AATTATAATG AAAAAGAGAC TGAGCAATCA GTCTTTAAA TCAGAAAAGC 2040
 GCATAGTATC AGGTATTGAA CAACCTGAT AATATGCGTT TTATTATGGA AATATTTGCT 2100
 TCATTTTCTC CTGAAATAGA GCTTTTGCTA TCCTATTTT CTCTATTCT AATGATTAC 2160
 TTCAACTTCT TACCTCTTG GAAAA 2186

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3236 base pairs

1120

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GTCACACGTT TGA	CTTCACG	TAT	TCATAA	GTATAAACTT	TAT	TTTTTATC	GGTTAGATAA	60
ATCTTCATGC CAT	TTTTTAGC	ATT	TATCTAAA	GGAGAAAATA	ACAT	TTTTTAT	AGCATTATCA	120
ACACCAAAGA TAT	GGTGACT	AGCT	AGACTA	TAAT	TTTCCTT	CTCCCAT	TAC TTGCTCGCGT	180
TTCATTGTAC CAG	CTCCGTA	GAAG	GAGATTA	ACATTATCAA	GTCCT	TTAAA	AATCGGCAAA	240
TTCATTTCCA AT	TCAGGAAT	TGCA	AATCCC	CCAATAACTG	GTAAT	TTTTTG	AGCATCCCAT	300
TGAGAAGTTA GA	CAGCTTC	CGAAG	AGATA	GCTTTGACAG	AATCAA	AGTC	AAAATTGCCT	360
TCTGTATCCT GA	TTTTTCTC	TAAT	TTTTTCT	TTTGATACCT	GGCTAA	CTTG	ATACTTATTG	420
GTATTCCAGA CT	ATGAAAAT	ATTT	CGAATT	TGAGTATTAA	AAATCAA	AGC	CAGTGACAGT	480
AATATCAGAA AT	CCTGCTAG	GATAT	TTGTC	AGCAGATTTT	TTCGCT	TGTT	TTTCTTTTTA	540
TTATTTTTTT G	AGACATAT	GCTT	CACCTT	CTGTTTCGTT	TTCTGT	CCCA	ACTTCTTCTT	600
TTTCTGCCAC CG	CAACCGTT	GTGA	AAGTCA	CTATCTGAGC	ATCTT	GATCC	AGGCGCATTA	660
CTTTAACTCC CA	TAGTTGCA	CGTC	CCTGTTT	GTGAAATATT	GGCAAG	ATTG	GTTCGAATCA	720
TGACACCTGT AT	CAGTGATA	ATCAT	CAAAT	CCTCATCCCC	TTGAAC	AGTC	ATAAGACCGG	780
CCAGCAAGCC AT	TTTTTTTCG	GTAAT	TTTAG	CTGTCTGCAT	TCCCTT	TACCA	CCACGACCTT	840
TTGTTGGGTA TT	CAGTAGCG	ACTGT	ACGCT	TACCATATCC	TTTTTCT	TGTG	ATAATAAGAA	900
CCTCATCTTG AT	CAGTAATC	AAGCT	GGCAC	CAACAAC	TGT	CTCTCA	CGAAGGTAA	960
CACCTTTCAC AC	CAGTGGCG	ATAC	GGCTCA	TACCACGAAC	GGCTG	ATTGA	TTAAAGCGAA	1020
CTGCATAACC AA	ACTTGTA	CCAAT	GATAA	TATCCATATC	TCCTTCT	GCC	AACAAGACAT	1080
TGATTAACTC AT	CTTCATCC	TTTAA	ATTCA	GCGCTTTGAG	ACCAT	TTTGA	CGAATATGG	1140
CAAAC	TCCTT	AACACT	GGTT	CTCTTCACAA	TACCGT	GACG	GGTTGTAAAAG	1200
CATCATCACT GC	GATCAGAC	TCAAC	ATTGA	TAACCGTCTG	AATACT	TTTCG	TCTTCATCCA	1260
ATTTCAAGAG AT	TGACTACT	GGTAG	CCCTT	TGGCAGTCCG	ACCATA	CTCA	GGAATTTCAT	1320
AACCTTTAAG AC	GATAGACA	CGTCC	CTTGT	TTGTGAAGAA	GAGCAG	ATGA	TCATGGGTGC	1380
TAGTTGACAC TA	ACTCACGA	ACAAAG	TCAT	CATCTTTCAC	TCCCGT	TCCT	TGGACACCAC	1440
GACCCACAG TTT	TTGAGCA	GTGAA	CTCGT	CCTGATCCAA	ACGCTT	AATG	TAGCCTCTGT	1500
TAGAAAGGGT AA	TCAGACA	TCCGAT	TCTT	CAATCAAGTC	CTCAT	CTCG	AGACTCAAGA	1560

1121

CCTGTCCAAT CATCAACTCT GTACGGCGCT TATCAGAAAA TTTACGTTTA ACTTCATCCA 1620
 ATTCGTCTTT GATAATTTGA GAAACACGTT CAGGCTTAGC AAGAATATCT GCTAAATCCG 1680
 CAATCAGAGC CAAGAGGTCA TCATACTCAG ATTGAATCTT ATCGCGTTCC AAACCTGTCA 1740
 AACGACGAAG ACGCATATCA AGGATAGCTT GACTTTGACG TTCAGAAAGC TTAAACTTGC 1800
 TCATCAACTC AGCTTGAGcT TCCGCATcCG tTTCACTAGC ACGGATGATA CGAATCAyTC 1860
 GTCGATATGG TCTAGCGCAA TCAAGAGACC TTCTAAGATA TGAGCGCGCG CTCCCGCTTT 1920
 TTCCTTATCA AAACGTGTAC GACGAACAAC CACTTCTTTT TGGTGCTCGA TATAAGCATC 1980
 CAAAATCTGA CGAAGAGACA AAATTTTCGG TATACCATTT TGGATAGCGA GCATATTGAA 2040
 ACCAAAATTG GTTTGCATTT GGGTCATTTT GAAGAGGTTA TTGAGAATAA CATTGGCTGA 2100
 GCGTCGCGC TTGACTTCAA TAACAAATCG AACACCTTCA CGGTTTGACT CATCACGTAC 2160
 TGCTGTGATA CCCTCAATGC GTTTTTCCTG AACCAAGCGA ACAATATGCT CATGCACCTT 2220
 GGTTTTATTG ACCATGTAAG GAAATTCFTGT TACAACGATA CGCTCACGAC CAGTCTTAGT 2280
 CGTTTCAATC TCTGTACGAG AACGTAGGAC AATCGAACCT TTACCTGTTT CATAAGCCTT 2340
 ATGGATACCT GATTTCCCCA TGACAAGAGC ACCAGTTGGA AAATCTGGTC CAGGCAAGAC 2400
 TTCCATCAAG TCCTTGGTAG TCACTTCAGG ATTATCCATG ACCAACTTCA CTGCATCAAT 2460
 gTTTTCAACC AGATTATGAG GTGGAATATT GTTTGCCATC CCAACCGCGA TACCAGTTGC 2520
 TCCATTAACC AAAAGGTTTG GAAAACGCGC TGGCAAGACC AAGGGTTCCT GTTCATTGGC 2580
 ATCATAGTTA TCAACGAAAT CAACTGTATT TTTGTTGATA TCACGAAGCA TTTCCAGAGC 2640
 AATCTTGCTC ATACGTGCCT CGGTATAACG TTGAGCGGCA GCACTATCTC CATCCATGGA 2700
 ACCAAAATTC CCATGACCAT CTACAAGCAT GTAACGGTAG CTCCACCATT GAGCCATACG 2760
 GACCATGGCT TCATAAATAG AGGAATCCCC GTGTGGGTGA TATTTACCCA TGACATCCCC 2820
 TGTAATACGA GCAGATTTTT TATGGGGTTT GTCTGGGGTC ACACCCAATT CATTCAATTC 2880
 GTAGAGAATG GCACGGTGAA CAGGTTTAA GCCATCTCGA ACATCAGGAA GAGCTCGCGC 2940
 TACGATAACA CTCATGGCGT AGTCGATAAA ACTTGCCTTC ATCTCCTTTG TCAGATTGAC 3000
 ATTCACTAAA TTTTTATCCT GCATTAATAA ATGCCTCATT TCACAATTAG TAAGTAACAA 3060
 CATTATACCA TAAATTCCTA TCTATTTAG CCTCTAAACC ACTAAAACGT TTACATCGAG 3120
 AACTATAAGG CATATTCGTG ACAAAGTTTT TTAAGTGA TAGAATGAAG TTGTCTAGGG 3180
 AAAACCCCTA ATAGAATAAG GAGATGGTTA nACAATGACT CTGACTAACA CACAAA 3236

(2) INFORMATION FOR SEQ ID NO: 181:

1122

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8651 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

AGGTCCTGAA GTATTGGAAC AGGAAGGTCA AGAGTTTGTG GAACATTTC AAAAACTCTT	60
GGAGTCAGTT GAAGTAGTAG CCATCTCAGG TAGTCTGCCA GCTGGCCTTC CAGTTGATTA	120
CTATGCGAGC TTGGTAGAAC TTGCTAATCA AGCTGGCAAG CATGTAGTCT TGGACTGCTC	180
AGGTGCAGCA CTTCAGGCTG TTCTTGAATC ACCCCATAAA CCAACAGTCA TCAAACAAA	240
TAATGAAGAA TTGTCTCAGC TTCTTGGAAG AGAAGTTTCT GAGGATTTGG ATGAATTAAA	300
AGAAGTACTT CAAGAACCTT TGTTTGCAGG GATTGAATGG ATTATCGTTT CACTTGGTGC	360
CAACGGTACT TTTGCCAAAC ATGGTGACAC TTTCTACAAG GTAGATATTC CTAGAATTCA	420
GGTGGTAAAT CCTGTTGGAT CTGGAGACTC TACTGTGGCA GGAATTTCTT CAGGACTTCT	480
TCACAAAGAA TCGGATGCAG AATTACTCAT CAAGGCAAAT GTCCTTGGA TGCTCAATGC	540
TCAAGAAAAA ATGACTGGTC ATGTCAACAT GGCCAATAT CAAGCTCTAT ATGATCAATT	600
AATAGTAAAA GAGGTATAAA ATGGCTTTAA CAGAACAAA ACGTGTACGC TTAGAAAAAC	660
TTTCTGATGA AAATGGTATC ATCTCAGCTC TTGCATTTGA CCAACGTGGT GCTTTGAAAC	720
GCCTCATGGT TAAACACCAA ACAGAAGAAC CAACTGTGGC CCAAATGGAA GAACTTAAAG	780
TCTTGGTAGC AGATGAATTG ACTAAATATG CTTTCTCTAT GCTTCTTGAC CCTGAGTATG	840
GACTCCAGC AACTAAAGCT CTTGATGAAA AAGCTGGTCT TCTCCTTGCT TATGAAAAAA	900
CAGGTATGA CACAACAAGC ACAAACGCT TGCCAGACTG CTTGGATGTT TGGTCTGCAA	960
AACGTATTAA AGAAGAAGGT GCAGATGCAG TAAATTTCTT GCTTTACTAT GATGTAGATA	1020
GCTCAGACGA ACTCAATCAA GAAAAACAAG CCTACATCGA ACGCATCGGT TCTGAGTGTG	1080
TGGCTGAAGA TATCCCATTC TTCCTTGAAA TCCTTGCTTA CGATGAAAAA ATTGCGGATG	1140
CAGGTCTGT AGAATACGCT AAAGTAAAAC CACACAAAGT TATCGGCGCT ATGAAAGTCT	1200
TTTCAGACCC ACGCTTAAAC ATTGATGTTT TGAAAGTTGA AGTTCCTGTT AACATTAAAT	1260
ATGTTGAAGC KTCGCTGAAG GTGAAGTAGT TTATACACGT GAAGAAGCAG CAGCCTTCTT	1320
CAAAGCGCAA GATGAAGCAA CGAACTTGCC ATACATCTAC TTGAGTGCTG GTGTATCAGC	1380
TAAACTCTTC CAAGTACTC TTGTATTTGC TCATGAATCA GGTGCGAACT TTAACGGAGT	1440
TCTTTGTGGC CGTGCTACAT GGGCAGGATC AGTTGAAGCT TACATCAAAG ATGGTGAAGC	1500

1123

AGCAGCTCGC GAATGGtCGC ACAACTGGAT TTGAAAACAT TGACGAACTC AACAAAGTTC	1560
TTCAAAGAAC AGCAACTTCA TGGAAAGAAC GCGTGTAAAG AAGTCCTCCT AGTTTtagGAA	1620
CATGAATCTA AAAAAATTTA AAAAAAGTTG TATGTAAAGG CTTACAAAAT AACTTACTTG	1680
TGCTATACTT AAATCACAAG TTAATATGAA TTAGAAAGTA ACTATATGAA GTATAATAAA	1740
AATAGGATAT AGTTTATTTT ACGAGCTAGG AAGGAAAAAT ACGGAAACAA TATTGCCAGA	1800
ATAAACTATA TTTAGATGCA CATTTcATTC ATTGTTTTAT AAAAGGAGAA GATAAACGGC	1860
TACTAAAAAG AGTTTTTAAAG CGTTAGTTGT AGGACTAGGT ATTGTTTCAA TATTCTTATC	1920
AGCCTTACCT ATGGTTAGTG GTTCTGTATT TGCAGATAGT GCCCTAACTA CAGTAGATAA	1980
AGCAAATGAT ATTGTTTTGA ATGTTGATGG GAATAAATTT TATAATGTTT CGGTTTCAGA	2040
AGATATTGTA AATGCTGGTC AAATTTTGGa AGATTATTTT TATGTAGATA AATTTGGAAA	2100
TATAAAFTTA AAAGGCACTC CTGAAGAGTT AGCAAAAAAT ATTGGTATTT CTGTACAAGA	2160
AGCAAGTTTG ATGTATGGAG CTGTAAGAAG GTTACCCAAC GTTTACGAAA GAGGTCCTGT	2220
AGGTTTTCGT TTCAATCTTG GTCCTCAAGT GAGGGGGATG GGTGGCTGGG CTGCTGGAGC	2280
TTTCGCTACT GGATATGCTG GATGGCATTT GAAACAATTT GCGGTTAATC CTGTTACATC	2340
TGGATTTGTT GCTGTAAATA GTGGTGCGAT TGGCTGGGCT GTAAAACTG CTGTAGAAAA	2400
TTATTGGACA GTTGCTGTAG CTACAGTAGA AGTGCCGTTT GTGAACCTTG TTTACACCAT	2460
AGATTTACCT TAGAGGTAT TTCTTTATGA ATCATTTCTT TAAAAAATA ACTGTATTTT	2520
GTTTTATAGT TTCTTGTTGTT CTTTGTATTAT TAGACTTAAT GAATTTTAAA AATGTAGCTA	2580
CTTTTTTATT TTTCTGTCTT CCTGTTTTTG TTTTGATTTA CAAAAATAAA TAAAAACAGA	2640
GCCTCTGTTT GATGAATTTT AGAACATAGT TAAGTTTTAA AAAAAAGTTGT ATGTAAAGGT	2700
TTACAAAATA ACTTACTTGT GCTATACTTA AATCACAAGT TAATACAAGG TGAGTGTTAC	2760
TAAGTAATAT TAGGCATGAT CACAGGTGAA TTAGAAATCA GCTGATTTTC TAGTTCATTT	2820
GTGGTCATTT TTTGTACTTA TATACCTTTA AGATATAAAA GGAGGTTGAC ATGTATCGAA	2880
TTCTAAATCC AATGAATCAC AATGTCTCGC TTGTcAGAAA TGATAAGGGA GAAGAGGTGA	2940
TTGTAATGG TAAGGGAATT GCATTCGGA AGAAGAAGGG GGATTTGATT GCTGAAAATC	3000
AGGTTGAGAA AATCTTTCGG ATGAAGACCG AAGAGTCCAG AGAAAACTTT ATGGCTCTTC	3060
TCAAAGATGT TCCGCTTGAT TTTATCACAG TGACCTATGA AATCATTGAT AAGCTATCAA	3120
AGAAATATCA TTATCCGATT CAAGAGTATC TCTATGTAAC CTTGACAGAT CATATTTACT	3180
GTTCTTATCA AGCTCTAACT CAAGGAAGGT ACAAGGATAG TAATCTGCCA GATATTTCCG	3240

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CTAAGTATCC	TGTCGCTTTT	CAAATCGCAA	ATGAAGCTTT	TGAAATTTAC	CGTCAGAAGC	3300
TAGCAGATCA	TTTTCTGAG	GACGAAATTA	TTCGGATTGC	TTATCATTTT	ATTAATGCTG	3360
AAGGTGAAAA	TGAAGTGGAA	CTTGTGGAGT	CGATTGATAA	GAGGAAAGAA	ATTCTCAGGA	3420
ATGTGAAGA	AGTTTTAACG	GACTATGCAA	TTCAACGAAC	TAAAAAGAAT	AACCATTTCT	3480
ATGATCGCTT	TATGATCCAT	TTGAATTATT	TCTTGGATTA	TTTAGACAGA	TCTAGAGATG	3540
ATAACCAATC	ACTTCTGGAT	ATGGAAGATC	ATATTAAACA	ATCCTATCCA	AAAGCCTTCG	3600
AGATTGGTTC	CAAGATCTAT	GATGTGATTA	CGCAACATAC	GGGTCTTGAT	TTGTATAAAA	3660
GTGAACGAGT	TTATCTAGTT	CTACATATCC	AACGTTTATT	GTCATAAAAA	TTTATTTAAA	3720
ACTATATAAG	GAGAATTCTA	TCATGAATAG	AGAAGAAGTA	ACATTGTTAG	GTTTTGAAAT	3780
CGTAGCCTAT	GCTGGCGATG	CTCGTTCAA	ACTATTGGAA	GCCTTGAAGG	CTGCTGAAGC	3840
TGGTGATTTT	GAAAAAGCGG	ACGCTCTGGT	AGAGGAAGCT	GGTAGCTGTA	TTGCAGAGGC	3900
TCACCACGCG	CAAACAAGTC	TATTGACTAA	GGAAGCTTCA	GGTGAGGACT	TGGCTTATAG	3960
TGTAACCATG	ATGCATGGCC	AAGACCACTT	AATGACAAC	ATCTTGTTAA	AAGATTTGAT	4020
GCATCATTTA	ATTGAACTCT	ACAAGAGAGG	AGTTCATAA	TGAATAAACT	AATTGCATTT	4080
ATCGAGAAAG	GAAAGCCTTT	CTTTGAAAA	CTATCTCGTA	ATATCTATCT	TCGTGCTATT	4140
CGTGATGGTT	TCATTGCAGG	TATGCCTGTT	ATTCTCTTCT	CAAGTATCTT	TATCTTGATT	4200
GCCTTTGTAC	CAAACATCAG	GGGCTTTAAA	TGGCTTGATG	AAGTTGTAGC	CTTCTGATG	4260
AAACCTTATA	GCTATTCTAT	GGGTATTCTG	GCTCTCTTGG	TAGCTGGTAC	AACAGCTAAG	4320
TCATTGACTG	ACTCAGTAAA	CCGGAGCATG	GAAAAACCA	ATCAAATCAA	GTATATGTCA	4380
ACATTGTTGG	CAGCAATTGT	TGGTTTGTG	ATGTTGGCAG	CTGATCCTAT	CGAAAGTGGT	4440
CTAGCTACTG	GATTCTTGGG	GACAAAAGGT	TTGCTTTCAG	CCTTCCTTGC	TGCCTTTGTT	4500
ACTGTAGCCA	TCTATAAGGT	TTGTGTTAAG	AACAACGTCA	CTATTCGTAT	GCCTGACGAA	4560
GTCCACCAA	ATATCTCACA	AGTCTTTAAA	GATGTGATTC	CATTCACTCT	ATCTGTTGTT	4620
TCTCTTTATG	CTCTTGACTT	ATTAGCACGT	TATTTTGTG	GTTCTAGTGT	GGCAGAATCA	4680
ATCGGTAAAT	TCTTCGCACC	ACTCTTCTCA	GCAGCAGACG	GATACCTTGG	TATTACCATT	4740
ATCTTTGGTG	CCTTTCCTT	CTTCTGGTTT	GTTGGGATTC	ATGGTCCATC	TATCGTTGAA	4800
CCAGCTATCG	CAGCTATTAC	CTATGCCAAT	GCCGAAGTTA	ACTTGAACCT	TCTCCAACAA	4860
GGGATGCATG	CAGACAAGAT	TCTTACTTCT	GGTACACAAA	TGTTTATCGT	TACCATGGGT	4920
GGTACAGGTG	CGACATTGGT	CGTTCCATTT	ATGTTTATGT	GGTTGACAAA	ATCGAAACGT	4980
AACCGTGCAA	TCGGACGTGC	TTCAGTAGTT	CCTACCTTCT	TCGGTGAAA	TGAACCAATC	5040

1125

TTGTTTGGTG	CACCTCTTGT	TTTGAATCCA	ATCTTCTTCA	TTCCATTTAT	CTTTGCTCCA	5100
ATTGCAAACG	TATGGATTTT	CAAATTCCTT	ATTGAAACTC	TTGGAATGAA	CTCATTCACT	5160
GCTAATCTAC	CATGGACAAC	TCCAGCTCCA	CTAGGTCTAG	TTCTTGGAAC	TAACTTCCAA	5220
GTGCTATCAT	TCATTCCTGC	TGCCCTTCTA	ATCGTGGTTG	ACGTTGTCAT	TTACTATCCA	5280
TTCCTTAAGG	TCTATGATGA	ACAAATTCCT	GAAGAAGAAC	GTTCAGGTAA	GTCTAATGAT	5340
GAATFGAAAG	AAAAAGTTGC	TGCAAAC TTC	AACACTGCAA	AAGCGGATGC	TATTCCTTGAA	5400
AAAGCGGGTG	TCGATGCAGC	ACAAAATACC	ATCACTGAAG	AAACAAATGT	CCTCGTTCCTC	5460
TGTGCAGGTG	GAGGAACAAG	TGGTCTCCTT	GCAAATGCTT	TGAATAAGGC	AGCAGCAGAA	5520
TACAATGTCC	CTGTGAAAGC	AGCAGCAGGC	GGCTATGGTG	CTCACCGTGA	AATGTTACCA	5580
GAGTTTGATC	TTGTTATCCT	TGCCCTCAA	GTGCTTCAA	ACTTTGAAGA	TATGAAAGCA	5640
GAAACAGATA	AGCTCGGTAT	TAAACTAGCG	AAAACAGAAG	GCGCTCAATA	CATCAAATTA	5700
ACTCGTGATG	GAAAAGGTGC	TCTTGCATTC	GTACAAGCGC	AATFCGATTA	AGGCTAGAGA	5760
CTCTGAAATA	GTCTCCCATC	GTTACGGAAA	TCGCTATGGC	GAATTCCTTA	TTATTAATTC	5820
GTGCGTAAAA	AGATATCGTT	TTTACCTCCT	CATGTCACAA	TTGCGTACT	TGGTACAAGA	5880
AGTGAGATGG	AGAAGGATGG	CTCACTGACT	CCTCTCCTCT	CACTTTTACT	TTATTTAAAT	5940
CAAGAAATAG	GTGAAAAAAA	TGACAAAAAC	ACTTCCAAAA	GACTTTATTT	TTGGTGGCGC	6000
AACAGCTGCT	TATCAAGCAG	AAGGTGCTAC	ACATACTGAT	GGAAAAGGAC	CAGTTGCTTG	6060
GGATAAATAT	CTTGAGGATA	ACTACTGGTA	CACTGCCGAA	CCAGCTAGTG	ATTTTTACAA	6120
TCGATATCCA	GTTGACCTCA	AGCTAGCAGA	AGAGTATGGT	GTCAATGGTA	TTCGAATTTT	6180
TATTGCTTGG	TCACGTATTT	TCCCAGCTGG	TTACGGCCAA	GTAATGCTA	AAGGTGTTGA	6240
GTTTTATCAT	AATTTATTTG	CAGAGTGTC	CAAACGTGAT	GTTGAGCCTT	TTGTAACTCT	6300
TCATCACTTT	GACACGCCAG	AAGCTCTCCA	CTCAAATGGA	GACTTCTTAA	ACCGTGAAAA	6360
TATCGAACAT	TTTGTAGACT	ACGCTGCCTT	CTGTTTTGAA	GAATTTCCAG	AAGTAAACTA	6420
TTGGACAACC	TTTAATGAAA	TTGGACCAAT	CGGTGATGGT	CAATATTTGG	TTGGGAAATT	6480
CCCTCCAGGT	ATCCAGTACG	ACCTTGCCAA	AGTCTTTCAA	TCACACCACA	ATATGATGGT	6540
GTCTCATGCA	CGCGCGGTAA	AATTGTACAA	AGAGAAAGGC	TATAAAGGGG	AAATTGGTGT	6600
TGTTACGCC	CTGCCAACTA	AATATCCTCT	AGATCCTGAA	AATCCAGCAG	ATGTTGCTGC	6660
AGCTGAGTTG	GAAGATATCA	TCCACAATAA	ATTCATCTTA	GACGCAACTT	ATCTAGGTCG	6720
CTATTCAGCT	GAAACCATGG	AAGGTGTCAA	CCATATCTTA	TTAGTCAATG	GTGGTAGTTT	6780

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GGATCTTCGT	GAAGAAGATT	TTACAGCATT	AGAAGCTGCA	AAAGACTTGA	ATGATTTCCCT	6840
AGGAATCAAC	TACTATATGA	GTGACTGGAT	GGAAGCCTTT	GATGGAGAAA	CTGAAATFAT	6900
CCATAATGGT	AAAGGTGAAA	AAGGAAGCTC	TAAGTATCAA	ATCAAAGGTG	TTGGTCGTCG	6960
TGTAGCTCCT	GACTATGTAC	CACGCACGGA	TTGGGATTTG	ATTATCTACC	CTCAAGTTTT	7020
GTATGACCAA	ATCATGCGTG	TGAAGAAA	TTATCCTAAC	TACAAGAAGA	TTTACATCAC	7080
TGAAAATGGT	CTCGGCTATA	AAGATGAGTT	CGTTGATAAC	ACTGTTTACG	ATGATGGTCG	7140
TATTGATTAC	GTGAAGCAAC	ACTTGGAGGT	TTTATCTGAT	GCGATTGCAG	ATGGAGCTAA	7200
TGTAAAAGGT	TACTTCATTT	GGTCATTAAT	GGATGTCTTC	TCATGGTCAA	ACGGTTATGA	7260
GAAACGTTAT	GGTCTCTTCT	ACGTAGATTT	TGAAACTCAA	GAACGTTATC	CTAAGAAATC	7320
AGCTCACTGG	TACAAGAAA	TAGCGGAAAC	TCAGATTATA	GACTAGTAGA	ATTAGTCATT	7380
AGATATAGAA	TTTTAGTGAG	TCAAAAAGAT	GTTCAAAGAT	TTTATCCAAT	CTATTTATGA	7440
AAAAAAGTTT	ATATTATAAA	TTTCGAAAA	TGCTCTCAA	TACCGTGTTT	GACGAGTGAA	7500
GAATTGAAAA	GTCTTGAAAA	ATGGTATGTC	TCGACTGGTA	AAGAATGGAT	TTGTCAATCA	7560
GATGATGAGC	TGGAAGAATT	TAAAAATCTA	TTTTTAAATT	TTATCAATCC	TGAAGAATGG	7620
GATACTATCT	CCTTTGATTC	AGATTTTATG	CCGTTTCAAC	AATCGTAACC	AATTTCTCAA	7680
AAAAGTTAAA	TCTTATATTT	AGTACTCTGT	AAAACCTTA	TCTAATCACG	TTGCTTATAC	7740
TCAATGAAAA	TCAAAGAGCA	ACTTTAAACT	AGGAAGCGAG	TCGCAGATTT	CTCAATGCAT	7800
AGCTTTGAGG	AATTGGGCAA	AAAGTCTTTG	ATATAGAAAA	ACGCATAGTA	TCAGGTGTTT	7860
CAACACCTGA	TACTATGCGT	TTTATGTGG	GAAGATTTAC	TTTTTTTCTT	CTGAAATTGA	7920
GTTGTTACCC	AGGCTCTTTC	AGTTTATTAA	GGCTTGATGA	CTTTAATGTG	TTTAGATAGC	7980
TTAAAAAGGA	TTGAATCACT	TAGTTTAGAA	TCTGAAACAA	TAGTATCAAG	ATTTGATACA	8040
TTATAAAAAG	TATAAAAATC	AAACTTATTG	AACTTGCTAT	GATCTGCGAG	TAAATATTTT	8100
TTATTAGAAT	TATTTAAAGC	GATGCGTTGA	GCCTCTCCCT	CTTCCTCGCT	AAAAGTAGCT	8160
AGAGCTCCGT	TTTGAATACC	ATTACAGCTA	ACGAAAGCTT	TAGAAAATTG	GAGATTAGAG	8220
AGATTTTGTA	GGGTCAATGT	ACCAACAAAA	GCACCTGTAA	TATCGCGATA	ATTTCCACCT	8280
ATTAAAAATCA	AATCTGTTAA	TTTTCGTTTCG	CTTAAAATCA	GAAAAACAGG	TAGACTGTTG	8340
GTTACGACGC	GGATATGTTC	AATAGGCAAC	TCACGCGCAA	AAAACTCTAA	TGTTGTTCCCT	8400
GGTCCAATGA	AAATAGTTTC	TCTTTCTTCT	ACTAGACTGC	CTGCAAAATG	GGCTATTTCT	8460
TGTTTTTCTG	CCGTTTGGAG	GGCTTGTTTT	TCAATATTTG	ATCGCTCATT	AGTCAAAAGG	8520
GAGTTGGTTC	GAAGTTTTTC	AGCTCCACCA	TGCACACGAA	TCAGCAAATC	TTTATCAGCT	8580

1127

AATTCCTGTA AATAGCGCCT TGCAGTCATA TCTGAAACGG CTATTTTCGTC CATAATCTGT 8640
 TTAACGTGTTA T 8651

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AATCTCCAAT CAGTGCCACT TCAGCTACAA AGAAGAGGAG GATAATAACT CCGTTCACAA 60
 GGACAGACAA GAATAATTGA TAGAAGGAGT CGGTTTCACT TGCTTGACTT GGTCTTGTA 120
 TGATWTGGAG ACTGGCAAGC AGAATGATTC CAATGCTAAT CACACACAAG AGGGCTGTAA 180
 ATCGTAGGCT ATCAAAGAAA GCAAAGAAAC TAGCAATAGC AGTGAGGAmG ATTGGAATTG 240
 CCAAGAGTTG ACTATATTGT TGGAGAACCT TGCTAGCGT CCAGTCCTTT TCCTGGTGA 300
 TAAATCGTCT CACAACGAAA CTACCCAAGA GGAATGAAAA GAAGAAGAGT GTTGTCGCTA 360
 CTAGGATAGA GATGATAGAA AAAAGAGTTA AAGGAGCTAG CTGCTCAGGG AAGCGACTGT 420
 TAATGCTTGC TATATGTCCA TAGTAAGCAT GTTTGATGTG ATAGATACTA AAGAAAAAGG 480
 AAGATGCAGA AAACAGAATG AGCAAGAGAA AGGCTGTGTA ACTGTGTGTG ATACTTGTTT 540
 CCAACTTACT TGTAGGAGAT TTGATCGCTT CCACTAGCCA AGACCAAAAA TCAAGCACTT 600
 GCTCTTTCCA TTTATCCCTA GATTTTGGAG CTGGTTCGGG GATATAAGGA CTTTCTAAAG 660
 ATTTACTGAT AAGAAGTGGC TCTTTCGTGG TTGCTTTTTC CTGAGGAAGA GCTTCTTGGC 720
 TCTCTTCAGC TATAGTGA CTTTCTGTTT CTTTAGAAAG GTCTGGCTCT TCTTCAGTAG 780
 AATTAGATGC CTTCTTTTCT TCTATTTCTG TTCTCGCTTC ACTGTCTTCA GGAGCTTCAA 840
 TTTTCTCTTC TTGCTGGCTT TCCAATTCGA CTTAGCTTG AGGGACTTCC TCCTCTAACT 900
 GAGTATTTTT TTCAATTGGT GTATCGAGAT CGGCTATCGT TTCTTCAGCC TTGTCTGCAA 960
 CCTCTTGAGC TTGCTCTTCA GGCTTGTTC TGTCTGTTGT TTTTACAAAA TCATTACTTT 1020
 CAAACCATTC TTGTTTCATG GTAGAACCCT CTTTTTAGTT AGATAAATAT GTTTCCATAG 1080
 TAGCAAATGT AAGCGTTTTT GTCAACGCTCT GCTTGGTGTG GATATTAGAT CAATATTATC 1140
 ATCAGATCTC GCAATGAGTT GATCCTTGAC ATCGGTTTTT TCAGTTTTGT AAGGGTTGCT 1200
 TAATCCCGTA CCTCTTGATT CAGGCTTTTC TCTTGTGAAT TGGAAGATAG AACCATAGTT 1260

1128

GCTTGAGATG	TCCCAGTTAA	TTCGTTGGCT	TTCTTTCTGG	TCTAGGATGA	TTCTGAGATA	1320
ATCTTTGGCA	GTCAGTTCAA	CCTTGCCATG	GACTTGGATA	TTTTCAGCGT	GGAAGTGATT	1380
CTCTGTTGAC	TCTAGCTGAC	TATCTGTAAG	AACTGTATCA	AAGATATTAA	CGATATTGGG	1440
CGTTGTGAGT	TTACTGTTTT	TGATACGACT	TCCTTCAATT	CGGAGGATAT	AGCTGTTTGT	1500
ATTGAGGGTC	GCATTTTCAA	GGCTAGCATT	TATGATGGTG	GTTTGTCCGC	GATTGGCTGA	1560
GATGTTGATC	CCTTTTAGAG	TTCTCCCTTT	TGGTAGTCGG	AGAATAACTT	CTTCAAACG	1620
ACTAGAGTAG	CTACTTGCGA	TATGAAGAAT	CCCACCAATT	CCAGAAGAGA	GAAACGGAGT	1680
TTCAGACAGT	TTCTTATCAG	TGAGACTCAG	AGTTCATCG	TTCTGATTGG	TGATAAGATC	1740
ATGGTGAGCA	GAAAGAGATG	GATGGTAAGA	AATGTGGATT	TGATCATCGA	AAGAGTCTGT	1800
GATGGTGAGC	GTGTGTTGGT	GGAGAGTAAT	TTCTAGGTTT	TCGACTTCCT	TGCCAAAGGT	1860
TAGCTTTTCC	GTACGGCTAT	CATAGACAGG	TTCTTTGGAC	ATGGAAAGTA	GGCTCTTAA	1920
CCCGTCAGAT	TGGATACCTA	CAAAAAGCAG	GATAAAGCCG	ATAACGGTAG	TCACCACACC	1980
AAAGATGAGA	AATCCTTTTG	TCCATTTACG	CATGCTGATT	ACCTCTCTTT	CCTTTTTTAA	2040
GAACAAATG	TACCAGACGA	ACAATGAGTA	GACCGAAGAA	GCGAGTTGCA	TAGGAAATGC	2100
CAAGTAAAAC	TAGCGAAGAA	GCACCGATAG	CCAGTAAACC	AGAACCAAAA	ATCAAGATAA	2160
AGGCTGATTT	GGCTTGGGCG	AGGACAGTGA	AACTTTCAAC	TAAAAATAGG	AATCCGCCGA	2220
TGATACCCAG	TATGGAAACT	GCAAAGAAAG	CCAGAATGAC	AGTCAAAGCG	GCTACAAGAA	2280
TTGCGAACAG	GGTCACGAGG	ATGGCGATTC	CCAGAGGAAT	GCCGATAGGT	GCTGCAAGGA	2340
GGGCTAACAA	GGCGATATGT	AAAATTTGTC	GGTATTTTTT	TTGAGCGGGT	GCTTCATTGA	2400
TTTTTTTATC	GAGAAGATG	GATAGAACTT	CGTGGCCCGC	TTCTTTGGGA	GTCCCAAAC	2460
TAGCGATGAG	TTCTTCTTCT	CCTTCGACTC	CAGCATCGTC	AAAGAGCTCT	CTGAAATAGT	2520
CCATGGCTTC	GATACGGTCA	GCTTCAGGTA	GTTTCTTGAG	ATAGAGTTCT	AGCTGAGTCA	2580
GGTATTCAGT	TCTTGTGATG	GCGGATACTC	CCTTCTATGA	TGCCATTGAT	GGTGTCTGTA	2640
TAGAGTGCCC	ATTCATCTTT	TAGGGTCAAG	AGCTGCTCTA	TACCACCGTT	TGTCAAGGAG	2700
TAGTATTTGC	GCATGCGACC	TTGGAACCTT	CTAGAATAGG	TTGTCAGAAA	GCTATTGCCT	2760
TCCAATTTTT	TGAGAATGGG	ATAGAGTGTG	GATTCTTTGA	TATTAGCGAT	CAGCTTAATG	2820
GTTTGGCTAA	TCTCATAACC	ATAAGAATCA	CCCTGCTCCA	GTACAGCCAA	GATGAGAAAT	2880
TCAATCAAGG	CAGAGGATGT	TGAAAAGTAC	ATGGGAAACC	TCCTTTTCTA	ATGTGTAAGA	2940
TTTTTATATA	TAATTTTCTT	ACACATACAT	TGTACATCTA	AAAGAAAGCC	CTGTCAAGAG	3000
AAATGTGTAA	AATTTTTATA	TATAAAAAAC	TTCTAGCTAA	AACTAGAAGT	TTAAAGGATC	3060

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TTATCCGCTC TGTCCACTGT AAAGAGGGCC ACAGTCATCA GGATATCGAT GAGCAAGAGG	3120
GCAGCTACAG ATGGTACCCA AGAGTGGAAC AGGTCAAAC TGTAACCAA GAGGGTTGGC	3180
CCAAAGGCTG CTAGGATATA GCCTCCTGTT TGAGATAGGC CGGACAATTG GGCTGTCTTT	3240
TCAGGGGCGC TTGTCTTGAG TGAAAAGTTG ACCATGAGAT AAGGGAAGAG GGCCTGGTT	3300
GCGGTTCCGA TGAGGAGATG GATGGCAAGC CAGTAAATGA AATTATTTGAT TGGGAAAAAG	3360
AGCATGGAAA TGCCGACCAC ACCAGCTAGT GAAACCAGAG TGAGCATGAG CTGACGGTTG	3420
CGAGTAGATA AACTGGTTGT CAGGCTTGGG ATGGTCATTG AAAAAGGAAT GCTAATCAGA	3480
GATAAGATAG AAGTCAGCAA GCCAGCTTCG TGAAGTGGATA GACCTGCATG GATAGACATG	3540
GTAGGTAACC AGGTCATGAC GGTGTAAAAG ATCAAGGATF GAAAACCTGA AAAGATAATA	3600
ATTGCCCAA CCTGTTTATT ACGCATGACC TTTATTTGAC TTTTTTGTTT GGTTTGTGGA	3660
GCTAGTCTAT GATTATAGCG GTGATTTGGG AGCCAGACCA AAAAAGTTGC TAGACAGAGT	3720
AACGTGAGGA GAAGGATAAG TCCTTTCCAA GAACTGGCTT GTGTAATGGG CACAGCTAGA	3780
TAGGAA	3786

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TCAGCTAAAA AACATTGCTA AATTGATTGA AGCTGGTGCT ACACATTCCG ATTCAACTTC	60
TCACACGGCG ACCACCAAGA ACAAGGTGAG CGTATGGCAA CTGTTAAACT TGCGGAAAAA	120
ATTGCAGGTA AAAAAGTTGG TTTCCTTCTT GATACAAAAG GACCTGAAAT CCGTACAGAA	180
TTGTTCGAAG GTGAAGCTAA AGAATATTCA TACAAAAC TGAAAAAAT TCGTGTGCA	240
ACTAAACAAG GAATCAAATC AACTCGTGAA GTGATGCGT TGAACGTTGC TGGTGCTCTT	300
GATATCTATG ATGATGTTGA AGTTGGTCGT CAAGTTTTGG TTGACGATGG TAAACTTGGT	360
CTTCGTGTGG TTGCTAAAGA TGATGCAACT CGTGAATTTG AAGTTGAAGT TGAAAACGAT	420
GGTATCATCG CTAACAAAA AGGTGTGAAC ATCCCTAACA CTAAAATTCC TTTCCCAGCT	480
CTTGCTGAAC GCGATAACGA CGATATCCGT TTCGGTCTTG AACAAAGTAT CAACTTCATC	540
GCAATTTTCA TCGTACGTAC TGCAAAAGAT GTGAACGAAG TTCGTGCAAT CTGTGAAGAA	600

1130

ACTGGAAACG	GACATGTTCA	ATTGTTTCGCT	AAAATCGAAA	ACCAACAAGG	TATCGATAAC	660
TTAGATGAAA	TCATCGAAGC	AGCTGATGGT	ATTATGATTG	CTCGTGGTGA	TATGGGTATC	720
GAAGTACCGT	TCGAAATGGT	TCCAGTTTAT	CAAAAAATGA	TTATCAAGAA	AGTCAATGCT	780
GCAGGTAAAG	TTGTTATCAC	TGCAACAAAC	ATGCTTGAAA	CAATGACTGA	AAAACCACGT	840
GCAACTCGTT	CAGAAGTATC	AGATGTATTC	AACGCTGTTA	TCGACGGAAC	TGACGCTACA	900
ATGTTGTCTAG	GCGAGTCTGC	AAACGGTAAA	TACCCACTCG	AGTCAGTAAC	TACAATGGCT	960
ACAATCGACA	AGAACGCTCA	AGCTCTTCTT	AATGAATACG	GACGTCTTGA	TTCAGATTCA	1020
TTTGAGCGTA	ACTCTAAGAC	AGAAGTAATG	GCTTCTGCTG	TTAAAGATGC	TACTAGCTCA	1080
ATGGATATCA	AATTGGTTGT	AACTCTTACT	AAGACAGGTC	ATACTGCACG	TTTGATTTCT	1140
AAATACCGTC	CAAATGCTGA	CATCTTAGCA	TTGACATTTG	ACGAATTGAC	AGAACGTGGC	1200
TTGATGTTGA	ACTGGGGTGT	TATCCCAATG	TTGACAGATG	CTCCATCTTC	AACTGACGAT	1260
ATGTTTCGAAA	TCGCTGAACG	TAAAGCGGTA	GAAGCAGGTC	TCGTTGAGTC	AGGCGATGAT	1320
ATCGTTATCG	TTGCTGGTGT	GCCAGTAGGA	GAAGCTGTTT	GCACAAACAC	AATGCGTATC	1380
CGCACAGTAC	GTTAAGAAAA	ATATAAAAAAC	CTATCATATC	CAGCTTTAGA	GCTTGTGTGA	1440
TAGGCTTTTT	GTATAGAGGG	TAAGAAATAG	GCAAAACTTT	CATAATGGAT	TGATACTCTT	1500
CGAAAATCTC	TTCAAACCAC	GTCAGCGTCG	CCTTACCGTA	TATATGTTAC	TgACTTCGTC	1560
AGTTCTATCT	ACAACCTCAA	AGCAGTGCTT	TGAGCAACTG	CGGCTAGCTT	CCTAGTTTGC	1620
TCTTTGATTT	TCATTGAGTA	TGAAATAAGA	TATGCACAAA	TTGATTAGAA	AGTCAAATGA	1680
ATTTCTACAA	ATGTTTtagc	AATCGTAATG	TACTTGTCTA	GATTTCGATCT	GATATATTTT	1740
CGATTTAATG	ATATGGTATT	TAAAACCTCC	AAAGTAGCTT	ACTCCATTCT	TTTACTTACG	1800
TGAGTGTAGA	TGTTATTTAC	TGTTTTAGCG	TTTTTGTGTT	CCACTCTAAC	CATTATAGCA	1860
TTCTTCTCAG	CTAGTGTACT	AAGGAGTGTG	TGCCTGAAAA	TATGGGAAct	AAGGGGCTGG	1920
TTTATCGGTT	TCTCTAGTTT	AGTATTTGCC	TTTTGCAAAG	TGATCTTAAA	TGCCTTTCTC	1980
TAAATTTACA	TATCACTATT	GTTTAAACAAA	ATCTAATCTA	TTTTAGGTCA	CTTATTCCTT	2040
TTTTGAAATG	TAGAATGAAC	TTTTTCAAAG	TTTTTTCGAAT	CTTTTAAAAAT	CTGTTTGCTT	2100
TATATCGCCA	TTCTCCCCC	TTTTTTAATT	CTCCCTATAT	AGCCTGACAG	CTTCCCGAT	2160
GGTACGAATA	TGGTTGCTTT	CGTCTAGGTG	GATGTCGGGG	TATTCGGGAT	TGAGTTTTTT	2220
TGAGGCAGCC	TTGGCGGAGT	TTCTTGACAT	AGTTAGTGCC	GTCTACTTGG	AAGATGCCGA	2280
TGGTATTATA	GTCAATCTGT	GGGGTATTCT	TGATAAATAG	GTAGTCGCTG	TTTCTTATCT	2340
TTGGCTCCAT	GGACTTGCTG	ACGACATAAG	CGATTGGGTC	GTAGTCGTCT	GGGATAATGG	2400

1131

AAACTCCATA	TCTAAATCGT	TGTCCTGCAT	CGAGCGGCTA	CCTGCAGAGA	TAAACTACCT	2460
AACACGAGAG	TAAGTAGTCT	GTCTGTAGTC	GTCCAGTCTG	ATGATTTTTA	CGATACTTCG	2520
TTTTTCTGAT	CATACAGTTG	CCTCTCGGCA	TAGGTCAGAA	CTTTACCTTG	TCTGGGTGGT	2580
TCCCGTTGGT	CGTAGATAGA	TTGGATATCG	CTAGGAGAAT	CCTTTTGAAC	TGGAGGAAAG	2640
AGGGCATCGA	TCAAGCTACT	GAATACTTTA	ACTAAGTCAA	ATATAGTATT	TTTCTTAGTA	2700
GACCTAACCC	TTTTTTCATA	ATTTCTAATG	GTGTTTTTAC	TTATACCTAT	CTTAGTACCC	2760
AATTCTTATT	GAGTCCAACC	ATTACTAGTC	TATATGTTT	TATAGTTGAT	TGAGTTTGGA	2820
ATAGTACGCT	GTAGCTGCTA	AAACATTTCT	AGAAATTAAT	TTGACTTTCC	TAATAGAGTT	2880
GTTCATATCT	TATTTCAATC	TATTATGTTT	TTCACCTCTA	ACAATCGCAA	TCTCTTCTTT	2940
ATCCATGAAT	GAAATCGCTT	TCTATTTTTG	TAAGTAAAGC	ATAACACGAA	ATCCACGAAA	3000
ATGAAAACCT	TTGTGTGTT	TTCGTAAAAA	ATTTGTTGAC	AGAGCACGAA	ACGC	3054

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TGTGATTTTC	yGAAAATTTG	GTAAAATATA	TCTTAATCAT	TTTCAGGAGG	ACAAAAATTT	60
GACAAGATAT	CAGAATTTAG	TAAATGGAAA	ATGGAAATCA	TCTGAACAAG	AAATTACGAT	120
TTATTCACCA	ATCAATCAAG	AAGAATTGGG	TACAGTTCCA	GCCATGACTC	AGACTGAAGC	180
TGATGAGGCT	ATGCAAGCTG	CGCGTGCAGC	CCTGCCAGCA	TGGCGAGCTT	TATCAGCAGT	240
TGAACGTGCG	GCTTATTTGC	ATAAACAGC	AGCTATTTTA	GAACGCGATA	AGGAAGAAAT	300
TGGTACTATC	CTTGCCAAAG	AAGTAGCAAA	AGGGATTAAA	GCAGCAATTG	GAGAAGTAGT	360
GCGTACAGCA	GACTTGATTG	GTTATGCTGC	TGAGGAAGGT	CTCCGTATCA	CTGGACAAGC	420
AATGGAAGGT	GGTGGTTTTG	AGGCAACAAG	TAAAAACAAA	CTGGCTGTTG	TCCGTCGTGA	480
ACCAGTTGGT	ATCGTGCTAG	CGATTGCTCC	CTTTAATTAT	CCAGTTAATT	TATCTGCTTC	540
TAAAATTGCA	CCTGCCTTGA	TTGCAGGGAA	TGTGGTCATG	TTTAAGCCAC	CAACACAAGG	600
TTCCATTTCT	GGACTCTTGT	TGGCTAAAGC	ATTTGAAGAA	GCAGGGATTG	CGGCAGGTGT	660
TTTCAACACC	ATTACAGGTC	GTGGTTCAGA	AATTGGGGAT	TATATCATTG	AGCACAAAGA	720

1132

AGTCAACTTC ATCAACTTTA CAGGTTC AAC TCCTATTGGA GAACGTATTG GTCGTTTAGC	780
TGGTATGCGT CCTATCATGT TGGAACCTGG TGGGAAAGAT GCAGCTCTTG TACTAGAAGA	840
TGCAGATTTG GAACATGCTG CCAAGCAAAT TGTTCGCGGA GCCTTTAGCT ACTCAGGACA	900
ACGTTGCACG GCCATTAAAC GTGTCAATTGT TCTCGAAAGT GTAGCAGATA AATTAGCTAC	960
TTTGCTTCAG GAAGAAGTTT CTAAATTAAC AGTTGGTGAT CCATTTGACA ATGCTGATAT	1020
TACACCTGTT ATTGACAATG CTTACGCCGA CTTCAATTGG GGCTTGATTG AGGATGCACA	1080
AGAAAAAGAA GCTCAGGCTC TTACACCAAT CAAACGTGAG GGCAATCTTC TCTGGCCAGT	1140
GCTTTTGTGAC CAAGTTACAA AAGATATGAA AGTGGCATGG GAAGAGCCAT TTGGTCCTGT	1200
TTTACCAATC ATTCGTGTGG CTAGTGTAGA GGAAGCTATT GCCTTTGCCA ACGAATCTGA	1260
ATTCGCGCTT CAATCATCAG TCTTTACAAA TGATTTCAAA AAAGCCTTTG AAATTGCTGA	1320
AAAACCTGAA GTAGGTACAG TCCACATTAA TAATAAAACC CAGCGTGGTC CAGATAATTT	1380
CCCATTCCCT GGTGTCAAAG GTTCTGGAGC TGGAGTGCAA GGAATTAAT ATAGCATTGA	1440
AGCGATGACA AATGTCAAAT CCATTGTTTT TGATGTGAAA TAACGTGTAA AACCAGGAAA	1500
TTGTTTCCT GGTTTTATTT TTTTGCTATA AAATAATAAT AATTATAGAA AAAATACGAA	1560
CTTTTGGTA TTATAATAGA TTGAAACCGG	1590

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CCTGCAGTTG TCAGACCTGT AATTTCTTTT TTATCTGTAA TAAGAATCGT TCCAGCGCCT	60
AGAAAACCCA CACCTGATAT AACTTGAGCT CCTAATCGTG TAGGATCTCC TGTCCTCAAT	120
TTATAAGATA CGTATTCATT CGTCATCATA ATCAAACATG CAGCTAGACA AACAATACTA	180
TAAGTTCGGA TGCCTGCAGG CTGGGATTTG CTCCTCTCT CTAAACCAAT TATACTACCA	240
ATGACTACTG ATAAAACAAT CCTGACAACCT ATTTCAATAT TTGATAACCC AAGACTAGTG	300
GCTGTCATGA TTATTTCCTT ACTTTACGCC CCGGTCTTTG TGTGAAGTAT AATACCGTTC	360
CAGAAATAAT CATCAGAACA ATTTGATAAA CAAATACCAG AGCTTGTGCA TTAGATGTTG	420
CTGTTTCATC ACCTGCAGAT CGAATCGTAA TACCTAATGG TTGAGCTAGG GGATGGTAAA	480
GGAATACAGA TAAGTCGAAG TCAGTTAATA AAGAGTTAAA GTTTAAAGCA ATAACAGAGA	540

GAACAACCGG	TAAAAATAAT	GGAATGATAA	CCTTCATCAT	AGTATAAAAA	GGTGAAGCAC	600
CCATACTTCT	TGCTGCATCT	TCCATCTCAT	CATCAACACT	AAATAAAATA	GCACGTACCA	660
TTCTATAAGA	AAATGGGATT	TTTACAACCTA	TATATGCAAT	AAGTAGAATT	ACCAAACCTAC	720
CTACCAAAAT	CTGATTCGAAG	ACAAGAAAT	GTGGCTGATT	AAAAGTAAAT	AATAAACTTA	780
CTGCTAAAAG	TGTACTTGGT	AGTAACCAAG	GAAGTAGAGC	ACCATATTCA	AATAAGAAAT	840
CAAAACGAGA	TTTATGTTTT	CTGACAACAC	GAGCAAATAC	AACTGCGAGA	ATTGTTGCTG	900
TTGTGCGAGC	AATAATAGAA	TAAATAAAGC	TGACCAAGAA	TGGAGAGAAT	GCCGCACTAT	960
TACTAAAGAA	TAAGCGATAA	TTTTCTAAAAG	TAAAGTTTGA	TAATGTTAAG	TTACCTGTTT	1020
GAATTGCAAC	TGGATCTGTA	AATGAGTATA	ATACTATAAA	AATTAGTGGA	AGCATGAAAA	1080
CTGTGAACAA	TCCATATGCT	ACAATGTGAG	CAATGATATT	CCAAGGCTTA	GACGCAATTT	1140
TTTGTTTTTT	AAGAGGCGCT	TTAGTCTTAG	AGATAGAAAT	ATAAATTTCCA	CCTTTTTCTA	1200
TCTTATTCAT	GATAGTAAGC	AAAATGTAG	TTGCAATACC	TAAAAATAAT	GCAAGTAGGG	1260
CAGCTAAATC	ACGAGAATTC	CCCATCCCTG	CAAATGTAAT	AATCATTGGA	TTTATAGTTT	1320
GAAATCTTTT	ACCACCAACA	ATCATGGGTG	CTGCTACTGC	AGATAAACCA	CTAAGAAAAA	1380
CCATAATAGT	AAGTGCAAAT	AGAGTTGGAA	TTAAGGTTGG	TAACACTACT	TTTCGGAAAA	1440
CAGTAAATGG	TTTTGCTCCC	ATATTTCGAG	CAGCCTCAAT	AGTGTGATAG	TCAACGCTTC	1500
GAATTGTATT	TGTTAAAAAC	AATGTATGAT	TAGCAGTTCC	TGAAAATGTC	ATAATGAATA	1560
AGACTGCACC	ATACCCAATA	AACCAGTTAG	GGTCTAAAGA	AGGGATAACA	TTTTGTAAAA	1620
ATTTTGTAAAT	CAATCCATAA	GGACCATAGA	CAAATTTATA	TCCAGTCGCT	AAAACCACTC	1680
CTCCATAAAT	TAAAGAGGTC	ATATAACCTA	ATTTTAAAAAT	TTTAGCACCT	TTAATATCAA	1740
AGTACTCTGT	AAATAGAACA	CAAAGAATAC	CTACGACATT	AACTGTAATA	ATGAGTGAAA	1800
ATGCTAACTT	AAAAGTGTTC	ATAATACTCT	GAAGTGCCCT	CTGAGATTTT	AGAACACGAT	1860
GTACAGCATC	AAGGGAAAAT	TCTCCTCCTT	TTACAATAAC	ATTCACTACT	AGATCAAAGT	1920
TTGGATAAAT	AATAAATGTT	ACTAAGAACC	AGATTAACCC	TAAACGAATA	AGCCAATCTT	1980
TTAAATTTAA	TTTATGACGC	ATACTGCACC	TCCTTAAAAAT	TGCAGAACGT	CTGATGGTGT	2040
GATAAATAAT	TCCACACTTT	CTCCGACAGA	TCTAATAGCA	GCCTGACTAT	CAATACTTGT	2100
TACATTAAGA	ATCTGACTTT	CAGAACTTTT	TATTGTATAG	TGAATTGTAA	CTCCAGAAAA	2160
CTCAACATCA	ATAATGTGCC	CTTTTAGAAT	AAAATCTTGT	TCAGTTTCAC	GATTGAATCG	2220
AACTTCTCT	AATCGAATGT	ATCCTTTTTT	ATCCTCTAAG	AAAACGCTTG	TATTTTTCAA	2280

1134

TAATACTTCG	TGGACTGTTT	CATCGGTCAA	AACATTAATA	TCTCCAATAA	AATCACATAC	2340
AAATTCAGTT	TGAGAATTAT	GATAAATCTC	TACTGGTGTA	CCGACCTGTT	CGATGTATCC	2400
ATTGTTAAAG	ACTGCAATTC	TATCAGATAA	AGTCAAGGCT	TCCTCTTGAT	CATGAGTAAAC	2460
ATATAAAGTA	GTAATACCTA	ACTCTTTTTG	AAGTCTTTTC	AACTCTTTTC	TCAAATCTAC	2520
ACGTAATTTT	GCGTCAAGGT	TTGACAATGG	TTCATCTAGA	CAAAGAATTT	TAGGTTCAAG	2580
AACCAGAGCA	CGAGCCAATG	CTACCCTTTG	TTGTTGACCC	CCAGATAATT	CTGATACATT	2640
ACGCTGTAAC	TGTTGATCAG	AGATCTTAAT	TTTTGCTGCC	ACTGCTGATA	CTTTAGCTTT	2700
AATAACATCT	GGAGCTACCT	TCTTAACCTT	TAAACCAAAT	GCAATATTAT	CAAAAACAGT	2760
CATAGTTGGA	AATAGCGCAT	AAGATTGAAA	TACAATACCA	ATTCCACGCT	TTTCAGGTTT	2820
CAAAATGAGTG	ACATCTGTTC	CATTAACCTC	AATACTTCCT	GATGATGGAT	CTAGAAAACC	2880
TACCAATGCT	CTCAAAGTAG	TTGATTTACC	ACATCCTGAA	GGCCCAAGAA	ATGTAAAAAA	2940
TTCCCCCTCA	TGTATATCTA	AATTCAGATT	ATCAATTGCA	ACAAAATCAC	CATATTTAAT	3000
TTGAATATTA	TCAAATTTAA	TCATCTCACT	AACTCCCTCT	ATTACTAAAC	CAAAGCCTC	3060
TCTTTATTTT	TTCCATAAAT	TTAGAAATAA	TAGAGAGACT	TGGACATAAA	AATTAACTCT	3120
TATTTCTTAT	TGTACGTATT	CTAATTCAGC	TTTTTCTACC	CATTCATCCA	AATGCTTTCC	3180
AACAGCTTCC	CAGTCAATAT	TTTGTGGTTT	CACTTGATCA	ACAAATTTCT	TCGTATCTTC	3240
AGGTAGATCT	TTGAGGGCAT	CTTTATTTGC	AGGAATAGAT	CCAAAGTTCT	TACTATATTC	3300
TACTTGAAAT	TCTGATFGAC	CAAACCAATC	AATAAATCT	TTAGCTAACG	CTTGT'TTTT	3360
ACTAGTGCTT	AAAACCATAG	TTTGTTCAGT	TACAAATGGT	ACACCAATCT	CAGGAGTCAT	3420
AACTTTGAAA	ACAACATTTT	GTTCTTTTTG	TCCAAC TAAT	GCACCAGAAC	CCCACATCAT	3480
TCCATATTGT	ATTGGATCTT	CTTTGTCTAA	CATCTTAACA	ATTGAACTTT	CTCCCTTTTG	3540
AAGAGTGTAT	GCATTTTCA	AATATCTTTT	TGCTACTTCC	CAACCTTTT	CGGAAACACC	3600
TAATTCACCT	TTATCATCAA	GGTATCGAAC	TAAGATACTT	GCTAGAATTG	CCCGTCCTGT	3660
ACCTCCTTGA	AGACCAGAAA	TTGAATATTT	ACCTTTATAC	TTACTACCTA	ATTCAGTCCA	3720
ATCTTTAGGC	ATTTCTTTTA	CATCAGGCGC	CCCAATTAAA	ACTAATGGTT	GAACAATCAC	3780
AGGATTATAA	TAATTATCTT	TATCTGATAA	AGATTGATCA	ATTTTATCTA	ACCATTTAGG	3840
CTTGTA CTGT	ACTAGTAATT	TTTGATCTCT	AATTTTATTT	GAATCAACAG	CACCAATTCC	3900
AAATACCATA	TCTGCAACTG	CATTATCTTT	CTCAGCAATA	ACACGGTCTG	CTAATTGAGC	3960
GCCAGCGATA	TCAACCATTT	TTATATTAAA	ACCAGCTTCT	TTTGCTTTAG	CAGTTAACCA	4020
ATCACCACGA	CCATTTGAGA	CTGAGTTCGA	ATAGATAACT	AATTCCTGAC	TTTTATCAGC	4080

1135

TTTTTCTTCA GATGAAGAAG CAGTCGTAGA ATTTGAACCT CCAGAGCAAG CAGCAAGTGT 4140
 AGTAAgAGCA ACTCCCGTTG CAAGTACAGT AGACCAAACCT TTCATTTTTT TCATGATAAG 4200
 TTCTCCTTTT TTATTATTTT ATTTAAATTT TTCGTGATAT GGAACAAATT GTCTCATATC 4260
 TTCAAATACA GTATAGTCAA TACGGTTTAC AGTAATAGTT GGAATCTTCT CTAATAAAAT 4320
 TTCAGTTAAT TCTGCTCTGA CTTTAGTAAA CTCTTCTTCC TCCTCTTCGG TTAGAGGAAT 4380
 CCGAAGATAC CCAATTGAAA TATGGAATTG ATATCTATCA TGATTAGGGA AACAAACACC 4440
 TGCTTTTTCT GAGACATAAG TACGAATTC TCTAATCTC TTTGCAGAAG CTTCATCTGC 4500
 AGTTTCAACT AGTATGTTTT GTTTCCCAT TTCAGTTATA CGCATATGAA TTTCTTCATC 4560
 CAACAATGGA AAAATTTCAA GTTGTTTAGC AAAGTAATCA TGTATTTCTT GTAAAGGTGT 4620
 ATCTAGAGGA AGATTACTGC TCCAAAACTC gtTCACGATT TTCATGGCAC AACAATTTCAA 4680
 TTACAGTCAT GTGAATAGAA TTCCTTGGAG TTAAAGTAAA CTTATCGATA AATGGTAATT 4740
 CTCTATAACG TGATTGAATA ATATCAACAA CTCCATCAA ATCTTGTTTA GTATAAAGAT 4800
 TTGCTACAAC TGTATTCCCA GGGAAATGAT TAAATTCCCC ATTCTCGG 4848

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GTATAAGCA ACACCTTCTT GCTTGCCATA AGTTGTGAAA TGGGTAGAAAT CGATATCTAC 60
 AATGAGTTGG TTTAGCTGGT GAAACTGTAA AAAGAATTCG ACCAATTCAA GGTGAGGCA 120
 TCGCAAAC TA TGGACTGTTT CCTCGTCAGT TCTGGAAAGA AAACGGGATA AGGTTGGCTG 180
 TGAAGCAAGC TGCCCTCCTT CCAATAATTT TGGAAAGTAG GCATCAGCTG ACAATTCTTT 240
 ACAAGCATAG TCCGTTCAT AACCTGTTAA CAGTTGAAAG AGGAACTGGA CAAGGATATC 300
 TGAATCCGAA TAACGACAGT AGCGGCCTTG GTCATTCTGTT ACTAAATACT TAGAAATCCG 360
 CTCTTTTAGT TTCAACTGGG AAAAAAGTTC CTGAAAAAAG ATAAGACCAC CATACTGGGT 420
 TAAATGACCT CCATCGAAAG ATAGTTGGTA AAAAGACTTG TTTTGGGAAGT GATGATTTGG 480
 TAAACTGTTT ATGTGAGTTT CCTTCTTTT TGTGTTTTT TCTACACTTA TACCATAAAG 540
 GGGAAACTCT TTTTGTCTA GTAAAAACA CCCATTGGGT GAAAAAAGAA ACCATCCAGG 600

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ATCTAAGCTA	AGGCAAGGAT	TCTGGATGGT	TTTTAGATTT	GGGTGAATA	ATTGGGGATT	660
TAGGAGAAAT	GATGGTATCT	TCCAAATCAA	AATCAACTTC	ACTCCATAGT	CTCAACTGAT	720
TGATTTTCCC	ATCTTGATAG	GTCACATCCT	TGCAAGGAT	AAACTGAGTC	AACACCTCAT	780
GTTGACCTTG	ACACCTGATG	TCATCTACCA	AGAGCCAGAC	ATCCTCTACC	AACATGAGGA	840
TTTTTCTCCT	GTGAAGATAA	GGCAAATCAG	GTTCTGCTGA	CCAATAAGCC	CCCTCAATAT	900
AATGCACTCC	CTCCCTTCT	TTATGGTGAC	AAAACAGGGA	GTGAGGATAG	TATTCATAT	960
CCCAGGATCC	CGTGATCTT	TCCGGAGCTT	TCCCATCTAC	AATGCAGGTC	GAATGACTCC	1020
AAGCACTCTT	TAAGAGATAA	CGTTCATATA	TCTCCCGATA	AGAATAACGC	CCAGCATCTA	1080
TGAAAATAGG	TTGGCCTTGA	TACTGTAAGC	AAAAACTATT	CTCGTCACTA	TGACTATGGG	1140
CACTTCCTAG	CGGACCAFTT	TTGAAAAATA	GATAACGATG	TTCATCCTTA	ATGCAGACAT	1200
GTCCAGAGTC	TTCAAAGATC	ATGGACTTAG	GCTGCCAAGC	TCTCTTTTCA	AATTCCTGCA	1260
GTCGCTTGAC	CTTTTCTCGC	CCCAGGAACA	AGAGGCTAAG	CAAATCAACT	TTAACATCCA	1320
GACCGTTAAG	AAGGTCTTCC	TGGTTCAAAA	CCACAGCAGA	CAGGCTCAAA	ATTTCTGTCTG	1380
TTTCTGTAGA	ATCGCTATCA	CCAAAAGCCA	AAGTCCGTCC	ATCTAAGCCT	GTCATCATTT	1440
GAATATAGGT	CGCCATCTTT	TCCAGCAACT	CTTGGTAACT	ATCTTGCAAG	TCTGGAAGCA	1500
AGAGACACAA	ATCCAGCAAG	GCTTTATAAA	CCTCTACATG	ATAGAGAATC	GACTGTTCAA	1560
ACTGGCTTCC	ATCTCCTAAA	ATCTGTGTCT	CAATTTGCTG	TTTCAACTCC	TCTGAAGCAA	1620
AATGGTAAGC	TTCTTCTAGA	TCCATCTTAT	CTGAAAAGAA	ATGATAGATA	GCAAGCATCG	1680
GAATTGTTTG	TAAAATCCCC	CAGTTACTAA	GGGTGTACTT	GGCGCGATAG	TAGCTTTTCA	1740
TAAAGTCAAT	CTGCTTTTCT	AGACTGACCA	AAATTTTCTC	TAGTTCTTTC	TCCTCTAGCA	1800
AGTCAAATTT	CAAGAGGAGC	AAGAGTAGTT	TCAACCAAGT	AAAGGAACGA	ATACCCGTAT	1860
CCAAGTTTCT	AGTCATCAAG	GATTGAGGAG	AAAATTCTCT	CACCTGCTCA	ATCCAATCAA	1920
ATAGAAAGAA	CTTGCACTTT	TGAATATAGT	CCTTATCTCC	TTCTACCAGA	TACCCTATCA	1980
TAAACTGCAA	GAGATATTCT	TGTCGATTGA	GCATATAAGA	CCATTCTGGA	TCATCTTCAA	2040
ATACTTGATC	CCATACCATC	GGCTGGATTT	GATGGATTTT	TGAACAAGGC	TCCATATCCC	2100
AAGGACTATC	AAACATAAAA	CGATTGTCCA	TCAAGCGTTC	AAGGGAACCTC	TTGACTTTCT	2160
CATAGTCTTT	TGAACAGTGC	GACAAGATAT	AATCACGACA	TTGATTTCCA	TCGACTCTTT	2220
CAAAAAATTG	TCTTCTTCT	TCTTTCATTA	TCTATTACCA	GAAAAAGAAC	TACTTAAAAA	2280
GCAGTTCTTT	TGTCTTTCCC	ATTACACTTT	CCTTTTCTAC	ATGGATGACC	ACACCTTTTG	2340
CAATCTGCAA	GGAGACCAAG	TCATCTTGGA	TAGAAATGAT	TTTTCCATGA	ATTCCAGACA	2400

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ATAACAACAC TTCATCACCA AATGTTAAAG AAGCTAAATA CTCTTGTCGT TGCTCCATCT 2460
 GTTTGCGAAG CAACTTTTGC TGACGAATAG AATGAAAGCT TGACAGTAAA AGGGGACTCA 2520
 CTGCCAAGAC AATCACTATT CCATAAAACA ATGTTGTATC CATTAAGCTA TAATCTTAAG 2580
 CCAGCTTCCG ATAATTCCGA TGATAACTGT TAAAATAACG AGTTTATATG TTGTCCATTT 2640
 CTTTTCTTTG ATCAAGTAGT AAATAAAAG TGTAAATAGG GCTGGTAGAA GAGCTGGAGC 2700
 AACCTTATCA AGCATTCCCT GAATACTTAC GATACTTTGT TTAGCGTCTG CTTTAACTTC 2760
 CCCTGCAGCA AAGGTAATCG GCACCATAAT CTTAACAGAT GTCGCTGCCA AACCAGCAAT 2820
 TACGtTACAC CGATAATATT GGCAATACGA GAAATCGTtG CCATCTGtTC GCTTAGtTTA 2880
 TCAATCACAG TTGTTCCTAG TTTGTATCCA TACAGACCAG TTGACAATTT AATCGCTGTT 2940
 AAAATCGTAT TCATCGCAAG GAAGAACAAG ATTGACCAGA CAACCAAGCC TTCTTGAGCA 3000
 AACGAAGCTG CGATGGTTGA GAACAATGGA GCTAAACAGA ATTGAGAAAG AGAATCCCCA 3060
 ATACCTGCCA ATGGTCCCAT CAAGGCCATC TTGATGCTAC GTGTTCTTTT TGCCGGACGG 3120
 CCATTTTCCA ACATTACAAG ATGCAAGCTG GTAATAAAAG GCAGGAAGTG TGGGTTGGTA 3180
 TTATAGAATT CACAGTTTTC TTCCAAGGCT TGGTAGAAAC CTTCTTGATC CTCTCCATAG 3240
 TGTTTTTCA AAGCAGGATA CATCACATTG GCATATCCCA ACCCTTGATA GTTACTATAG 3300
 TTAAATCCAT TTTGACAAAA GAATGCCCGC AAAGACGTTT TAAGATAATC ACGTTTTGTT 3360
 AATTTGTTAG ATCCAGTCAT CGTGTGCTTC CTCCTCTACC ACATGATCCG CTGTTTTTGG 3420
 CTGTATTATA AATTCAATCA AAGCAAAGAT AGTACCTACA ATTGCAATAC CAATTGTTGG 3480
 GATGTTTAGA TAAGCTGCAC AAACATATCC CAACAAGACA AAGGGAATCA ACTCTTCTTT 3540
 AGCCATCACT GACAAGATCA TCGCAAAACC GATAGCTGGG AGCATTTTAC CAGCAACTGT 3600
 CAAACCTGTA AGTAATACCG GTGGAATGTA GTCTACGACT TTCAACAAGG TATCCATTGA 3660
 AAGGGCACCA AGCAACCCAA GGTAATCCA ATAAAGGCAA ACAACCAAAT TGTTCATTT 3720
 AGAGTGAAct TAAATTTCTT CAAATTATGG TTTTTCAAGT GCT 3763

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5053 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

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CAATCTCTGA	GTATGTGCGG	TCAATACTAW	CAAAGGGAAT	yCCTGACGTC	AAGTAATGTT	60
CAATGGmCT	ATAGGTAATG	GCAACCACTC	CATCAACTTT	ATTATGACGC	AACATCTCCA	120
GATAGCTTG	CTCTCTATTT	GTACCATTGA	TAGAACATAA	GAGTAATTTG	TTATTTCTCT	180
TATAGACTTC	ATTTTCCACA	TGCATAGCAA	ATTCTGAAAA	GAAGGGATGC	CAGATACTTG	240
GTACAATGAT	TGCAATCGTT	TCTGTTTCGAT	TTTTTTTCAT	TCCTCTAGCG	TAGTAATCTG	300
GAATGTAATT	CAAAGTTTTA	ATCGCTTGTT	CCACTTTTTT	CAAAGTFACT	TCTTTAATGC	360
CTTTTCTTTT	ATTAATTACA	CGTGAAACAG	TTCCAACACT	AACTCCTGCT	TCTAAAGCAA	420
CATCTTTCAT	GGTAATGAT	TTTCTTTGTT	CTACCATATT	ATCACCTCCT	TTCAATATAT	480
AGTATCATGC	AAATGCTTTT	TAAGCAACTA	TTTCTCAATC	ATTTTGGCC	AGATCATTTA	540
TCCCATCATG	AATAAAATCA	CTCCAATTAG	CTTTTGAAAA	TACTTCAATT	TTCATGTGTA	600
AACATCTACA	TAAAACAGGA	AAAGCCTTGG	TTTCATGGCT	TTTTTCGTAT	CTTCTATAAA	660
AAAAGCAAGA	GTTTTAGATG	GCTATAAATC	TAGATGTACA	TTTTGCTTAA	ATGATTGAAG	720
GTCTTTTCTT	AACAAAAACA	CCCCCAAAT	TAGACTTTTT	CTGTCTAACT	TTTGAGGTAC	780
AGTTCAAACG	CGAAATAGCG	TTTTTTTGTT	ATTTTGGTT	ACTCATCTAA	TCGAATAAAC	840
ATCATGGCAT	TTAACAAAGTA	TATGAGTGAG	ACCGTGTTTA	TATTATTTGA	ATAGATGAGT	900
CTCTTATTTT	CAATAGGAGG	AATAATAAAA	TTAGAAATAA	TGATATCATA	AGGTGAATCT	960
TCTAAAGATT	CCTTTGATAA	TTCTAATTCA	GTCCAAACTT	CCAGTCAAAA	ATTATTGCTA	1020
CAATAATAAG	AAAGTGCTC	TGCAACGAAT	TTTGCATGAT	ACTGATCAAA	ATTACTCATA	1080
ACTAAAACCT	TTAGTTTAGG	CTGATTTTGT	AGCAAATTAA	TCACCAAATG	TTGGGTATGA	1140
GTGATGAAGG	TATAAGATAG	ATGATTTACC	ATCATTGAAC	TAGAACAAC	CTCAAGAGTC	1200
TCTAAATAGT	GAGAAAGCTC	TTTTTTTATA	TCTGAAACAA	ATTTTGAAA	AATATTTTGA	1260
AAGTTCCTGA	TTGTATCCC	TTTTTGATCA	AATAAATAA	ACTCAGTAAA	CAACTCTTGA	1320
CGATACAGAT	GTGCGGTATT	ATGCAGATGC	CAAATCAGAT	TATCCTTATT	CTCCATTTCA	1380
ATCTGATACT	TGACTGAAAT	CTGATCAATA	AAATCACTCA	ATAGATGGTA	AGATTTTCA	1440
ACATAACTAT	CCTTTTAC	GCATTTTCATA	AAGAGACTTT	CATCTATGAA	AAACATTTT	1500
TGAAAGTAAG	ACACAAATAA	TTGGCAAACA	ACTTCTTCAT	CTAAAGAGAT	ATTGTATTCT	1560
GATTCAAAAC	TCTGAGCAAC	ACCTTCTATT	CCTTCTGCCT	GCATTAATAA	ATCCAAACTT	1620
TGGTCGTAA	AAGAATCTTT	ATCTACTTCC	ATAAAATGAC	CAAACTTTAT	TCTATATAGG	1680
TTCGTAACATA	GGAGCAACTT	TAGCATTCTA	TGCGTTGACA	AATTCATTGG	AAAGCTTGTT	1740
TCCTTATAAA	CCAATTCTAA	CAATGAGAT	AGTGCTCTG	ATGAAAAATT	TTCAAATGGC	1800

1139

CATTCTAGGA	AATAATATTT	TTCTGAAAA	TATTGTGCAA	AAAAGTAACG	AATGTCTCTC	1860
TCATTTCCAA	TGATTTGAAC	AGGGGTCAGA	CTAACTTCAA	ATTGAAATG	CCTTTTAATC	1920
ACTTTATFGA	TTTGGCTAAT	AATACGATAG	AGCGAAGATG	AACTGATATA	AAATTCTTTA	1980
CAAATACTCT	CAGCTTGACA	ACCTTCATTA	AAGAAGATGA	ATTCTAAAAAT	CGAAAAATGA	2040
GTTGAATGTT	TAAAGAAATG	ATGGTAAACC	ATTTCAATAT	CACTATCATC	GGTATTAATA	2100
ATGCGTATAC	CATTAGTAGA	AGAATGAAAA	ATCAAGTCAG	GAAAAGCAGA	TTTAACATGG	2160
GATAGATCAT	CTTTGACTGC	ACGTTCTGTA	CAATTTAATA	ACTCTGCTAG	TTCAGAACGA	2220
TGAAACCAAC	GTTTATGTTC	AAATAATAAT	TCTAATAAAT	CTAATTGCCT	ATGACTTTTT	2280
TTAGATAATA	AATCTCTCAT	GAATATCTTT	CTCTCTTTAT	AAATTATCGG	ATTAAACCTC	2340
TTGCAATTAT	ACCACAAAGA	ATAGGTATAG	CATGATATAA	CGACTTTTCC	TAAAATCTTT	2400
TATTTTCGTAT	AATAACACTA	CGGAGACAAT	ATATAAACAA	TTTTCTTATT	TTACCGTCTA	2460
TTGAGGGCGT	GAATACAGAA	TCAAATTCAA	GTCTAAAGAT	TATATTTTTA	ATTTTAAAAA	2520
TTATATAATA	GCAACAATTA	AAGAATTTGA	TTTTTTAAAA	TTATATAATA	ATAACAATCG	2580
AAATAATTGA	CTTTTCTATA	TTAAAGTTAT	ATAATAGTAA	TAATCAAAGA	AATTGATTTT	2640
TTGATATTAA	AATAAAAAAG	GAGGGTAGGC	AGTGTGTGA	TCAATTATTG	CTGGAGGTCT	2700
TATTGGTCTC	TTGGCAGGTA	AAATCACTAA	AAAAGTAGTT	CTATGGGAAT	CATCGCAAAT	2760
GTATTCGCTG	GTTTAGTCGG	GGCATATGCA	GGACAATCTC	TTTTAGGTAG	TTGGGGTCCA	2820
GCAATCGCTG	GAATGGCTTT	GCTCCCATCT	ATTGTAGGTG	CAGCGATTGT	GATTACTGTA	2880
GTGTCATTCT	TFACAGGTAG	AAAGTAAACT	TTTCGCCAGT	AAAGTTAGCA	AACTATTTTT	2940
AAATCAATGA	CGGGAAAAAT	AGTTTAAATG	TTAAATCGAA	AGGATTGTAT	ATGTCAAAAG	3000
CAAAGAAAAAT	ATGTTTCATT	ATTTTCTGTA	TTTTAATCTT	GACAATTTTC	CTTCCTGTTT	3060
TGATAGATTA	TCATCAAGTT	AGTGATCTAG	GTATTCATCT	ACTTAGCTGG	AGACAGAACT	3120
CCGTAGTTGA	ATTCTATCTT	GCTAGATATG	TCTTTTGGGG	GACAGTGGTT	CTATCAACTT	3180
TAGTTTTATT	ATCCATTTTA	GTTGTGATGT	TTTATCCTAA	ACGTTACTTG	GAAATCCAAC	3240
TTGAACTAA	AAACGATACA	TTAAAAATTA	AGAATTCGGC	AATCGAAGGT	TTTGTTAGAA	3300
GTTTGGTGAG	TGATCATAGA	TTGATCAAGA	ACCCAAGTGT	TCATGTAAAT	TTACGAAAAA	3360
ATAAATGTTT	CGTTCATGTA	GAAGGTAAAA	TTCTTCCTTC	AGACAACATC	GCTGACAGAT	3420
GCCAAATAAT	TCAAAATGAA	ATAACTAATG	GATTGAAGCA	GTTTTTTGGT	ATTGAGCGTC	3480
AAGTAAAACT	TGAAGTTGCA	GTAAAAAATT	ACCAACCAAA	ACCTCAAAAC	AAAAAGACTG	3540

1140

TTAGTCGTGT GAAGTAAGGA AGTAAAAAAT GGAATGGC'TT AAACAATATC GATATCCAAT	3600
TATCGCTGGT CTCATAGGCG TATTTCTGGC TTGTTTGATT GTCTCCTTTG GCTTCTTCAA	3660
AACAATATTT GTATTGATTT TAGGAGCACT GGGAGTTGCA GCTGGATTAT ATATCGAAAA	3720
AAACTATATA GATAAATAAA AAAATAAAAA TTACTAATTT AATTAAAGGA GTTTCATATG	3780
TCAAACGAAA AAAACACAAA CACTAACGTA GAAAAGAAAG ATGCTACTGT TGTAGCTCAC	3840
GAAATCAAAG GGGAACTTAC TTACGAAGAT AAAGTTATCC AAAAAATCAT TGGTCTTTCA	3900
CTAGAAAACG TTTCAGGTCT TTTGGGAATC GATGGTGGTT TCTTCTCAA TCTTAAAGAA	3960
AAAATCGTTA ACAGCGATGA CGTAACAAGT GGTGTTAACG TAGAAGTTGG TAAAAACAAA	4020
GTTGAGTTG ACTTAAACGT TATTGTTGAG TACCAAAAA ATGTTCCAGC TTTATATTCA	4080
GAAATCAGAG AAATCGTATC TTCAGAAGTT GCTAAAATGA CTGACTTGG AATTGTTGAA	4140
ATCAACGTAA ACGTTGTCGA CATCAAAACT AAAGAACAGC ATGAAGCAGA CTCAGTAAGC	4200
CTTCAAGATC GCGTATCTGA CGTTGCTGAA TCAACAGGAG AATTCACTTC AGAACAATTC	4260
GAAAAAGCTA AATCTGGTCT TGGATCTGGT TTCTCAACTG TTCAAGAAAA AGTTAGCGAA	4320
GGTGTAGAAG CTGTTAAAGG TGCAGCAAAT GGTGTAGTAT CTCACGAAAA CACTCGTGTA	4380
AACTAAGATA AAATAAATAT AACAGGAGAA ATTATCATGT CAGTAGAAGA AAAATTAAT	4440
CAAGCTAAAG GTTCTATTAA AGAAGGTGTT GGGAAAGCCA TCGGTGATGA AAAAATGGAA	4500
AAAGAAGGTG CAGCTGAAAA AGTTGTTTCT AAAGTAAAAG AAGTTGCCGA AGACGCTAAA	4560
GACGCTGTAG AAGGTGCTGT AGAAGGTGTT AAAACATGT TGAGTGGCGA CGATAAATAA	4620
GGTAAAAGT TACTTTATCT TTTTAGTAAT ATTAGTCAA AGAGTCTGAG TCAAGATGAT	4680
TCTCAGAAAA CAAAAGCTA GAGATTCCCA ATTGCGGAAC TCTAGCTTTT TAATTTTGCC	4740
TCTTCTCTT ATTATATTC AGCAGGTTGT TGGCCATGAG TACGAATCCC ATGTCAATTC	4800
TCACTTGACG CTTACCTCTC AGATGACATC TCTTATAACC CAAACAAACC TTTATCTGCC	4860
CAAAGACAGA TTTCATATCA ATCTTACGTT TAGCGAAAAT TTGTCTACCC TTGGAAGATA	4920
AAAGTGCCTG ATATTCTTTA GTTTTAAAC ACTGGTAACG TTCATTCATA TACAGTCTCT	4980
TTTGAGGGGC TGATTCAGGT TCATAATCGC AGTCAACATT GATTTCAAGG CTGTTTGCTT	5040
TCTATCTCCC CGG	5053

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AATTCTCTTT TTTCCAACAA AATGTATGAC CTGCACTTGA ATACTTCTCA TTGTTTGATC	60
ATTCATCTAC TTTCATATAA TCTTTTACAA AATCATAATA TGACATAACA CACTATCCCT	120
TTTAGACAAT ATTCCAATTA GCCTTATTAA TTCAAAATA TTGTATTAGT AATTATAACA	180
GATGTATAAT AGAAAAGCAA TGATAGATAT TATCAATTAA GCGAATTTAT ATCTAAAAGG	240
GATATTAAAG AAAGGAGATA TGCTTATGAA GATTTACAAA AACTATTTG CTTATGTCCA	300
AGATAAGAAA TATCTTGGGG TTTTGGCCAT AATTTTTTCT GCTATATCTG CTGCACTTAC	360
AGTATATGGA TATTATTTAA TCTACAAAT TCTAGATAAG TTAATAATTA ATTCAAATT	420
ATCCGGTGCA GAGAGTATAG CATTAATAATC TGTTATTACA CTAACAAGTG GAGCGATATT	480
TTATTTTGTC TCAGGAATGT TTTCACATAT CTTGGGATTC AGGCTTGAAA CAAATTTAAG	540
AAAAAGGGaA TCGATGGTCT GGAAAAGCA AGTTTTAGGT TCTTTGACTT AAATCCATCT	600
GGTCAAATAA GAAAGATTAT AGATGCAAT GCTGCACAAA CTCATCAGGT GGTAGCACAC	660
ATGATTCCCC ATAGTTCTCA GGCAATAATC ACACCCGTAC TTGTAAGTGC ACTTGGCTTT	720
ATAGTAAGTA TAAGAGTTGG CATAATTTTG CTTGCTCTTA CTATAATGG TGGCTTAATT	780
TTAGGGGCAA TGATGGGCGA GCAAGAATTT ATGAAGATAT ACCAAGAATC CCTATCTAAA	840
CTAAGTGCTG AAAGTGTGA GTACGTGAGA GGAATGCAAG TTGTAAAAAT ATTTAAAGCA	900
AATGTAGAGT CTTTTAAAAG CTTTTATAAG GCGATAAAAG ATFACTCAA GTATGCTTAT	960
GATTATTCCC TATCTTGTA AAGGCCTTAT GTTTGTATC AATGGTTATT TTTTGGACTG	1020
ATTGCAATTT TAATTATTCC TATAGTTTAT TTTATGACTA GCTTAGCTAG CGCAAAGGTG	1080
ATTTTACTTG AGCTTATCAT GATTTTATTT TTATCAGGAG TTCTCTTTGT TTCATTCATG	1140
AGAATGATGT GACTCCATG TATATTTCTC AAGGAAATTA TGCAGTAGAT ACTTTAGAGG	1200
CGCTTTACGA AGATATGCAA AAAGACAAAT TAGTGCATGG TAATGTCAAT AATTTTAAAA	1260
ACTATAATAT AGAATTTGAG AATGTTAGCT TTGCTTATAA TGATAAAGCT GTCATTGAAA	1320
ATTTATCCTT TAATTTAGAA GAAGGAAAGT CCTACGCACT TGTCGGTTCA TCTGGATCAG	1380
GCAAATCAAC AGTAGCAAAA CTTATATCAG GTTTTACAAA TGTTAATAAA GGAAGCATAA	1440
AGATAGGCGG GATAGCAATA AGTGAATATT CTGACGAAGC CTTAATTAAG GCCATTTCCCT	1500
TTGTTTTTCA AGATTCAAAA TTATTCAAGA AGAGCATTTA TGATAATGTA GCGTTAGCTA	1560
ATAAAGATGC GACGAAAGAT GACGTTATGA GAGCCTTAAA ATTAGCAGGA TGCGATTTAA	1620

1142

TATTAGACAA	AT'TCCCAGAA	AGAGAAAATA	CAATCATAGG	CTCAAAGGT	GTTTATTTAT	1680
CCGGTGGAGA	AAAACAAAGA	AT'GCAATG	CTAGAGCAAT	TTTAAAGGAT	TCCAAAATTA	1740
TTATTATGGA	TGAAGCATCA	GCATCTATG	ACCCAGATAA	CGAGTTTGAA	TTGCAAAAAG	1800
CTTTTAAAA	TCTTATGAAG	GATAAACAG	TTATCATGAT	TGCACACAGG	CTATCTACAA	1860
TTAAAGACCT	TGATGAAATT	ATTGTCATGG	ATAGTGGAAA	AATTATAGAA	AGAGGGTCTG	1920
ACAAAGAATT	AATGTCAAAA	GATACAAGGT	ATAAGAGCCT	GCAAGAGATG	TTTAAACAGTG	1980
CGAATGAATG	GAGGGTTTCA	AATGAAAGAG	TTTTATAAAA	AAAGATTTGC	TCTTACAGAT	2040
GGAGGAGCAA	GAAATTTAAG	TAAAGCAACA	CTGGCTTCAT	TTTTTCGTTA	TTGTATAAAC	2100
ATGCTTCCTG	CCATATTACT	TATGATTTTT	GCTCAGGAAG	TTTTGGAAAA	TATGGGCAAA	2160
AGCAATGGCT	TTTATATAGT	AT'TCTCAGTT	TTGATTTTGA	TAGCAATGTA	TATTTTGCTT	2220
TCTATCGAAT	ACGATAAATT	ATATAACACA	ACCTATCAAG	AAAGTGCAGA	TTTAAGAAATA	2280
AGGACAGCGG	AGAATTTATC	AAAATTACCT	CTATCTTACT	TTTCTAAACA	TGACATTTCC	2340
GACATTTTAC	AAACAATCAT	GGCTGATATT	GAAGGCATAG	AGCATGCAAT	GAGCCACTCA	2400
ATACCAAAGG	TGGGCGGCAT	GGTACTGTTT	TTCCCATTA	TATCTGTAAT	GATGCTAGCG	2460
GGCAATGTCA	AGATGGGTTT	AGCTGTAATT	AT'TCCATCTA	TTTTAAGCTT	TATATTTATA	2520
CCTTTATCTA	AAAAATATCA	GGTTAATGGA	CAGAATAGAT	ATTATGATGT	CTTAAGAAAA	2580
AACTCAGAAA	GCTTTCAAGA	AAATATCGAA	ATGCAAATGG	AGATTAAAGC	ATATAATTTA	2640
TCGAAGGATA	TTAAAGATGA	CTTATATAAA	AAAATGGAAG	ATAGTGAGAA	AGTACACTTA	2700
AAGGCGGAAG	TAACTACAAT	TTTAACTTTG	TCTATATCTT	CAATATTTAG	CTTTATATCT	2760
CTTGCTGTTG	TGATATTTGT	CGGCGTAAAT	CTAATTATTA	ATAAAGAGAT	AAATCTCTCT	2820
TACCTTATAG	GATATTTACT	AGCTGCTATG	AAGATAACAG	ACTCTTTAGA	TGCATCTAAA	2880
GAGGGCTTGA	TGGAATATT	TTATTTATCG	CCCAAAATAG	AAAGATTAAA	AGAAATTCAA	2940
AATCAAGATT	TACAAGAAGG	CGATGACTAT	AGCTTAAAAA	AATTTGATAT	TGATCTAAAA	3000
GATGTTGAGT	TTGCCTACAA	TAAAGACGCA	AAAGTTTAA	ATGGTGTAAG	TTTTAAAGCT	3060
AAGCAGGAG	AGGTCACTGC	TTTGGTAGGT	GCAAGTGGCT	GCGGTAAAAC	AACTATCTTG	3120
AAACTTATAT	CAAGACTTTA	TGATTATGAC	AAGGGACAAA	TCTTAATCGA	TGGCAAAGAT	3180
ATAAAGGAAA	TATCAACAGA	ATCCCTTTTT	GATAAGGTGT	CTATTGTTTT	CCAAGATGTG	3240
GTTCTCTTTA	ATCAAAGCGT	TATGGAAAAAT	ATTAGAATCG	GTAAGCAAGA	TGCAAGTGAC	3300
GAAGAGGTTA	AAAGAGCAGC	AAAAC'TGCA	AATTGCACAG	ATTTTATAGA	AAAAATGGAT	3360
AAAGGTTTCG	ATACAGTTAT	TGGTGAAAAC	GGAGCTGAGC	TATCAGGAGG	AGAAAGACAA	3420

1143

AGATTATCAA TAGCCAGAGC CTTCTTAAAA GATGCGCCGA TATTGATCTT AGATGAGATA	3480
ACAGCAAGCC TTGATGTTAA CAACGAGAAA AAGATTCAAG AGTCTTTAAA TAATTTAGTT	3540
AAAGATAAAA CTGTTGTAAT CATTTCCACAT AGAATGAAAT CCATAGAAAA TGCAGACAAG	3600
ATAGTAGTTC TTCAAAACGG AAGAGTAGAA AGCGAAGGTA AGCATGAAGA GCTTTTACAA	3660
AAATCAAAAA TTTACAAAA TTTAATAGAA AAGACAAAA TGGCAGAAGA ATTTATTTAT	3720
TAGGAGGACT ACAATGGATA ATAAAAAATT AAAAGTAAAA GATTTAGTAA GCATCGGTGT	3780
TTTTGGCGTA ATTTATTTTG CCTTCATGTT TGGAGTTGGT ATGATGGGCT TGATTTCAAT	3840
ATTGTTCTTA ATATACCCGA CAGTATTAGC CATAAGTGCA GGAAGTGTG TTTATGTTATT	3900
TATGGCTAAG GTTCAAAAAGC CATGGGCACT ATTTATATTT GGTATGATAT CACCACTTGT	3960
GATGTTTGCA GCTGGTCATA CCTACGTAGT TGTGGTTTTA TCACTTATAG TAATGATAAT	4020
AGCAGAATTA ATTAGAAAAGA TTGGTAATTA TAATTCATTT AAATACAATA TGCTTTCTTA	4080
TGCAATCTTC AGCACATgGA TATGTAGCTC TTTAATGCAA ATGCTTTTfAG CAAAAGAAAA	4140
ATATATGGAG TGGTCTTTGA TGAATATGGG AAAAGATTAT GTTGATGTAT TAGAAAAGTT	4200
AATAACTTAT CCTCACATGG CTTTAGTfAGC CTTAGGTGCT TTCTTAGGAG GAATTCCTGG	4260
AGCATATATA GGCAAGGCTC TATTGAAAA ACACTTTfCA AATGGATTAT ATTGTTGGGG	4320
ATACTTfACT CCTTGCTTAA TTTTATGGTG CTATCTGAAT TAAACCCTAT AGTTAAGATG	4380
TTTTTGAGTA TACCTATfGT TATTAGAATG TTTATTTTAC CATTfTATGGC AGCAAGCTTT	4440
ATGATAAAGA CCTCGGATGT AGGCGCAATA ATTTfCATCGA TGGATAAGCT TAAGATTTCA	4500
AAGAATGTAT CCATACCTAT TCGGTTATG TTTAGATTCT TCCCATCTTT TAAGGAGGAG	4560
AAGAAAAACA TCAAAATGGC TATGAGAGTA AGAGGGATAA ATTTTAAAA CCCAGTCAA	4620
TATCTTGAAT ATGTTTCTGT GCCACTACTC ATTATATfCAT CTAATATATC AGATGACATT	4680
GCAAAAGCGG CAGAAACAAA GGCAATAGAA AATCCAATTG CCAAGACCAG ATACATTCGC	4740
GTAAAGATAC AGCTAATTGA TTTTGTTTAT GTTTTAGCGG TTGCTGGACT TATTGTGGGA	4800
GGCTTAATAT GGTTGAAATA AAAAAATTAA GTCTTGATTA TGGTGAAGAG CATATATTAG	4860
ATGATATATC ACTATCCATA GCCGAGGGAG AGTGCGTGCT ATTTACAGGA AAAAGTGGAA	4920
ATGGTAAGTC ATCTTTAATA AATTCAATCA ATGGACTfAGC TGTAAGGTAT GATAACGCAA	4980
AGACAAAGGG CGAAATAATT ATTGATGGTA AGAATATAAA AAATTTGGAA CTTTATCAA	5040
TCTCAATGCT TGTTTCAACT GTTTTCAA ATCCTAAGAC ATATTTTTTT AATGTCAATA	5100
CGACATTAGA ATTATfATTT TATTTGGAAA ATATCGGTCT TGCAAGAGAA GAGATGGACA	5160

1144

GGCGTTTGAA GGATATACTT GAGATATTCC CGATAAAAAA TCTTTTGAAC AGAAATATAT	5220
TTAATCTATC CGGCGGTGAA AAACAAATTC TTTGCATGTC AGCTTCTTAT ATAGCAGGTA	5280
CAAAGATTAT AGTTATGGAT GAGCCTTCAT CGAATTTAGA TATTAAAAGC ATAAGTGTTT	5340
TGGCAAAGAT GCTAAAGATA TTTAAAGAGA AAGGCATAAG CATAATTGTT GCAGAGCATA	5400
GAATTTATTA TTTGATGGAC ATAGTTGACC GTGTATTTTT AATAGATAAA GGAAAGCTTA	5460
AAAAAACTTA TACTAGAAGT GAATTTTAA AGCTAGATAA AAATGAATTA AATGCTTTAA	5520
GTTTAAGAGA TAAAGAATTA AGTAAATTA AAGTTCCTTA TTTAAAAGAA GGTGGAGAGT	5580
ATCAGATAAA AAATCTTAGT TACAAATTTA CTGATGATGA GTGTTTAAGC TTAAAAGATA	5640
TTTCGTTCAA GCTTGGGAAA ATTTATGGCA TAATAGGATC CAACGGACGA GGAAAATCAA	5700
CGCTTTTAAG ATGTTTAATA GGTCTTGAGA AAAAATCAAA AGAAGAAATT TATTTTAAGG	5760
GAGAGAAGCT ATCTAAAAA GAAAGACTCA AAAACTCTTC ACTTGTTATG CAAGATGTAA	5820
ATCATCAATT ATTCACAGAT GAAGTATTC ACGAGCTTAG ATTAGGAGTA AAGAATTTTG	5880
ATGAAGAAAA GGCGAAAATC ATTTTAAACC CCAATTATTC ACCCCAAATC TAAAAACCAT	5940
CCAGAATCCT TGCCCTTAGCT TAGATCCTGG ATGGTTTCTT TTTTCACCCA ATGGGTGTTT	6000
TTTACTAGAC AAAAAAGAGT TTCCCTTTA TGGTATAAGT GTAGAAAAA ACACAAAAAG	6060
AAAGGAAACT CACATGAACA GTTTACCAA TCATCACTTC CAAAACAAGT CTTTTTACCA	6120
ACTATCTTTC GATGGAGGTC ATTTAACCCA GTATGGTGGT CTTATCTTTT TTCAGGAACT	6180
TTTTTCCCAG TTGAAACTAA AAGAGCGGAT TTCTAAGTAT TTAGTAACGA ATGACCAACG	6240
CCGCTACTGT CGTTATTCGG ATTCAGATAT CCTTGTCAG TTCCTCTTTC AACTGTTAAC	6300
AGGTTATGGA ACGGACTATG CTTGTAAAGA ATGTGCAGCT GATGCCTACT TTCCAAAATT	6360
GTTGGAAGGA GGCAGCTTG TTCACAGCCA ACCTTATCCC GTTTTCTTTC CAGAACTGAC	6420
GAGGAAACAG TCCATAGTTT GCGATGCCTC AACCTTGAAT TGGTCGAATT CTTTTTACAT	6480
G TTCACCAGC TG	6492

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AACTGAAGGT AAAGGCTTCG ACGCAGAACG TGACGCTGCC CAAGCTGCC TTGATGACCT	60
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1145

TAAGAAAGCT	CAAGAAGACA	ACAACCTGGA	CGACATGAAA	ACAAAACCTG	AAGCATTGAA	120
CGAAAAAGCT	CAAGGACTTG	CTGTTAAACT	CTACGAACAA	GCCGCAGCAG	CGCAACAAGC	180
TCAAGAAGGA	GCAGAAGGCG	CACAAGCAAC	AGGGAACGCA	GGCGATGACG	TCGTAGACGG	240
AGAGTTTACG	GAAAAGTAAG	ATGAGTGTAT	TGGATGAAGA	GTATCTAAAA	AATACACGAA	300
AAGTTTATAA	TGATTTTTGT	AATCAAGCTG	ATAACTATAG	AACATCAAAA	GATTTTATTG	360
ATAATATTCC	AATAGAATAT	TTAGCTAGAT	ATAGAGAATT	ATATTAGCTG	AACATGATAG	420
TTGTATCAAA	AATGATGAAG	CGGTAAGGAA	TTTTGTACC	TCAGTATFGT	TGTCTGCATT	480
TGTATCGGCG	ATGGTACCAG	CTATGATATC	ATTAGAAATA	CAAACATATA	AATTTGTAAT	540
ACCGTTCATA	ATTGGTATGA	TTTGGACAGT	AGTTGTATTT	CTTATGATCA	ATTGGAATTA	600
TATAGGCAAA	TACTAAGAAG	AGACAAAAAT	ATATAAATAT	TTCTGTACTT	ATAGGATATT	660
TAAAATCAAA	ATAAAGTTAA	TTTACTTATT	TGCAGAGGTT	GCAACCCAGC	CTCTGTTTTT	720
CGATAAAAAG	GGACGGAATC	TCATTTGTTT	GGGTTTGTTC	TCATCAATAG	AAAGGAACAA	780
AGAGTGTTCG	TAACTGAACA	CGGGTTTCAG	AATTTCTTAC	TAAATATAAA	AGAAAGGAAT	840
TGAACCCGAC	CTAAATGGTG	GTTTCGATTCA	GAACATCAAT	AGAAAGGAAT	AAGGGTGTTC	900
GTAACGAAAC	ACGGGCTATG	GACTGTGCCA	AAAAGATAGT	TTTTTCTAGG	ACGTAAGCGT	960
CCGTCGTCFA	AACTCCTAGA	TGGCTGTGTC	CGTTTGACGC	CCTTTGTATC	TTGAATTATG	1020
AACAATACTG	AATTTTATGA	TCGTCTGGGG	GTATCCAAAA	ACGCTTCGGC	AGACGAAATC	1080
AAAAAGGCTT	ATCGTAAGCT	TTCCAAAAAA	TATCACCCAG	ATATCAACAA	GGAGCCTGGT	1140
GCTGAGGACA	AGTACAAGGA	AGTTCAAGAA	GCCTATGAGA	CTTTGAGTGA	CGACCAAAAA	1200
CGTGCTGCCT	ATGACCAGTA	TGGTGCTGCA	GGCCCAATG	GTGGTTTGG	TGGAGCTGGT	1260
GGTTTCGGCG	GTTTCAATGG	GGCAGGTGGC	TTCCGGTGGT	TTGAGGATAT	TTTCTCAAGT	1320
TTCTTCGGCG	GAGGCGGTTT	TTCCGCAAT	CCAAACGCTC	CTCGCCAAGG	AGATGATCTC	1380
CAGTATCGTG	TCAATTTGAC	CTTTGAAGAA	GCTATCTTCG	GAACGAGAA	GGAAGTTAAG	1440
TATCATCGTG	AAGCTGGCTG	TCGTACATGT	AATGGATCTG	GTGCTAAGCC	AGGGACAAGT	1500
CCAGTCACTT	GTGGACGCTG	TCATGGCGCT	GGTGTCAATTA	ACGTCGATAC	GCAGACTCCT	1560
CTTGGTATGA	TGCGTCGCCA	AGTAACCTGT	GATGTCTGTC	ACGGTCGAGG	AAAAGAAATC	1620
AAATATCCAT	GTACAACCTG	TCATGGAACA	GGTCATGAGA	AACAAGCTCA	TAGCGTACAT	1680
GTGAAAATCC	CTGCTGGTGT	GGAAACAGGT	CAACAAATTC	GCCTCGCTGG	TCAAGGTGAA	1740
GCAGGCTTTA	ACGGTGGACC	TTATGGTGAC	TTGTATGTAG	TAGTTTCTGT	GGAAGCTAGC	1800

1146

GACAAGTTTG	AACGTGAAGG	AACGACTATC	TTCTACAATC	TCAACCTCAA	CTTTGTCCAA	1860
GCGGCTCTTG	GTGATACAGT	AGATATTCCA	ACTGTTACAG	GTGATGTGA	ATTTGGTTATT	1920
CCAGAGGGAA	CTCAGACTGG	TAAGAAGTTC	CGCCTACGTA	GTAAGGGGGC	ACCGAGCCTT	1980
CGTGCGGGTG	CAGTTGGTGA	CCAATACGTT	ACTGTTAATG	TCGTAACACC	GACAGGCTTG	2040
AACGACCGCC	AAAAAGTAGC	CTTGAAAGAA	TTGCGGGCTG	CTGGTACTT	GAAAGTAAAT	2100
CCAAAGAAAA	AAGGCTTCTT	TGACCATATT	AAAGATGCCT	TTGATGGAGA	ATAATACTCT	2160
TCGAAAATCT	CTTCAAACCA	CGTCAGCGTT	GCCTTGCCGT	ATATATGTGA	CTGACTTCGT	2220
CAGTCGTATC	TACAACCTCA	AAACAGTGTT	TTGAGCAGCC	CGTGGCTAGT	TTCCTAGTTT	2280
GCTTTTFACT	TTATAGATTT	TTTAAGACTT	TCCTAAGTAA	TGACGGACGG	TAGTGACCTC	2340
CTTCGAAGTT	CCATACCTAA	ACTTTGAACC	TAAGTTTAA	AGTTTCCGGA	CAGCTGAAAC	2400
CAAGCTGTTT	CAGGTGTTTT	CATTACGGCA	GAAAGTCTTC	GATTTAGTTG	TGAAATGGTG	2460
AATGATACTC	TTCAAAAATT	TCTTCAAACC	ACGTCAGCGT	CGGCTTGTC	TGGGTATGGT	2520
TACTGACTTC	GTCAGTCTTA	TCCACAACCT	CAAACAGTG	TTTGAGCTGA	CTTCGTCAGT	2580
TCTATCCACA	ACCTTAAAAC	GGTGTTTTGA	GCAGTCFTGT	CCTAGCTTTC	TAGTTTGCTT	2640
TTTGATTTTT	ATTGAGTATG	AATTACCTAA	ATTATGATGC	ATAGTTGATG	GGATATATAT	2700
AATAGATTGA	AATAGAATAT	GAACAAATTG	ATAAGAGGAT	TTTAAAGTAA	TCTCTAACAA	2760
TGCTTTAGAA	ACTATGGTGT	GCTATTCTAA	ATTCAAATCA	CTATAACTTG	TTTACGTTTT	2820
AAAAAAGAGC	CGTCGGGCTC	TTTTTACTTA	TCTTCAGTTC	CCTGCATTC	TTTTATCACA	2880
GCTAGTCTAG	TCTGGATATC	CTTTTCCAAG	ACCTTAAACT	TGTAAGTCAA	GTCTTCTTGG	2940
TATTCCTTGA	TAAGTCTTTT	TTGCTGGTTA	ATGATTTGCA	GGCTGTTTTG	GATAATATCC	3000
ACATCGTCCT	TGATAGCTTG	AACGCGGTCA	GTGGTATTCA	AGACTTCATC	TGTGATGGTT	3060
TGGCGATTTT	TTGTAACCAG	ATAACTTCCG	GCTGCAGCTC	CTGCAAATAG	CAGTAGGTTG	3120
GATAATTTCA	TAGCAACTCC	TTAAGCGTTT	TTGATGGTTT	CAGCGACTTG	AGCAAGTTTG	3180
TCAAAGTCTG	GTTTCGTGGC	GATAAAATCA	ATCTTGAGGT	CATCGTCAGC	ACTGTAGCGA	3240
GGCACAAGGT	GAACGTGAGT	ATGAAAAACT	GTTTGACCAG	CGACTTCTTC	ACAGTTGGAA	3300
ATGATATTCA	TACCAGCAGC	CTTAGTACT	TTTATGACTT	TTTGAGCTAC	TTTTGGTACT	3360
TGGGCAAAGA	GTTGGCTGGC	GCTCGTAGCA	TCCATCTCCA	AAAGATTGCG	ATAGTGTCT	3420
TTTGGCACGA	CCAAGTGTG	TCCTAGTGT	ACTTGAGAGA	TATCAAGAAA	GGCAAGGACC	3480
TGCTCATCTT	CATATACTTT	TGAAGCAGGA	ATTTCCCTTG	CGATGATTTT	ACAAAAATG	3540
CAATCTGACA	TAAAATCTAC	CTCTACTGTA	CTGAATTTTG	ATATAATATA	GCTACATTAT	3600

1147

ACCAGATTTG GAGAAAATAT GTTAGAAATT AAAAACCTGA CAGGTGGCTA TGTTCATGTT	3660
CCTGTTTTGA AAGATGTGTC CTTTACTGTT GAAAGTGGGC AGTTGGTCGG TTTGATTGGT	3720
CTCAATGGTG CTGGGAAATC AACGACGATC AATGAGATTA TCGGTCTGTT GGCACCTTAT	3780
AGTGGCTCCA TCAATATCAA TGGCCTGACT CTGCAAGGAG ATGCGACTAG CTACCGCAAG	3840
CAGATTGGCT ACATTCCCTGA GACGCTAGT CTGTATGAGG AATTGACCCT CAGAGAGCAT	3900
ATCGAAACGG TTGCTATGGC TTACGGTATT GAGCAAAAAG TGGCTTTCGA ACGAGTAGAG	3960
CCCTTGTTAA AAATGTTCCG TTTGGAACAG AAATTAGACT GGTTCCCTGT TCATTTTTCA	4020
AAAGGGATGA AGCAGAAGGT CATGATTATC TGTGCTTTTG TGGTGGATCC AAGTCTTTTC	4080
ATCGTGGATG AGCCTTTCCT TGGTCTTGAT CCGCTGGCTA TTTCTGATTT GATTCAGCTT	4140
TTGGAAGTGG AGAAGCAAAA GGGCAAGTCT ATTCTCATGA GTACCCACGT GCTGGATTCCG	4200
GCGGAGAAGA TGTGTGATGC CTTTGTCAIT CTTACAAGG GAGAGGTGCG TTCCAAAGGC	4260
AATCTCCTGC AACTACGTGA AGCCTTTGAT ATGCTGAGG CTAGTTTGAA TGATATTTAC	4320
TTGGCTCTGA CCAAAGAGGA GGATCTATGA AAGACTTGTT TTTAAAGAGA AAGCAGGCCT	4380
TTCGTAAGGA GTGTCTTGGT TATCTGCGCT ATGTGCTCAA TGACCACTTT GTCTTGTTC	4440
TGCTTGTCTT GTTGGGCTTT CTAGCCTACC AGTACAGTCA ACTCTTACAA CATTTTCTTG	4500
AAAATCATTG GCCTATCCTT TTGTTTGTAG GAATTACGTC TGTTTTACTT TTACTTTGGG	4560
GAGGAACTGC CACCTATATG GAGGCTCCAG ACAAGCTCTT TCTCTTAGTT GGAGAAGAGG	4620
AAATTAAGCT CCATCTCAAG CGTCAAACG GCATTTCCCT AGTCTTTTGG CTCCTTGTAC	4680
AGACCCTTTT CTGCTGTTA TTTGCGCCTT TATTTTTAGC AATGGGTAT GGCTTGCCAG	4740
TTTTTCTGCT CTATGTGCTT TTATGGGGG TAGGAAAATA TTTCCACTTT TGTCAAAGG	4800
CCAGCAAAT TTTCACTGAA ACTGGACTGG ACTGGGACTA TGTTATTTCT CAAGAAAGCA	4860
AGCGTAAGCA AGTCTTGCTT CGTTTCTTTG CCCTCTTTAC GCAGGTCAAG GGAATTTCAA	4920
ACAGCGTTAA GCGTCGTGCC TATCTGGACT TTATTTTTAA GGCTGTTTCAAG AAGGTGCCTG	4980
GGAAAGATTG GCAAAATCTC TATCTGCGTT CTATCTGCG AAATGGCGAC CTCTTTGCTC	5040
TCAGTCTTCG TCTTCTCTTG CTTTCCCTTG TGGCGCAGGT TTTTATCGAG CAAGCTTGGA	5100
TTGCGACAGC AGTGGTAGTT CTCTTTAACT ACCTCTTGCT CTCCAGTTG CTGGCCCTCT	5160
ATCATGCCTT TGACTIONCAG TATTTGACCC AACTCTTTCC GCTGGACAAG GGGCAAAGG	5220
AAAAGGCTT ACAGGAGGTA GTTCGAGGAT TGACCAGTTT TGTTTTACTT GTGGAATTAG	5280
TTGTTGGGTT GATTACCTTC CAAGAAAAC TAGCCCTTCT AGCCTTACTA GGAGCTGGTT	5340

1148

TGGTTTTACT	AGTCTTGAT	TTGCCTTATC	AGGTAAAACG	TCAGATGCAG	GACTAACATT	5400
GCTGATACGA	CACTAAAAAA	GAAGTTGAGT	TCAGTCTGTC	TCAACTTCTT	TTTGTACT	5460
ACAGGATAAT	GGTTGGTCCG	TAGAGACTTA	TACTCTTCGA	AAATCTCTTC	AAACCACGTC	5520
AGCGTCGTCT	TACCGTACTC	AAGTACAGCT	TGCGGCTAGC	TTCTTAGTTT	GCTCTTTGAT	5580
TTTCATTGAG	TATTAAGTTG	GTCTTGACTT	GGTCAAAGTG	GAAGCGGTCA	TAGGCCCGCC	5640
AAGCGGCGCG	AGTTGGAGCA	TCTGGATCAA	GAGCGCTGAG	TCCCATGAGA	AGACTGGAAG	5700
TCTGGTAAAA	TTTTTCTAGT	TCAATCAAGA	ATCGATTATC	CACTGTTTCA	GCCTGGCTA	5760
GAAAACCAAG	AATAGAGTTT	AATTGCTCCT	GAAAGCGGAC	GTCGTCAGCG	CTTGCCTGTT	5820
TGCATGCTTG	GTAGGCTTTG	TTTAAGTCAG	TAATCAAAGT	ATGAGCTCTT	TTGATGGGGT	5880
CTGTATCTGT	CATGGGAATG	CCTCCTTTAA	TCTGGGTGCC	AGTCTTACTT	CTGGCAACTG	5940
TGTTTTGATA	CTGTTAGTTT	ATCACTTTTA	ATTCTTTTTT	TTTATTCAAA	TCTTTAATTG	6000
TCATTGAAAT	GTCTTGAATT	GCGCTGAGTG	AATTTTATGA	TAAAATAGTT	GTAAGCTCAT	6060
CATGATGTTG	TAGAAAATAA	TCCTTTTAGG	AGTTTTCAAA	GACTGTTTAG	GATTGGGTGT	6120
GCTTGGGCTA	GACCTTTTCT	GTATTCTTTT	TCTTAGGAGG	AGAATCCAAT	GAAATATATG	6180
ATTATTCAGA	CGCAGAAAAC	AGTCTATAAA	GTAAACATCG	ACGATATCTA	CTATATCCAA	6240
ACACATCCAA	CTAAAGCCCA	TACCGTACAG	ATTGTTACAG	AAGAAGCTAG	TTTTAATATG	6300
CTTCAAAATT	TAAGTAATCT	TGAGAACCAA	TGTGGGGAAA	CCTTGATGAG	ATGTCATCGA	6360
AATTGTTTGG	TTAATCTTGA	TAAATTAAAA	TCGATTGATT	TTCAAGAAAG	AATCCTTTTT	6420
CTCGGAGAAG	AAGGTCAATA	CGCTGTCAAG	TATGCCAGAC	GTCGCTATAG	AGAAATTCGT	6480
CAAAAATGGT	TGAAAGAGGG	AGAGTAAGAA	GATGAGAATA	TTTGTTTTAG	AGGATGATTT	6540
TTCCCAACAG	ACTAGAATTG	AAACGACGAT	TGAGAAACTT	TTGAAAGCAC	ATCATATCAT	6600
TCCTAGCTCT	TTTGAGGTAT	TTGGCAAGCC	GGACCAACTG	CTGGCTGAAG	TGCATGAGAA	6660
GGGGGCCCAT	CAGCTATTCT	TTTTGGATAT	TGAGATTCTGA	AATGAAGAGA	TGAAGGGACT	6720
GGAAGTGGCT	AGAAAGATTC	GGGATCGGGA	TCCTTATGCC	CTGATTGTCT	TTGTGACGAC	6780
TCACTCGGAG	TTTATGCCCC	TGTCTTTTCG	CTACCAAGTG	TCTGCTTTGG	ACTACATTGA	6840
TAAGGCCTTG	TCAGCAGAGG	AGTTTGAATC	TCGGATCGAG	ACAGCCCTCC	TCTATGCCAA	6900
TAGTCAAGAT	AGTAAAAGTC	TGGCGGAAGA	TTGCTTTTAC	TTTAAATCAA	AATTTGCCCA	6960
ATTTCAAGTAT	CCTTTTAAAG	AGGTTTACTA	TCTCGAAAACG	TCGCCCAGAG	CCCATCGTGT	7020
TATTCTCTAT	ACCAAGACAG	ACAGGCTGGA	ATTTACAGCG	AGTTTAGAGG	AGGTTTTCAA	7080
GCAGGAGCCC	CGTCTCTTGC	AGTGCCACCG	CTCTTTTCTC	ATCAATCCTG	CAAATGTGGT	7140

1149

GCATTTGGAT AAGAAAGAAA AACTGCTTTT CTTT

7174

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CCACCAGGGA AAATCATTGA AGTTGGTAGT CACCAAGAGT TAATGCAGGC GCAAAGTTTC	60
TACCATCATC TATTCAATAA ATAAGGAGAA TGTCATGAAT CCTAATCTTT TTAGAAGCGT	120
CGAGTTTTAT CAGAGACGTT ACCATAACTA TGCACAGTG TTAATTATAC CTCTTTCATT	180
ACTATTTACT TTCATCTTGA TTTTCTCCCT TGTGTCACA AAAGAAATTA CTGTTACTTC	240
CCAAGGAGAA ATCGCCCCA CA _g TGTCATT GCCTCCATTC AGTCAACCAG TGATAATCCT	300
ATCCTAGCTA ATCATTTAGT GGCAAATCAA GTAGTTGAAA AAGGGGACTT ACTCATCAA	360
TACTCTGAAA CAATGGAAGA AAGTCAGAAA ACTGCCTTAG CAACTCAATT ACAAAGACTT	420
GAGAAGCAA AAGAAGGACT TGGAATTTG AAACAAAGCT TAGAAAAAGC GACTGATCTT	480
TTTTCTGGCG AGGATGAATT TGCTACCAT AATACCTTA TGAATTTTAC TAAACAATCC	540
CATGATATTG AACTGGGTAT CACAAAGACT AACACCGAAG TTTCAAATCA AGCTAATCTT	600
TCCAATAGCA GTTCATCAGC TATTGAACAA GAAATTACAA AAGTTCAACA ACAAATGGA	660
GAATATCAAG AGTTGAGAGA TGCTATCATA AATAACAGAG CACGCTTACC AACTGGCAAT	720
CCGCACCAGT CAATTTTGAA TCGTTATCTT GTAGCCTCAC AAGGACAAAC ACAAGGAACT	780
GCAGAGGAGC CATTTTTATC TCAAATTAAT CAAAGTATTG CAGGTCTTGA ATCATCTATC	840
GCAAGCCTCA AAATTCAGCA AGCTGGTATC GGAAGTGTAG CAACTTATGA TAACAGTTTA	900
GCAACCAAAA TTGAAGTACT CCGCACTCAG TTTTACAGA CAGCCTCACA GCAACAACATA	960
ACTGTGGAGA ATCAATTAAC AGAATTAATA GTACAACACTAG ATCAAGCCAC ACAGCGTTTG	1020
GAAAACAATA CCTTAACCTC CCCAAGTAAA GGTATCGTTC ATCTGAACAG CGAATTTGAA	1080
GGTAAAAATA GAATTCCAAC TGGTACAGAA ATTGCTCAA TATTCCTGT CATCACAGAT	1140
ACAAGAGAAG TACTAATCAC TTACTACGTA TCTTCTGACT ATCTACCTCT ACTAGATAAA	1200
GGACAAACTG TAAGATTAAA ACTGGAGAAG ATTGGAATC ACGGCACCAC CATCATCGGC	1260
CAACTTCAGA CAATTGATCA AACTCCTACC AGAACAGAGC AAGGAAATCT CTTTAAATTA	1320

1150

ACCGCTCTTG	CAAACCTATC	TAACGAGGAT	AGTAAACTCA	TCCAATATGG	CTTACAAGGT	1380
CGCGTCACTA	GTGTAACCTAC	AAAGAAAACA	TATTTTGATT	ATTTCAAAGA	TAAAATTTTA	1440
ACACATTCTG	ATTAATTTTC	AGATAACACT	CTATAACTAT	TTATTATCTT	ATCAAAAAGG	1500
AGAATCATAA	CATGGATAAG	AAACAAAACC	TAACTTCATT	TCAAGAACTA	ACAACCTACCG	1560
AACTCAATCA	AATTACAGGT	GGAGGATTGT	GGGAAGATTT	ATTATATAAC	ATTAATAGAT	1620
ATGCTCATTA	CATCACATAA	GAACCTCATC	ATCCAATACA	ACTATAAAAA	AATAAGACCG	1680
AGAAACAAGT	ACTCTCGGTC	TTATTTTTC	TCATTCTGTA	TGTATCACAG	TAAGTACCTG	1740
ACGAAAGACT	TGATTTTGAC	AGGTGGTATT	TAGACTGGTA	TTAGGATGGC	TTTCCACAAT	1800
CTTCATGACG	GTATAGAGAC	CAACTCCTCT	CTCCTCCCCT	TTAGAACTGG	CTCCAAAGGA	1860
GAAGATTTC	GAAATATCGA	TGCCCTCTTC	TTTGATGGAG	TTTTTCGATGA	TAAAGGTCTC	1920
CTGTGCTCCA	TTTTTTAAAA	AGGCGATTGA	AACATGAGGT	TGACTAGCTT	CCACACTGGC	1980
TTCAATAGCA	TTGTCACAAA	GGATAGACAC	AATGGTTAGA	AAATCAAGTA	GACTCATCCC	2040
CTCGACCTGA	ATCTCCTCAG	GAACCTCGAC	ATTAAAGACA	ATGTTCTTAT	CTCTGGCTTT	2100
TAAAAATTC	CCTGCTAGAA	GACTTTTGAG	GGCTTTATCA	CGAATATTTA	CCAATCTGCC	2160
CAGGTATAT	TTATTGTTCT	GCAATTTCTG	ACTGGAATCC	TTTAAGACGG	AGCCATAGAC	2220
CTCTTTTATC	TGCTCCATAT	CCTCCTCTTC	AATGCCCAGA	CGTAAGCTAG	TCAAGAGGTT	2280
GGTATAATCA	TGACGAAAGC	TCCGTACTTC	CTTGTAAGC	TCCTCTATAT	GCCGACTATA	2340
GCGTTCCATA	TCTCTATAGC	GCAGGGCCTG	CTCTTGTTCC	AATCTCTCAT	AGAGTTTTTC	2400
CTTCAAAATAG	GTATCCAATT	TCTTGATAAC	CCCCATAAAA	AAGAGTAGGT	AAAAGACTAG	2460
GATGAGATGG	CGAACAGTCT	TTGATTGAAT	ACTTTGTTCA	TATTCAAAAA	AAGACAGACT	2520
TTCCATGACT	AGATAGTAGC	CACCCATTAT	CCAGTTAATC	TGAGTCAGGG	ACTTTTGAAA	2580
GGCTTTATCG	AGAATCTCCT	TTCTCAAGCT	AGTAAAATCG	TAGTCCAACC	ATTTCAAAAA	2640
AGCTAGAGAA	ATGAAGAAAT	TGAAAATTAT	TATACATAAC	CCAGTAAATG	AGTAGCCATC	2700
ATATACTTGC	CCTTGTCCTA	AAAATGGAAG	CACAAAATAG	GAGACTCCTC	TATAAAAGAG	2760
ATTCACCAAT	ATCATTGGAA	AGAGACCATA	AAAGAAAAGG	AGTTTTTTAG	GAAGCCCTCT	2820
CAATAATAAG	AAAGATAAGC	CTATGCCGTA	CAAGGGTTCC	ATAAAATAAG	ATAGGTAAAC	2880
ATTTCTACT	ATATAGCTAA	TCATCACAAA	AACAAAGGCC	AACAGTATCT	TCAAAAAGAAA	2940
GGCCTTAAAA	ATCCTCTCGA	AAGTAAGATC	AATTCCATCC	ACCTTAAAGA	AGATGACAAT	3000
TTCTAGTCCA	TTAGTAACAA	GTGTATACAA	CAATATCCAA	GCAATGTTCA	TAAATTCTCC	3060
TAGCTCAGTG	TAATTTATTG	ATGGCCTCAG	ACACTCCTC	GACCTTATAA	CGGGCGATTA	3120

1151

GACAACCTCC ACCATTGGGA GAGAAGAGCA GTTTTTCTTT CTTATCCAAA TGCACCACAT 3180
 TTGCAGGATT GATGAGAAAA GAGCGGT 3207

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTGAATCAAG TGTACTGCAC CAGTTCGTGC ATCAGGCATA ACAACATCTA CAGATATAAT 60
 ATTGTTTTCT GAGTCCGCTT CATAAGTTAA AATCATAAAT TTTTCGATAT TCGAATTTTT 120
 AGTAGCTTGT TCAATTCTTT GAATCATTTT ATCAGAAACT AACTCCATCT GAATTGGAAA 180
 GGAATGACTA TTTTCATCAT TTTTGTAGGA AGAATGTTGA TTAAGATAAA GTGTATTCAT 240
 CTGAGCATAT TCAATAAAGT AGCCACTCTT ATTTTTTTGT ACCAAAGGAA ATTGGTTTGT 300
 AAGTCGCTTC TTACCCTTTA TAATTAACAA TACTTTCCCA TATTTTCTG TATTTGTTTC 360
 AAATCTFAA TATCCCAAG TCTGTCCTGC TAATTGTAAT TTATACTCAA ACAAACTGTC 420
 TGATGCAAAAT GCAGTATCAA TATGATFAGG TCGCGTCCAT GCATAACCAT TCGACACTAT 480
 CATTGTCTCT CTTTTTCTA GACGTCATC TACATAATCT TTTTGCCCTT TCATCAAAGT 540
 ATCTACAATT TTTTGTGCCT CAAGCGAATC AAAGAGATCC TGATTCAACA TAATCTTCC 600
 TCCTCCAAAT ACTTTTTAAT GAATTATACC ATTTCTTAA AGAAATTAACA ACAATAATTA 660
 TCTTTTTCTT AAAGTCTGT GTCAGAGTAA TTTAGAAAAT TATATCTTCT ATAGTAAAAT 720
 CAATTAAGAAA CTGAACAAAT TTATTGGGAA ATTCAAATCG CTTTCTGAAA ATATTTTAGG 780
 AACCGTAGTG TAATATTCCA GATTCAATTC ACTATAAAAC TGACCTTTCT CCTGCAAAAG 840
 AAAAAGGAAA GACTTCCTTT CGTGCCTTTC CTCTTACTTG CTAATTGTTT GATTATTTTT 900
 GGTAAGCTAC TGCTTGTCTG ATAAAATCCT GAATCGGCTC TCCTTGGTGG AGAGCTTTTA 960
 CTATTTTCGA ACCGACGATA ACACCATCTG ACACCGCATT GAAGCGTCC AGATCGGCTT 1020
 GACTAGATAC ACCAAAACCT GTCAAGACTG GGATGTCGGC CACTTGATGA AGTTGCGCCA 1080
 AGTGCTTGTG CAAATCTGCA CGGTAATTGC CTGATTTCCC TGTCCTCCA TTGATGGCAA 1140
 CGGCATAGAT GAATCCCTCC GCCCCTTCAA TCAACTCTTT CTGGCGCTCA ATTCCTGTGG 1200
 TCAAGCTTAC TAAAGGAATC AAGGCGATAT CTGTATTTGC CAAAAATGGT TCTACAAAGT 1260

1152

TGGCATGTTT	ATGAGGCAGG	TCTGGGATAA	TCAAGCCCTT	CACAGCTGTA	TCAGCCAGAT	1320
CTTTGACAAA	GTTCTCCACA	CCGTACTGAA	AGAGGGGGTT	GAAGTAGGTC	ATGATGACCA	1380
GTGGAATCTC	TGTTTCAATG	GTTTTCAAGG	TTTCAACTAA	AGCCTGGGTA	GAGGTCCCGT	1440
GGGCTAAACT	GCGCAAGCCA	GCTTCTTCGA	TAACAGGTCC	ATCTGCAACA	GGGTCTGAAA	1500
AGGGAATACC	CACCTCAATT	GCAGAGACAC	CCAAATCTTC	TAAAAAGTGA	ATTGTTTCAG	1560
CAAGACCGTC	CAAACCTTTC	TCGTGGTCAC	CAGCCATGAT	ATAGGGAACA	AAAATTCCTT	1620
TTCCAGCTGC	TTTAATAGCA	TTTAATTTTT	CTGTAGTGT	CTTAGGCATG	AGCTTCTCCC	1680
TTCTTTGCTG	CATCTGCTTC	CAAGCGGTCC	TTGACTTGAA	CCACATCCTT	GTCCCCACGA	1740
CCTGATAGGC	AGACAATCAT	AGACTTTTCT	GGTCCAAGTT	CTTTGGCCAA	TTTCACCGCA	1800
AAGGCGATAG	CATGGCTAGA	TTCCAAGGCT	GGGATAATCC	CTTCCACACG	AGACAAGAGT	1860
TGGAATCCTT	CCAAGGCTTC	TTCGTCTGTC	ACAGGGACAT	AGCTGGCACG	TTTAATATCG	1920
TGGTAGTGAG	AATGCTCTGG	ACCGATACCA	GGATAGTCCA	AACCTGCTGA	GATAGAGAAG	1980
GCTTCAAGAA	TTTGACCATG	GGCATCTTGG	AGCACATCCA	TGAGGGAACC	GTGAAGGACA	2040
CCTGGACGAC	CCTTGGTCAA	GGTAGCTGCG	TGGTGTCTG	TATCCACACC	AAGCCCTGCT	2100
GCTTCAGTTC	CATACATAGC	TACTGACTCA	TCTTCTACAA	AGGGATGGAA	GAGCCCGATA	2160
GCATTCGACC	CACCACCAAC	ACAGGCTACT	AGGGCATCTG	GCAGATCTCG	ACCTGTCAAG	2220
TCACGGTACT	GTTGTTTAGC	CTCTCGACCG	ATGACACTTT	GGAAGTCACG	AACGATTTCT	2280
GGAAATGGAT	GAGGCCCCAA	GGCAGAACCA	AGGATATAGT	GGGTATCGTC	GATATTAGCC	2340
ACCCATGAAC	GAAGGCTGC	ATTGACCGCA	TCCTTGAGCA	CGCGCGAACC	ATCTGTTACA	2400
GCCTCGACCT	TGGCTCCCAA	AAGCTCCATG	CGGAAGACAT	TGAGGGCTTG	GCGTTTGACA	2460
TCTTCCTCAC	CCATGTAGAT	GGTACATTC	ATGTTAAAGA	GGGCTGCAGC	AGTTGCAGTT	2520
GCCACACCGT	GCTGACCAGC	ACCCGTTTCT	GCGATAATTT	TCTTTTACC	CATGCGTTTG	2580
GCAAGCCAAA	CTTGTCTTAA	GGCATTGTTA	ATCTTGTGGG	CTCCTGTATG	GTTAAGGTCT	2640
TCCCCTTTGA	GATAAATCTT	GGCTCCGCCA	ATATGCTGGG	TCAAGTTTTT	TGCGTAATAA	2700
AGAGGAGTTT	CACGTCCCTAC	GTAAGGGCGC	AAAAGCTGGT	TTAATTCCTC	TTGGAAACTT	2760
GGGTCTGCCT	GACTTTCACG	GTAGGCCTTC	TCCAACCTCCA	AAACTGCTGT	CATCAATGTT	2820
TCTGGGACAA	AACGTCCGCC	GAATTTTCCG	TAAAATCCAT	CTTTATTTGG	TTCCCTGATAT	2880
GCCATGCTTT	ACCCCTCTCTA	TAAATCTTCT	AATCTTTTCA	TGATCTTTTT	GTCCATCTGT	2940
CTCCACTCCG	CTCGATACAT	CTACTGCATA	GGGAGTAAAG	TGTTGAATTG	CTTTTACTAC	3000
ATTATCTTCA	TTAAGGCCAC	CTGCGATAAA	GAAGGGCTGT	GCTAGTCCAG	TCGTATCCAG	3060

TTGACCCCAA	TCAAAGGGCT	GGCCACTTCC	TGCCACAGGG	GCATCAAAGA	GTAGATAATC	3120
TGCCTGAGAA	TTGGGGACAT	GCCCATTTCC	ATCTACCTGC	ACAGCCTGAA	TACTGGCACA	3180
AGGCAAATTC	TCAAATAAAT	CATCTGCCAC	CTGACCGTGA	ACTTGAACCA	AGTCCAAGCC	3240
AACTTTGTCA	ATCGCTTCCA	GCAGTTCTAC	CCGACTTGGT	GAAACAAATA	CTCCAACCTT	3300
TTTCACATCT	GCAGGAATAA	GCTTTGCCAA	CTCAGCTGCC	TCTTCTAAAG	TCACCTGTCT	3360
TTTACTAGGT	GCAAAGACAA	AACCGATATA	GTCGGCTCCT	GCTGAAACGG	CTGTTTCCAC	3420
CGCTTCTTTG	GTCGATAGTC	CACAAATTTT	AACCTTTGTC	AATCTGCAAC	TCCTTGATTC	3480
TCTGGGCCAC	ATTTTCTGCC	TGCATAAGAG	CTGTCCCTAC	CAAAATCCG	TTAAAGTATG	3540
GGGCTAGTCG	TTCCGCATCC	TGCCCTGTGA	AAATGGCAGA	TTCAGAAATG	TAATAGCGAC	3600
CTTCCTCAAA	GTAAGGGGCT	AAATCTACAC	TGGTCTGCAA	GTCGACCTCA	AAGGTAGTCA	3660
AGTTGCGGTT	GTTGACCCCG	ATAATCTCAG	CACCAAGTCT	GTGGGCTACC	TCTAGTTCAG	3720
CTAGATTGTG	AGTCTCCACT	AAGACTTCCA	GACCAAGCTC	TGTCGCGTAG	TCATACAGTT	3780
CCTTGAGGCG	TTCTTCGGAC	AAGGCTGCCA	CAATGAGCAA	GATAACTGTC	GCACCTGCAT	3840
TGCGAGCGCG	GATGATTTGC	TTTTCATCGA	TGATAAAGTC	TTTGTGAGC	GTCGGAATCT	3900
CTACCTGACT	GGAAATTTCC	CGTAGATAAT	CCAAATGCCC	TTTAAAGAAA	ACCTCATCTG	3960
TCAACACCGA	AATCATCACT	GCTCCGTTTT	CTTCATAAGT	CTGGGCCTGT	TGCACAATAT	4020
CCACATCGAG	ATTGATATCT	CCCAAAGTAG	GGCTAGCTTT	CTTGACCTCA	GCGATTACCT	4080
GCAAGCGGTC	CTGATGATTC	TTCAAAAATT	CTGCCAAGCG	ATAGGTCTGG	CGCAGAGGCT	4140
GGATTTGCTC	CAGCTTCATC	TGCTCCACCT	CACGCGCCTT	CTGCTCTAAG	ATTCTGTGCTA	4200
AAAATTCCTG	ACTCATTTTT	GGTACTCCTG	TAACAGTCTG	AGTTTTTCAA	GGGCCTTGCC	4260
TCTAGCAATC	ACTTGACGGG	CCAAGGCAAC	CCCTTCCTTG	ATGCTATCAA	TCTTACCATT	4320
AGCATAGAAA	CCAAGACCAG	CATTCAAGAC	TGTCGTTTCC	AAGAATGGAC	TTGCTTCGTT	4380
TTTCAGAACG	CTAAGCAAAA	TTTCTGCATT	TTCCTGAGCA	TTCCCACCAC	GAATATCTTC	4440
CATAGCATAG	CCTTCCATTC	CCAAATCCTC	TGGAGTAAAG	CTTGACAAGC	TGATTTCGCC	4500
ATTTTCAAGA	AGTGCAATCT	TGGTTGTTCC	GTTCAAGCCA	GCTTCATCCA	ACCCTTCTGG	4560
TCCAGCAACC	ACGATGGCAC	GTTTGGCACC	CATATTTTTC	AAAACCTGAG	CTGTACTTTC	4620
TAGGAGTTCT	GGACGACTAA	TTCCAAGAAG	CTGTGTTTCT	AAAGCCATTG	GATGAATCAG	4680
TGGACCAGTC	AAGTTCATAA	TCGTTGGAAT	TCCCAATTCC	AAACGAGCTG	GCATGATGTA	4740
TTTCATAGCT	GGGTGCATAT	TTTTAGCGAA	GAGAAAGACG	ATTCCAGTTT	TATCAAAGAC	4800

1154

CTTACCTAGT TCAGCTGGTT TGAGGTCAAG ATTGATTCCC AAGGCTTCGA GGACATCTGC	4860
GGAACCAGAT TTAGAAGATA TCGAGCGGTT ACCGTGTTTG GCCATGTGAA TACCGCCACC	4920
AGCCAAGACA AAGGCTGCAG TTGTGGAAAT ATTAAACTG AAAGACTTGT CCCACCTGT	4980
ACCACAGTTG TCCATGGCAT CATGAATCTC AGTTGGAATA TGCTGGGCAT GTCCTCTCAT	5040
GACTTGGGCA ATGGCTGTGC GTTCTTCAGG TGTTCCCCC TTCATCTTAA GAGCTAAGAG	5100
GAGAGAAGCA ATCTGCGCTT CAGTTACACG CCCAGTTACG ATACGCTCAA TGACATCCGT	5160
CATTTCCACA CCTGATAAAT TTTCAAATTT TGCTAGTTTT TCAATAATCT CTTTCATCCT	5220
AGTTTCCTCA CTTTACAACC TCCTCGATAA AATTCCGAAT AGAAGACAAG CCGTCTGGCG	5280
TTCCAATGCT CTCTGGATGG TACTGGAAGC CATAAATCGG TAGGTTTTTA TGTGAATCC	5340
CCATGATGGC TTGGTCATCA GTCGAACGAG CTGTCACTTC AAAGTCTTCT GGCATTTCT	5400
CAATCAAAAT ACTGTGATAA CGCATGACCG CACGGCCATC CTCAATACCT TGATACAAA	5460
CAGATGGCGC TTCAAAGTTG ATATTGCTCT GTTCCCCTG CATGACTTTT GGAGCCAAAC	5520
CTAGCTTACC ACCAAAGACT TCTGCAATGG CTTGGTGGCC CAAACAAATC CCAAGAATCG	5580
GCTTCTTGCC TGCAAAATCA CGAATCATGT CTTCCATCTT TCCAGCATCA ACTGGCCAAC	5640
CAGGACCAGG AGAAAAGACC AGACCATCTG CTTTTTCAGC TTCTTCATAC AGCTTGAAT	5700
CATCATTTCT CAGAACCTGA ACTTCTGCAA AATTCCCAAT GTATTGGGCC AAGTTATAGG	5760
TAAAAGAATC ATAGTTGTCA ATCAATAAAA TCATGGTCTT AGTTCTCCAA TTCTAGTCAT	5820
AGATTTTGCT TTGTTAATGG TTTCTTGTA TTCGTTTTGG GCGATAGAGT CGTAGACAAT	5880
CCCTGCCCA GCCTGCACAT AGGCTCTTG ATTTTTGAGA ATCATGGTTC GGATGGCGAT	5940
GGCCAAATCC ATATCACCCG TCGCAGACAA GTAGCCGATT GCCCCAGCGT ATACTCCCCG	6000
TTTTTCCGTT TCCAGTTCAT AGATACGTCT CATCGCTCGA ATCTTTGGTG CTCCAGAAAC	6060
GGTTCAGCA GGAAGCGTTG CTTTCAAGGC ATCCATGGCA GTGAGTTCTG GAAGCAAACG	6120
CCCCTTGACT ACGCTGGTCA AATGCATGAC GTAGCGGAAG AGCTCCACTT CCATATACTT	6180
AGTGACTTGG ACACTGGTCG TTTCAGAGAT GCGGCCAATA TCGTTACGCC CCAAGTCTAC	6240
CAACATTCGA TGTTCCTGCTG TTTCTTCTC ATCAGAGAGG AGGTCAGTCG CCAAGGCCTT	6300
GTCTTCTTCA TCCGTAGCCC CTCTTGCTCG CGTCCCCTGCA ATCGGATTGG TTGTCACGAT	6360
GCCATTTTGG ACAGAAACCA AACTTTCTGG ACTAGCTCCG ATGATTTGAT AATCCCCAAA	6420
ATCATAGAAA TAAAGGTAAT TAGAAGGATT AGTCACGCGG AGATTTCTGT AGAAGTCAAA	6480
TGGATTTCCA GTAACCTCTG CTGAAAAACG CTGGCTGAGT ACACATTGGA ACATATCTCC	6540
GTTACGAATC AAGTCACGAG CTGTTTCTAC CATTCCCTCA AACTTATGTG GAGCGATATG	6600

1155

CGGTTTGAAG	TCTAACGGAG	ATAGATCCAA	ATCTTCAAAT	TCATTTGGAG	CAGGAATGCG	6660
TAATTCCTCA	AGCACTTGGT	TCAAGGATTT	TTCCAAGGCC	TCTTGACTGC	GCTCACTATA	6720
AAGTGCATCC	TCTATGACAT	GTATCTTCTC	CTTCTTGTGG	TCAAAGACCA	TATAGCTCTC	6780
ATAGACAAAG	AAATGCATGT	CTGGCGTCCC	AATGTATCC	TCAGGGATTT	GACCAATTTT	6840
TTCATAAAGC	GAAATCATAT	CGTAACCCAC	AAAACCAATG	GCTCCACCAC	CAAAAGGTAG	6900
CTCTGAGTGG	TGCTGACTCT	TATGAATCAC	TTCATAAAGG	AAATCCAAGG	GATCCCGATC	6960
AATCACTTGA	CCATTTTGAT	AGAGAACCCC	ATTTTCAAAC	TTAATCTCAA	AAACTGGATT	7020
ATAGGCTAGG	ATAGAAAAAC	GAGCTGTTC	CTTGTCTCTC	GGAATACTCT	CTAAAATAAC	7080
CTTATGTTGC	CCCTTTAAGC	GCATATAAGC	CAAGATTGGT	GATAAGACAT	CTCCATGAAT	7140
GATTTCGTCC	ATTGTAATTT	CCCTTTCAGT	TCTACTTCTA	GTCCGTGGTG	ACTGTATGAA	7200
AAATCCCCAC	GCAAAAATAAC	TTGCGTGAGG	ACGAAATTCG	CGGTGCCACC	TCAATTATAG	7260
GATTTCTCCT	ATCTCTCATT	CCTGTCTCAG	ATATCTCCTG	TAACAGGCTG	TGCGATAAAG	7320
GGCACTCCCT	TGAGAATGAT	GTTTTCTTCT	CTCGTTTCAG	ATGAACCCAA	CTTTACAGCT	7380
TTCTCTGCTT	GTTTTCAGCA	ACCACAAGCT	CTCTGTGAGA	GAAAGAACTG	TAATTTTTTCC	7440
ATCTATTATT	TTTTAGCTTC	TAGTAGTCTG	CAATCGCAGC	TAGGTCCTTG	CCTCCACGAC	7500
CAGAGACATT	GATGAAGAGA	TGTTCACTCT	GGTACACCTT	TATACTCTTC	GAAAATCTCT	7560
TCAAACCGCG	TCAACGTTCG	CTTGCCGTAG	GTATGGTTAC	TGACTTCGTC	AGTTCTATCT	7620
GCAACCTCAA	AACAGTGTTC	TGAGCTGACT	TCGTCACTTC	TATCCACAAC	CTCAAAACAG	7680
TGTTTTGAGC	TGACTTCGTC	AGTTCATCC	ACAACCTCAA	AACAGTGTTC	TGAGCTGACT	7740
TCGTCACTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGC	AGCCTGCGGC	TAGTTTCCTA	7800
GTTTGCTCTT	TGATTTTCAT	TGAGTATTAC	TAGCTTTTTT	CGTATTAGTC	CAGCCTTTTT	7860
GTTTGCTTTT	AGTAGTAGGC	ATGGAGCTGT	AGATAGAACT	CAAGTTCATC	AAAGCGACTT	7920
AAGGCCCTAA	TAAAAGATAA	ACCAAACGAC	GGATAGAAAA	AAGCCCACAC	ACAGAATATA	7980
CTTCCGTGTG	AGGGCGTTGG	TAACGCGGTG	CCACCTCAAT	TATAAAGGGA	CTATCCCTTT	8040
ACATCTCTGC	CTTGTTTAAAC	AACAAGCTGC	ACTGTAAGGT	GTGCGCACCG	AATTTTCATT	8100
GTTTCAAATT	CATTTTCAAA	ATCAGCCCAC	TTTCACTACT	TCCAACCACC	TATTCACAAT	8160
CACCACAGGC	TCCCTGAAGA	TCAAAAATAG	TTACTTTTCT	GATTTGTTGA	ACTTATTTTA	8220
ATACTTGTGT	TTTTCTTGT	CAAGACTTTT	TTACGATTTT	TTTGAAAATA	TCATTCGAAT	8280
ATGACCATGT	CTTCTTAGA	TCGAACATGA	ACATGTCCCA	CTTCTTAGAA	ATTGGATCCA	8340

1156

ACTCAATAGA	AACTGAATGG	AGGCTAAACA	GAACTTATTT	TAGAACACTC	CATCTTTTCC	8400
ACTAGGATTT	TCAAGAATTA	AACAATACTA	GAAACTCTGT	CTCCTAACAA	ATTTAGGAGA	8460
AACTTCAACA	GATGTGACAC	TTTCCCCTTT	AATAATGCT	AAAACACCTT	CTATCATTTT	8520
TTTAGCCAAT	TTAACATAAT	TGGGAGCAAT	TGTAGACAAA	GCTGGAGTAT	AATACTGAGA	8580
AATAGGAATA	TTATCAAATC	CAATGATAGA	AATATCATCT	GGAATAAGAA	TTCTTTTCTC	8640
ATAGCACGCA	CGAATCAAGC	CCTGAACCTT	TTTCATCTCCT	GAAACAAAAA	TAATGTCCGG	8700
ATAATTTTGG	GTAGTCAAGT	GCTGCATTGC	ATAAGAATAA	ACTGAATCAA	TTGTAGATAA	8760
GCCATAAATG	ACTTTTAAAT	CCATAAAGTA	ATTTTTATCA	TTCAGAAAAG	AACGCACACC	8820
TCTTTCACGA	TCCTTATTA	CATGGGATTC	TCCTCCCATA	AGCAACCACA	TATTTTAA	8880
TTTTTCTTCA	GTTACAGCTT	TCATCATATC	ATAAGTAGCT	TGAAAATTAT	TATTAGATAC	8940
ATAGACTACT	CCAGACGTTT	GAGATTCACC	GAAAACAAGA	AAAGGCATAT	GGTTCCTTCTT	9000
TAAATACTGA	ATTCTGATAT	CATCTACACT	TTCATAAAAA	ACAATAACAC	CATCTACTAG	9060
GCTACCTGTG	CTTGATATAA	TTGAATTACT	AATTGTATCC	TCCTCTCCAA	AGTACTCAAC	9120
TATAGCATT	ACACCAAAT	CTTTACACGT	CCGTAACACT	TTATCTAACA	GCGTATGAAA	9180
CCAAATTA	GGAAAAGAGT	CGATTTTTTT	TACAGAAATC	AATATATTTA	TAGCTTCTTT	9240
TTTAGTTAAA	TTTTTTGCAT	ACGCATTTGG	AATATACGAC	AATTCCTCTA	TAACTTTTTG	9300
AATCGCTTGA	TAAGTTTCTT	CTTTAACATT	TACTCCACCA	TTAATAACTC	GTGAAACTGT	9360
TTTTGGAGAA	AAACCTGATA	AACGTGCAAT	ATCATAAATA	GTTACCTTTT	TCCCATTAT	9420
ATTTTTCATT	TCAGTCCCTC	ATTACGAACA	TTCTAATATT	ACTATACAAT	ATTTAATTTT	9480
TTTTAAACAAG	AGAATTTAGT	AAATTATTTA	AGATCCACAA	ATTCACAAAA	TTAATTTTAC	9540
AAATATTTCTT	CCCCTTCAAA	AAAGTTTAAA	TTGCATTTCA	CACCTTTATT	TTTAAGAATG	9600
TTTCCAACCTT	CACGACAAAT	AAATTCATAT	GAGAAAAAAC	TGCCATAAAA	TTGTAGATTA	9660
ACTTTTTCAG	TAAAATGTGT	AGGATTTATA	AAAACATATA	ATAGCCTGTC	AATGTAACAT	9720
TTTAACATAG	AGTTAATTTT	TTCTTTAAAG	ATAACATTTG	TTATCAACTC	ATCAGGAGGT	9780
AAATGAAAGG	CAAACACCAT	TTCACAAATA	TCATAAAAAG	AAATAAATTT	GTATACTTGT	9840
ATCAAACAAT	TATTATCAAA	ATATTCTATT	TTACCTAAAT	CAAAATTGAT	TTTATAATCT	9900
TTCATAAAAA	CCTCTGAGCA	AAAATCTACT	CAAAAATTAG	ATGATTAAAA	CATCTAAAAA	9960
GCAAAAAGGAC	AAAAACATCT	GTCCCTTTGT	TTACTAAAT	TCAGCTAATT	TCTTCGACAT	10020
AAATAACACC	TACAATATTA	GCAATTTCTT	CCATCAGTCG	AAGATGTTCA	AATCTACCTG	10080
ATAATTCAG	AGTAATAAAT	GACGCTATTT	TTTTGTCCGG	AACATCAAAG	TATTCAAATC	10140

1157

TGTCAGAATT AACATCTCCA AACGCTGTTC TTGAATCGGT CATTCTGATA CCATTTTCTG 10200
 CACAATAAAC CAATACACGA TTATAGGCTT CTGTAGATTT AACCACTATA TACAATTCAA 10260
 TCATTTTAGA ACGATTTTGC AGATATTTTT TTAGTGTTG GAACATGGAT ATCACACCCC 10320
 AAACAGAAAT GGCTACTAAA AGAGCTCCCT CATAAGG 10357

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

CGGGACATTC TCAATCTTCT GTCTTTTGT TTTCTTCTT TCTATGATA CAATGGAAAA 60
 AATAAATTC AAGGAGTTT TTTTATGACT TATCCAAATC TCTTGGACCG CTTCTTAACC 120
 TAGTTAAGG TCAACACGCG CTCTGATGAA CACTCTACTA CTACTCCAAG TACACAGAGT 180
 CAGGTTGACT TCGCAACAAA TGTCCATAAT CCTGAAATGA AACGTGTTGG ACTGCAAAAT 240
 GTTFACTATC TACCGAATGG TTTTGTCTAT GGAACCTTGC CAGCCAACGA TCCGTCTTTA 300
 ACACGTAAGA TTGGTTTTAT ATCGCACATG GATACTGCTG ATTTTAATGC TGAAGGAGTC 360
 AATCCACAGG TAATTGAAAA CTACGATGGT GGTGTGATTG AACTAGGGAA TTCTGGTTTC 420
 AAATCGATC CAGCTGACTT CAAGAGTCTT GAAAAATATC CAGGACAAAC GTCATCACA 480
 ACAGATGGAA CAACCTTGCT AGGTGCTGAT GACAAGTCAG GAATGCTGA AATTATGACA 540
 GCCATTGAAT ATCTAACTGC TCATCCTGAA ATTAAGCACT GTGAGATTCG TGTGGTTTTT 600
 GGTCCAGATG AAGAAATCGG TGTGGTGCC AATAAATTTG ATGCAGAAGA TTTTGATGTG 660
 GATTTTGCCT ACACTGTGTA TGGTGGTCCA CTAGGTGAAC TTCAGTACGA GACTTTCTCA 720
 GCCGCTGGTG CTGAATTGCA TTTCCAAGGT CGTAATGTCC ACCCTGGTAC TGCCAAAGGG 780
 CAGATGGTCA ATGCCCTCA GCTAGCAATT GATTTTCATA ATCAACTTCC AGAAAATGAC 840
 CGACCTGAGT TAACTGAAGG TTACCAAGGT TTTTACCATC TAATGGATGT GACAGGTAGT 900
 GTTGAGGAGG CGCGTGCAAG CTACATCATT CGTGATTTTG AAAAAGATGC CTTTGAAGCG 960
 CGTAAAGCAT CCATGCAATC TATCGCTGAT AAGATGAATG AAGAACTTGG GAGCGACCGT 1020
 GTCACTCTCA ACTTGACAGA CCAGTACTAC AATATGAAAG AAGTCATTGA AAAAGATATG 1080
 ACTCCAATTA CCATGCTAA AGCCGTTATG GAAGATCTAG GTATCACGCC TATTATCGAA 1140

1158

CCAAATCCGGG	GTGGAACAGA	CGGCTCTAAG	ATTTCCCTTTA	TGGGAATCCC	AACTCCGAAT	1200
ATCTTTGCAG	GTGGCGAAAA	TATGCACGGA	CGTTTGAAT	ACGTAGCCT	TCAGACTATG	1260
GAACGTGCAG	TTGATACCAT	CATTGGCATC	GTAGCTTATA	AAGGCTAAAA	AGACGAGGTA	1320
GCTCAGCTAC	TTCGCCTTTC	TTTTTATTCT	ACTGGTTTTT	CTTGATTTC	AGTAGTTGTA	1380
GAAGATTCTG	TTGTTTCATT	TTCTGAAGTT	GATTCAGCAG	GTTTAGAATC	TCTTGTATTG	1440
CTTGGTTTTG	TTTCGTCGCT	AGCAGTTTCA	ATGTTAGATT	CTGCAGTTGC	GTTTGGTTGG	1500
TTCTCAGCAC	TGGTGTATC	ACCATTGCT	TCAGCATTC	TTGCTGGACT	TGTTTCTTCA	1560
CTTGCCTAG	CTTTGACTG	GATTTGATGA	TTCAAACTA	GAATAGCTTT	TGTCGATTCA	1620
AGTAAAGCTG	TTTTGTCTTT	ACTCTTAGCA	GAAAGTTGAT	CTAATAATGC	ATCCACCTTA	1680
TCAAAGTCCG	CATCAGATCC	ATTATTACTT	TCTAAATAAG	AGTGAAGCGA	CATGAGAATA	1740
TCGTAGAGTT	TTTGATAGAG	TACAAGTGTC	TGAGGATCTT	GCTCAGCATT	TTCCTTTTCT	1800
TGTTGAAGGG	CGTAGCGAT	ACGAGTCAAG	ACATCTTTTA	CCTGACTGTT	TACTTCATCC	1860
AAGTCTGCAT	CAGCCTTGTT	TGTGGCAGCT	TTTAGATTTT	CTACTTCTTC	TGCCAAGGAT	1920
TGCTGATTC	CTTCTTCATG	GATTTGTTCC	AAGAGTTGAT	TTGCCTTGCT	CAAAAGACTT	1980
TCTACTTCTT	CCTTGCTATC	TGTCGCAGAT	TATTGGTTGC	TATCTACCAT	GTACTCCTAA	2040
AACAGGAGAG	TTATAATCCA	AGATTACAAG	GCCTTACAGA	AATAAGAAAT	CCAGATAAGA	2100
CAATGTTTCG	CCAAGACGCT	ATTCGCTTCG	CACAGCAGCA	CGGATTCAAT	ATGCTTTAAT	2160
TTTAAAGFTT	AGGTGTCAAG	ACCTCTTTTT	AGTGTGCCCA	AAATTTAGAG	AAGTAATCAA	2220
TCAAATAACT	TTTATTTTTT	TCAAATTTTC	AGTAAACTGA	CCTAAAGCTA	ACTCAATCTG	2280
TCTTTGTAGA	TGCTTCTGCT	ATCAGCTAGA	AGTTGATCTA	CTTTTGCCAA	GACTGCCTTC	2340
TCATCAAAAAG	TTCCAGGTTG	ATAGTTGGAT	TGCAGGGATG	GAATCTTGTT	TTTCAAAGCC	2400
GCTTCATATC	CCTTAGTTTG	AACCTTGATG	TAGTGATTGT	GGTCGCCATG	AGGAATCACA	2460
AAACCTTCTG	AATCTTCACT	TATAATTCTGA	TTGGCATCAA	AACCATGACC	ATCTTCTTCC	2520
TCATGATGGA	CATGTAGTGA	CGGATTACTT	AATACAGAAC	TAGAAGAACT	TCCTACCTCT	2580
TCCGTGTTAG	AGTGTGATGG	GGGATTGTTA	AGAGATGACT	TAGGAATATA	GTGATAGTGA	2640
TCCCCATGTC	TTACTATATA	AGCATCACCT	GTATCTCTGA	CAATATCATT	AGGGTTAAAG	2700
ACATATGTGG	CTGCTAATTC	ACCTGCCGAC	AAGTCACTCT	CAGGAATGAA	ATGATAGTGA	2760
CCACCATGTG	GTAATAACTG	AGATTGAAAT	AGAATATGAG	CAAATTGATA	AGGGGATTTT	2820
AAAGTAATTT	CTAACAATGA	TTTAGAAACT	ATGATGTGCT	ATTCTAAAT	CAACTCACTA	2880
TATATAACCA	TCATCGGTAG	TATAACGTCC	CTGTAATTTT	GCTACAGATA	CTTCTGCACT	2940

1159

AGCTCCTTTA	TCGTCTTTAC	CATGTTCTTG	TTTTTGCGA	TTGATTTTCAT	CTTTTGTTCG	3000
TACATTTTCT	GCATGAGCTT	GATCTTTAAG	GTAACATAA	TACTTTCCAT	CTACCTTAAT	3060
AATATATCCT	CCCTAACCT	AACTGACGAT	ATCTTGATCT	TTCGGCTGAT	AGTTGGGGGC	3120
TTTCATTAAT	AGCTCTTAC	TAAAGAGCGC	ATCAAAAGGA	ACTTTACCAT	TATAGTAGTG	3180
ATAATGATCG	CCATGAGAAG	TTACATAACC	TTGATCTGTA	ATCTTAATAA	CAATTTGTTT	3240
TGCTTGAATT	CCTTCTTTT	GACTAACCTA	GTCTGGAGTC	AAATTTTCAG	TCTTCTTAGT	3300
GTCTTTATTA	CTGTTTACAT	ATGAAACACG	ATTTTTATCT	GTATTGGCCT	GTTAGCTATG	3360
TTGGTTTCTA	GCATAAACAC	ACAGACTTAA	GGAAAGGATA	ACAACAGATC	CAGCTGCTAT	3420
ATATTTCTTT	TTAAATTTCA	TAATTACCTC	ATTTCTATAA	TTATTTATAT	GATGTCTTCA	3480
TTATTAATG	ATTAAATAA	TTAATTAACC	AATTAATTA	CTAGTAAATA	TTCCACCTCT	3540
TTTTAAGTTG	TATGTCAAGA	AATTTTATAT	ATTAATAATA	AAATGAAATT	CTCCCAAAGT	3600
CAGAGTTTTA	TTTCTAACTT	TTGAGAGAAC	TTTCTTTTGG	ATTCAGACTT	TTTCTACTGC	3660
TATTCCTTAC	GCTATGAGAT	CAGATAAATT	CTTTTTTATC	ACTTCTCCAC	TTGGCAATCT	3720
TAATTCATC	GTTCCATCCA	TATTGAATAT	AACACTATCT	AAGCCTAATC	CGTAACTAGC	3780
TGTAAATTTT	TCTAATTTT	CTGTACAGG	ATCTACTGCT	GGAGCTTCCT	CTAATGCTGG	3840
ATCTAACATA	GGGTCACTCC	CCACATTTCC	TTCTGGATTC	AACATTCCAT	TATCCGTGTA	3900
GTTTTCTGGT	TTTACAGGTT	TTTCGTTTGG	TGCCTCTGGT	AAAGAATCTG	CTGGTTTATT	3960
TTCTGTGGT	TGGTCTCAA	CTGTCCAGT	AGATACTTTT	CCATTTTCAG	ATGGTTTATT	4020
TTCAACATTT	CCTTGAGGTG	CTTCTCCTGT	AAAATCTGCC	ATATTCTTTT	TAATGACTTC	4080
TCCCGATGGT	AAATATAAAT	CAATTGTTC	GTCCATATTA	AACAAGACAT	TTTCTAGCTT	4140
CATCCATAA	CTTTCAGCAA	ATTTTGCTAC	TTTTTCTTGT	ACAGGATCCA	CTGTAGGAAC	4200
TTCTTCTAAC	GTTGAATTAC	TAGTACTATT	CCCAGTTTCA	GAAAGTTTTT	CTTTTCTTAC	4260
CTTCTCACTA	GTCTTTGGTT	CTTCTACCTT	TTTCACTAAGT	TTTAAGTTTT	CTTGTGCTTT	4320
ATTCCTTTTA	AATTGTGGTA	GAATACTTGG	TTTATCAGTT	TGATTTTCTT	TTTCCAAGAT	4380
AGGTACTTCC	ACAATATAAG	TCGATTGATT	GTCCAAATAA	GCATTTGCCA	TGAAGGTAC	4440
AGGAATTTTA	TTTCCGGCCG	TTCTGGTTGT	TCCTTGGTTT	AATTTCCGAA	TCGGTAATTT	4500
GATTTACCA	ACTTTATAGT	TATTTTCTAA	ATAAGCATTT	CCATGAAATT	CATCAAACAC	4560
TCTGACTAAA	GCATCAGTTC	CTTTAGGCAC	TGCAAATGA	GGGTTCACTC	TTAAATAAGT	4620
ATCCCCTGCA	TGGAAAGGAT	AGAAAATCGT	TTGACTGGCC	ATTTTGTAAAG	CTAAAGAGGT	4680

1160

TGGAAGTGTGTA	AATGTACCAT	CATAACTTAC	TTCTGGATAA	TCTTTTGAAG	CGATAGTATA	4740
CTTAAATGTT	TGTCCTGGTA	AATAAGGTTG	ATCTAATTCA	AAGTTTGCAA	TATTCCCTAC	4800
TCCTTCTCCA	AATACTTTAC	CAGATACTTT	CTCCAATACT	TTTCCATCTG	GTGTTATTAA	4860
TTTTACTAGC	ATATTGATAC	CTAATTTTTT	CTCCAATTCA	GGCGGAAAAC	TAAAAGAAAC	4920
GCGTTTTTGA	CCATTGGCTA	GAGTAAAGTT	TTGATTATTA	AACGTACTAT	TTTTTAACAA	4980
ATTAACAACA	TTCGTTAATT	CTTCTCCAGT	ATAAACTTTA	TTCCCTTCTT	TTTTAGCAAC	5040
TCCTTCTTCG	GGTTTAAACA	GTTTCATAGT	ACTGTGAGAA	TGACCAATTC	CAACCGGTTT	5100
ATGTTTCATCA	ATCGGATCTG	CATGATGGTG	ATCTCCATGC	GGATAAATAA	TCGCATTTTT	5160
TTCTTTTATTC	ACGACAATAC	TTTCACGTTT	GACACCATAT	TGTTTCATAA	TGCCAGCAAT	5220
TTTTTCTTCG	ATTTTTTTAT	CTAAATCTTT	CATTTCTTTG	GCATTACTTG	GATAATCCTG	5280
TTCATGAGAT	GACAAAAGAT	CTAATCCATT	ATGACTAGTT	TTAACTTCCT	CTAAATGTTT	5340
TTGCGCAAsC	TAATTTGCTC	TTCTGTCAAG	TCCTTCTTGA	AGAAATAATG	ATTGTGGTCT	5400
CCGTGACTCA	TGACAAAACC	TGATTTCATCT	TCAGCGATAA	TACGATTAGC	ATCAAATCCG	5460
TATCCATCTT	CTTCATGTTT	CTCATGTGAA	GTTCCTGGAT	TGATTGGAAG	AGATGGAGAA	5520
GGTGTGCTA	GACTATGTGT	TGGAAGAGTC	GGTTGCCCAA	TTTGATTTGA	TTTTGGAATG	5580
TAATGGAAAT	GATCACCATG	TCTTACAATA	TAAGCTGTAG	CCGTTTCTTC	AACGATATCT	5640
TTTGATTAA	AAATATAACC	ATCAGATGCT	GAAGAGAGCT	CCTTACTTGT	CGTTAAAGAA	5700
GAAGGATTGC	TTGAAAGACT	GCCTAGACTA	GACACTACTT	CATTAGGTTT	TGCATTTGTA	5760
GAAACTGTAG	AACCAGTTCC	ACTGATAGGC	ACCATTCTGG	CAATCTTTTC	TTCTAAGGCA	5820
GAAAGCTTGC	TGTAAGGAAT	AAAGTGGTAA	TGGTCGCCAT	GCGGAATCGC	AACTCCATTT	5880
GGTGTACGAC	TGATAATCTT	AGCAGGGTCA	AAGACCAGGC	CATCTGATTC	ACTGTAACGT	5940
TGGGCGCTAG	GTGAATCATA	GAGTTCCTTC	AAAAGACTCT	GGAGATTTTC	AGATTTATTT	6000
GCTGGCTTGC	TAGTTGATCC	TTTTGCTACA	GATTGCGTGT	TATTGTCACT	AGCTGTTGAA	6060
GAATAGCTTA	ACTGACTCGG	TTGCATATTT	TTTCCAGCCA	GATGTGCTTT	AGCTGCTGCT	6120
AATTCACTAG	CAGATAAATC	GCTTTTGGGA	ATGTAGTGAT	AGTGACCTCC	ATGAGGAACG	6180
ATATAAGCAT	TACCCGTATC	TTCGATAATA	TCAGCTGGAT	TAAAGACATA	ACCATCATTT	6240
GTCGTATATC	GTCCCTGAGA	CCTTGCTACA	GCAACATTAG	AGTTAACCTT	CTCATTATCT	6300
TTGACATGTT	CTTGTTTTTG	ACGATTGATT	TCATCTTTAG	TTCGAACATT	ATCAGCATGA	6360
GCTGCATCTT	TCAGGTAGAC	ATAATATTTT	CCATCGACCT	TGATGATATA	ACCACCCTTG	6420
ACTTCATTGA	CAATATCAGC	GTCTTTAAGT	TGATAGTTTG	GATCCTTCAT	CAAGAGTTCT	6480

1161

TCACTAAAGA GGGCATCATA AGGAACTTTC CCATTATAGT AATGATAGTG GTCACCGTGT 6540
 GACGTTACAT AGCCCTGATC TGTAATTTTG ATTACAATTT GCTCAGCCTG AATTCCTTCT 6600
 TTCTGGCTAA CCTGGTCTGG TGTCAAGTTT TCACTTTTCT GACTTGACTG GCTGCCATCC 6660
 ACATAAGAGA CACGATTATT GTCCTTATTT TCCTGCGAAC GATGCTGGTT TAGTGCATAG 6720
 GCACATAGAC TCAAGGATAC GATAACAGCT GATCCAGCTG CTATATATTT TTTACTAAAT 6780
 TTCATAAATC CCTCATTTCA ATAAATGATG AAGTTTTTTC TCAACTTCTT TTACTTTATT 6840
 AAATAGTTTT CTAAACCCGG GGGTACC 6867

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CGTTCTAAAA ATGCAGTACG TTTGATTGAG AAATCAGTTA AAGGTATGCT TCCACACAAT 60
 ACACTTGGAC GCGCTCAAGG TATGAAGTTG AAAGTATTTG TTGGAGCTGA GCACACTCAC 120
 GCTGCACAAC AACCGAAGT TCTTGACATT TCAGGACTTA TCTAAGGAAA GGAACAATAA 180
 AGTATGTCAC AAGCACAATA TGCAGGTA CTGGAGCTGA AAAACGCTGT TGCACGCGTT 240
 CGCCTTGTTT CAGGAAGTGG TAAAATCACT GTTAACAAAA AAGATGTTGA AGAGTACATC 300
 CCACACGCTG ACCTTCGTCT TGTCAATCAAC CAACCATTCG CAGTTACTTC AACTGTAGGT 360
 TCATACGACG TTTTCGTTAA CGTTATAGGT GGTGGATACG CTGGTCAATC AGGAGCTATC 420
 CGTCACGGTA TCGCTCGTGC CTTTCTTCAA GTAGACCCAG ACTTCCGCGA TTCATTGAAA 480
 CGCGCAGGAC TTCTTACACG TGAATCACGT AAAGTTGAAC GTAAGAAACC AGGTCTTAAG 540
 AAAGCTCGTA AAGCATCACA ATTTAGTAAA CGTTAATTCG AAAGAATTAC TATACTTATA 600
 CAGAGCACCT TTCGGGGTGT TCTTTTTTTA TACTTTCTTA CTAAATTGGT GCAATTGACA 660
 CAGTTGTTGC GACTTTAGTC GCTTACAAAT GTGGCTGCAA CCTGACATGG TCAGTTGCCT 720
 CAAAACGTTA ATCAATACGA TTATATCAAC GTTTCAAAGC ACTCAAGGGT TTACCCTATG 780
 GGTGCTTTTT TCTATACTTT CTAAAAAAGT TTACCCTAAA ATTTGCCCTA AAATTACCCT 840
 ACTTATTTTT AAGATGTTGG TAGGCAACTT GTCCAGCAGA TAATGGAAC ATGTTTGAAG 900
 TATTAACATA AGTCTTAGTT GTAACGGTAT CGTATGAGT TAATGCTTCA GAAATGGCTT 960

1162

CTAAGCTCAT TCCTGCTTTT TTAGCAAGTG TCGCTCCTG

999

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATATTATCA CTGTTCTTGA AGGCAGAACA CAAGCTGTCA TCCGAAATCA CTTTCTTCGC	60
TACGATAGAG CCGTTCGTTG TCAAGTGAAA ATCATTACGA TGGATATGTT TAGTCCTTAC	120
TATGACTTGG CTAACAGCT TTTTCCGTGT GCTAAAATCG TTCTAGATCG TTTCCATATT	180
ATCCAACATC TCAGCCGTGC CATGAGTCGT TTTTCGTGTT AAATTATGAA TCAGTTTGAA	240
CGAAAATCTC ATGAATACAA GGCTATCAAG CGTFACTGGA AACTCATCCA ACAGGATAGT	300
CGTAACTCA GCGATAACG TTTTATTCGC CCTACTTTTC GCATGCACTT AACAAATAAA	360
GAAATTCCTG ACAAGATTTT AAGCTATCA GAAGACTTGA AACACCACTA TCAGATCTAT	420
CAACTCTTAC TTTTTCCTT TCAGAACAAA GACCCTGAGA AATTTTTCGG ACTCATTGAG	480
GACAATCTGA AGCAGGTTCA TCCTCTTTTT CAGACTGTCT TTA AACCTT TCTAAAGAAC	540
AAAGAGAAAA TCGTCAACGC CCTTCAACTA CCCTATTCAA ACGCCAAAT GGAAGCGACC	600
AATAATCTCA TCAAACCTAT CAAACGCAAT GCCTTTGGTT TTCGAACTT TGAAAACCTC	660
AAAAAACGGA TTTTATTCGC TCTGAACATC AAAAAAGAAA GGACGAAAT TGTCCTTTCT	720
CAAGCTTAGC TTTTCTTCAA CCCACTACAG TTGACAAAGA GCCTATTTTC GCTGATTCTC	780
CACTACATTT GACTGGATTC TAATTTTTTA GAGAAATACA AAAGAGCTAG CTTTAGCTAG	840
CTCTTTTCCT ATGCGGAGAG AGGGACTTGA ACCCTCACGA CCTAAAGCGG TCACAGGATC	900
CTTAGTCCTG CGCGTCTGCC AATTCCGCCA TCCC CGCTC GATTACTTTA CTAGTATATC	960
AACTTTTGGG ATGCTTGTC ACACTTTTTT TCAAATTTTT TCATTTTCAC CAACCAGGTT	1020
ACTCAAAAAG TTCATTTAGA TTTTCATCTA CTA ACTTAGC TCCGAGTGTA TTTTGTAAAT	1080
GACCTAGGGC AAATTGATGA TTTTCAGGCC AGATGGAAGC AACAGCTGGT TTAACAATCT	1140
CGATGTCATA TCCTAGATTA TAGGCATCTA TAGCTGTATG TAGGACACAG ATATCCGTC	1200
AGACACCTGT TAAGATAACG GTAGACACTC TACGCTCTCT CAAACGAATA TCTAGGTCAG	1260
TCCCTGAAAA AGCTGAGTAA TGGCGTTTAT CCATCCAAAA GACACGACTG TCTGAACCAT	1320
GCTCTTGATA AAAGATCCCC AAATCTCCAT ATAAATCCG TCCACTCGTC CCAATCAGAT	1380

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TATGAGGAGG AAATAACTTA CTTTCCGGAT GGAAACAATC GTTTTCTTCA TGAGCATCAA 1440
 TAGTAAAGAA GATATAATCT CCTCGTTCAA AAGCTAATCG AGTTACCTTG CTGATGGCAT 1500
 CCGAAATCGC CTGAGCTGGA GCACCTGCTG TTAGTTTCCC ACTATCAGCA ACAAATCTTT 1560
 CTGTATAATC AATCGAAATT AAAGCCTTTG TCATTAGTAA TCTCTTTTCT TCACTTCTTC 1620
 AAAAATATCT GAAATCAAGA CCTTAAGATA GGTTCCTTC ATTCCAAGTG AGCGACTTTC 1680
 AATAATCCCC GCAGACTCAA GTTACGAAG AGCATTGACA ATCACAGAGC GAGTGATTCC 1740
 GATACGATCT GCAATCACTG ACGCAGTCAA CTTCCCTTCA TTTCCATTTA ATTCCCCTAA 1800
 AATTGCTGAA ACAGCACGGA GTTCGGAGTA AGAAAGGTA TTGACCGCCA TGGTGACAGC 1860
 AGTACGACGA CGAATATTTT TCTCATCTTC TTCACGTTGG AAGTTAAGAA GCTGAATCCC 1920
 AACAACGGTA CTGGCAATCT CAACAAGAAC CAAGTCTCA TCTTCGAATT TTTTATCATT 1980
 ACGCCAAATA ATCAAAGAAC CAAGGCGAAT CCCCGATACA TGAATCGGTG CAATAGTCGT 2040
 CAAGCCATCT GGAATCAT CTCTACTCTC AATAGGGAAA ATACTCATAT CATGCTCAAC 2100
 AGGCAAGTTT GCTTCTGTTT CGTAAATCAT ATTAGCCCCT TGAACGTAGT CATCTGGGAA 2160
 AATCTTAGTT TGGAAGAATT GCTtACGCGA TCTGTATTG TTTTATAACG CATAAAATAG 2220
 CCAAGCAGAC GTCCTTACT ATTGATAATG CAGGCATTGC AATGAATAAT ATCCGCTAAC 2280
 TGACGCGTAA TAGCGTTGTA AGGGAGCTCA TCTCG 2315

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CGATTTCTTC CATTTCTTCA AATAAGAATA CTTTCATCTGA CATATGTGTT ACCTTCTTCA 60
 TCAAAAATTA TTTTGTAATC GATTACATG CAGATCGTAA CATAAAGAAA AACAGATGTC 120
 AAATATTTAAA CGTAAAAACA TGCTCACTAA AGAACTATAA GAGAAAAGGT AAACCTAGCG 180
 ACGCGATGAA CGCTGGGTCG TTTGGTTTCG ATTGCTCTCT TCCTCTTGTT TTTTCTGTTC 240
 TTCTTCTTGT TTTTCTCAG CTCCTTGGC CTCTTGTGTTG GCTTTTTCCT CAGCTTCCAT 300
 AATTAATTTA TCCGCCACAG TGTAGCTGTA GATTCCAGCT TCCATGTGCA CCACACTCGG 360
 TTCTGACAAT TGAGGCTTAA TCTTACTGTA ATATGGCAGT TTCTTACTCA TTTCAGATAG 420

1164

AGGAACCAAG	ACTTCGTCCG	AATCATTCAT	GGTCAATCGA	ATTAAATCGG	ATGTCACCTT	480
GCTTGGGGCT	AATTCACCT	TTTGGATAGC	CGCCTTGAGT	TCTGGGCTAA	TTTGAGCAAG	540
TTCTGAGACA	AAAACCTTGA	TTTGTTCACT	ATCATTAAAG	AGAAGTATA	AATAAGTTTC	600
TGGTAAACTG	TTCAGACTCA	CAGAACTAGT	CTCAAGCTGA	CCACTGGAAA	GAATAGGATA	660
ATGATTTTCA	CCAGAAATAT	AGTAGGCCAC	AATATCATAT	TCCTTGACCT	TAATAGTGAA	720
CTTAGTTGGA	AATTGATAGA	CAAGTTGAGC	TGATTC AAC	CAATAGTTAG	ACTTAATCTG	780
CTTTTCATAT	TTTGCCTTGT	CTAGCAGAAG	GTTAATCGTA	TAATCCGAAT	CCTGAATGCC	840
TGAAGCCTGT	CGAATATCAT	CAGCTGTAGT	TTGCACCGTT	CCCTCAACAC	GAATATCTTT	900
CATGGTCGCA	TAAGGACTGA	GCAAGTAGGC	AGAGACAAAC	AATAGAAGCA	GACTTGAAAA	960
TAAAATCGTG	AAGGCTCGCA	AGATATGGAT	ACCAGGAATC	TTTGCCTTGG	CTGGTTTTTC	1020
CTTTGTAGCC	TTTTTAGCAA	GCTTTTTATC	CTGTTCTCCT	TTCTCTTTAG	ACTCTGGTTC	1080
TTCTTTCTCT	TCTTTCTCTT	TGTCAGCCTC	TGAGGATGCT	ACTTTTTCTT	CAGACTCTTC	1140
CTTAGCTGAT	TCTGAATCTT	CCTGGTCTGT	TTCACTCTCC	TGGTCTGT	TATCCTCTGA	1200
CTTCTCAGAT	TCTTCTCCCA	TTTCAGCTTG	TCTTCTCTTT	TCCTTCTCCT	CAGCTAGAGC	1260
CGCCTCTTCT	TCAGCCTTCT	TTTTTAGATA	TTCTTGGT	CGTTTCTGCC	ATTCTGATAA	1320
CTCTTTCAAT	TCTTCGAGGG	TTTCTTTGTC	CTCATTTTTC	TTATCTTTTG	ACATTTACTT	1380
TCCTTATGAT	AAATCTTTTT	TCAACAATTG	ATAAAAATCT	GCTAGAGATT	TCAATTCCTT	1440
AGAAGCTTTC	ATCTTAGCTT	GGTAATCTTC	CTTGTGACTT	AGTAAGTGAG	AAAGCTTCTC	1500
TTCCAAACTA	TCCAAGGTCA	AATCGCTTTC	TTGAAGGTCT	TCTGCATAGC	CTTTCTTAAC	1560
AAAGTAAGCT	GCATTTTCAA	TCTGGTCACC	ACGACTAGCT	TCACGACCAA	GCGGCACAAT	1620
GACATGCAAT	TTTGCTATCG	CCAAGAGCTC	AAAAATCGTA	TTGGCACCAC	CTCGTGTAC	1680
AACAATATCA	GCCAAATCCA	TCAAGGGTTG	ATAGAGATCG	GTCACATAGT	CAACACGAAA	1740
AAGATTTTGC	CTCAACTCAT	TCAGACTAGA	ATCTCCAGTT	AGATTGATAA	TATTGTAGCG	1800
CTCTGTTAGT	TCTTTCTTAT	GGTCTGTAC	CAATTGGTTA	AAGACACGAG	CGCCTGCAGA	1860
ACCGCCAACA	AACAATACAG	TTGGCAATTT	GGGATTAAAG	TGGGTTTGAA	TATCCACCAA	1920
TTCATCTGGT	TCTGGAGTGT	TTTTGTCCGA	AACCTTGGTC	ACCGCTCCCA	CATGCTCAAC	1980
CTTAGCCAAA	CTCGAAGCTT	GTTCAAAGGT	TGAATACATC	TTAGTCGCAA	ATTTATAGGC	2040
GATTTTATTG	GCCAAGCCCA	TAGACAGGTC	AGATTCTGTA	ATAAAGACAG	GCACTCCTGA	2100
CACACGCGCA	GCGATAACAG	GCGGTACTGA	GACAAAGCCC	CCCTTTGAAA	AAAGGGTCTG	2160
TGGACGCAGT	CGCAACATGA	TAAAGAGCGA	TTGGACAATT	CCCCAACCAA	CTTTGAAGAC	2220

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GTCCAGCATA	TTTTGCCAAG	AGAAATAGCG	ACGCAATTTT	CCAGTCGCAA	TAGAATGGAA	2280
GGTGACATCC	AAACCTGACT	TAAGGATTTT	TTGGTGTTCG	ATACCACACT	TGTCCCCGAT	2340
ATAGTGGACT	TCCCAACCAT	CTTCGATGAA	CTTGGGCATT	AACAAAAGAT	TGAGGGTAAC	2400
GTGTCCAACC	GTCCCCCAC	CTGTAAAGAC	AATTTTTTTC	ATATTATTCT	TTTAACTCCG	2460
CTACTGTGTC	GATAAAGAGG	TCGCCACGTA	CTTCAAAGTT	AGCATACATA	TCCCAGCTAG	2520
CATTGGCAGG	ACTAAGAAGA	ACCACATCTC	CTTGAGTCGC	AAGCTCATAG	GCCTTGCGGG	2580
TCGCATCTGC	AATATCTGTC	GCCTCCACAT	AAGCGACACC	AGCCTTGCTCT	GCTGCCCGTT	2640
TGACACGTTT	TGCAGATTGA	CCCAGGATGA	CCATCTTCTT	GAGTCCAGTA	ATGTCTGGCA	2700
CCAATTCGTC	AAACTCATTG	CCACGGTCCA	AACCACCTGC	AATCAAGACG	ACCTTGCTGT	2760
TGTCAAATCC	TGACAAGGCT	TTTTGAGTAG	CCAAGATATT	AGTTGATTTA	CTGTCGTTAT	2820
AGAATTTAAC	ACCCTTGATG	TCATCCACAA	ACTGGAGACG	GTGTTTGACA	CCACCGAAGG	2880
CTGAAAGAGT	TTCCTTGATG	GTTTGATTGT	CCACATCACG	AAGCTTGGCT	ACAGCAATAG	2940
TCGCAAGGGC	ATTTTCCACA	TTGTGGCTAC	CTGGAACACC	GATTTTCATTC	GCTGCCATGA	3000
CTACTTCACC	ACGGAAGTAG	AGTTGACCAT	CTTCCAGATA	AGCTCCATCA	ACCTTTTCAA	3060
GTGTTGAAAA	TGGTACAACA	GTGGCTTCTG	TCTTGGAAGT	CAAGTCTTTT	GCCAAGTCTT	3120
GATTAAGTTT	CAAGACAAGG	AAATCAGCTG	CTGTCATCTT	GTTCTGGATA	TTCCACTTGG	3180
CTGCTACATA	TTCCGAAAAT	GACCCATGGT	AGTCGATATG	AGTTGGCATG	AGGTTGGTAA	3240
TAACCGCAAT	CTCTGGATGG	AATCTTTGAA	CACCCATGAG	TTGGAAAGAA	GAAAGTTCCA	3300
TAACAAGCGT	GTCCTTATCT	GATGCTATTT	GAGCAACCTG	ACTAGCTGGA	TAGCCGATAT	3360
TCCCTGATAA	AAGACCATGT	TGGCCAGCAG	CAGTCAAAAC	TTCCCAATC	ATAGTCGTTG	3420
TGGTTGTCTT	ACCGTTTCGAT	CCTGTGATAC	CAATAATCGG	TGCTTCTGAA	ATCAAATAAG	3480
CCAATTCAC	CTCAGTCAAG	ACTGGAATTC	CCTTGGCCAA	AGCCTTTTCA	ATCATGGGAT	3540
TGTGTAGGG	GATACCTGGA	TTTTTCACCA	TAAGGGCAAA	CTCTTCATCC	AAGAGTTCCA	3600
AAGGATGGCC	ACCTGTAATG	ACCTTGATCC	CTTCTTCCAG	CAAACCTTGG	GCAGCTGGAT	3660
TGTCCTCGAA	AGGTTTCCCA	TCATTTACTG	TCACAATGGC	ACCTAGCTTG	TCCAACAAAC	3720
GAGCTGCAGA	TTCACCAGAC	TTGGCCAAAC	CTAAAACAAG	GACTTTCTTA	TTTTTAAATT	3780
GATCTATTAC	TTTCATGTCT	CGAACTCCAT	TTCTACTCCT	ACTATTTTAC	CATTTTATG	3840
GAAATAAAAA	AGCCACAAAG	TGTGTTTGTG	ACTCTTCTCT	CTAACTGAAT	CTTACCATAT	3900
CATCTATGTG	ATAAATCGGT	AACTCGAATG	ACCTGATCCA	CTTGCTCCCA	AATCAGAGGA	3960

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TTATGGGTCG CAATAATAAT GGTCCGATTC GGATTTTSTA AAGATTCTAG GATGGAAAGT 4020

AATTCCTCAG AGTTTTTGGG GTCTAAGGAA GCGGTTGGTT CATCTGCGAG GATCAAAGGT 4080

GGATCCTTTA AAATTATCTT CGCTAGTGCA ACACGTTGTG CTTCTCCTCC TGATAACTCA 4140

AATATAGGTT GCTTCAAATC CAAATAAGAG AGGTTTACAC GGTTTAGAGC TTGTTTCATC 4200

AAAGAGATTT TCTCTTTTTC CTTCAACTTT TTACCAACTA AACCCAGATT GAGATTCTCT 4260

TTGACGGTTT GGCTTTCAAT TAAGCCAAAA TCTTGAAATA AGTATCCTAA GTAATCTCTA 4320

AAGAAAACAG AAGGCTTGAT GTCCTTAAGA GAAGTGCCAT CATAGATGAT TTGCCCTTTG 4380

TCATATGGCT CCAATCGTCC AATCATATTC AAGAGTGTG TCTTACCACA GCCACTTGTA 4440

CCGATTAAGG CATAAATTTT CCCACCTTCA AAATGAAGAT TCATATCTGA AAATAGCTGA 4500

CGGCTTCCAA ATTTTTTAGA TATATCTTTT AGTTCAATCA TCCTATTTTC CTTTCATAAT 4560

TGTCATAGAA ACACGAGATT CTTTCTGCGC TTGACGGTAA AGCGTCAAAA CTGCACTAGC 4620

TAGAAAGACC AATAAAGTGA GCAAGCCAAT CACCAAGTCT CGACTGCTTA AAATAAAGAG 4680

ACTAGCACCA AATACAAAAC TAGCAAATG GCTAACCATTA TACTGAGCAT GTGTTTCAAA 4740

AAATCGTAAA CCTGAAATTC GTTTAATCAA GATACTCTCG CGGAATGCT CGAAATATAG 4800

AAGATTGACA GAATAAAGA GTAACAAGGA ACTGGCTATT CCAACAATAG CTCCTAAGAT 4860

TAAAGTTGCT GTTTCAGTTT GAACTTCATT ATAACGAGTT AGATAAACAC TTCTTCCTTC 4920

TTTAAGATAG GATACTTGCT CATAAATTC AGCTTTCTTC AAGAGTTCTA GCCCACTCTC 4980

ATATCCTTTG ATAAAGAGTT GTTTTCCAGC ATTGATAGAC CAACTAGATA AGGATATAAA 5040

ACTATCACCT GTAGAAGTCG GCGTGAATAC CACTAAAATC GGATCAGTCA AATACTGAGT 5100

AGATACGGGA TTCTCACCGT TATTATAAAC AAACCGCTTT TCTCCCATTG AAAGATAACT 5160

AACGTGCGCT TTCATCTCAT AATCCAAAGG AGCACTTGCC TCCTCACCAG ATTTTCCATA 5220

ATAACTCAAT CTTTCTTCAA AAACCTTCTT AAGTTCTGCT TCTCGAGAGC GCAAATGTTC 5280

TGGGAGCAAG AGGATAAACT CACCTTTTTG GAGATGGGCT AACTTCTGTT TGGTCTCAGC 5340

ATCTACCACG ACCTTTTCCT TGTCCAAATA ACTGGGACTA ACATAGAGCG TATTAGCATC 5400

TGAACTATAG GTATCCAGTG TCTCTCCCTG TTCATTTTTT CCTTGTGGAT TGGCAAATG 5460

GAGCAGATTA TCCTTTACAT AAAGAGCTTG TTCTTCTTCG ATTGCTTCCT TGGCAAAGGC 5520

ATACCACTTG CTCTGATTTT CTGTATCTTT TCCTCTATCA CCTAAGCCAA AGGAAATCTG 5580

GTAATAGTCT GCTCTGTCCT GCCATGCTTG TTTTGAATT TCAAGTTCTT TCAATCGTTG 5640

GTAAGACGTC AAACCTGTCT TAACAGCGTA GCCTACTGTA AAAACAGCTA CTAAGTACA 5700

CAATAGGGTT AAAGCCATCA AGCGTTTAAG GGGTAATCTT CCCTTAATAA CGGGAACATA 5760

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TGCTTTGTAA CTCAAACCTCA TTAGGTAAAG GAGCATTAGT AAAATTGAAA TCGCCAATAA 5820
 AAACAACAGA TAGAAACTAA TCCCAAAACC ATAGGTGGCT AACAAGATAG GATAAAACAA 5880
 ACCTTGACTA AAAAGAACGA CTCCCCACC TAGGAAGGAA AGGAGGGCTG ATAGAAGGAG 5940
 CCATTTGATA TCAGTAGATA AAGAATGCCC CATGATGGAT AAGAGAGTCT GACCAGAAAA 6000
 GAGTTTTATA CCTGCTGCTC TCATTTCCCTT AATCCGAGTG ATAATCACTA AAGCAAAGAA 6060
 AGATAAGCCA AATATTGCTA AACTAATTAA AATAAGGGGA TTTAGTAATA TTCGAAAAGC 6120
 AAGAAAATAG GCGGATATCT TTCGGTCAGC ACTTGCTTTA TAACCCAAAT CTCCTAATTT 6180
 ATCGGCAAGC TTTTCTTTTCG TCAAGGAGCC TGACAAAAGG AGATAACTAT TTAGCGGAnT 6240
 AtACGTTTAC GACTTTCTTG GCTAGCTTCT TGGAAATCTT TTGGTAAAGT TCCCTGACCA 6300
 TAAGTTGCAT AAGTAAAGTG AGTCGTCCA TCCTTACTCG GCTCTACAAT TCTTCTAGCT 6360
 ATTAACTCT GTTCTGAGTT TGCAAAATTC TCCAATTCCT GTTCAAATAC CTCACGCGTC 6420
 GGTTCCTGAG TATCTTTTTT GACACGAAGT AAAGAAACGG AATCATAGCT TGCATATAAA 6480
 TATTGTGGCG CACGTAAGAC AATAATCCAA GCAAGGAAGA AGCTGAGAAA AAAAGTTGAT 6540
 AATAATATGA ATAGTTTCTT CATAGTAGAC TCCTTGTAAG CAAAATCCC CCTGTAATTT 6600
 CTTACAAGG GAACGATTTA AATCAATGAA CGATTAGTCA TAATCACAGT AAAATGCTAC 6660
 TTGTTCTCCC CATTTAGTCC AAATCCATGC AGG 6693

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1847 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

CCGGTCTATG TACCCACTAC TTTGGGACAA TATGGGGATC AGCTACCCAA AACTAATCGA 60
 GCGTTTGGTT GACCTTGCCA AGGAAAGTTT TGACAAGCGC GACGATTTGA TATAAAATGA 120
 AAGAGAGGGT AGAAGCCAGA ACCATCACTG CACGGTGACT AGAGTCTCTG GACTTCAGCC 180
 CTTTTTAAAG GAGTAGAAAT GAAATTAACA ATCCATGAAA TTGCCCAAGT TGTGAGGCC 240
 AAAAATGATA TCAGTATCTT TGAGGACACC CAGTTAGAAA AAGCTGAGTT TGATAGTCGT 300
 TTGATTGGAA CTGGAGATTT ATTTGTGCCA CTTAAAGGTG CGCGTGATGG CCATGACTTT 360
 ATTGAAACAG CCTTTGAAAA TGGTGCAGCA GTAACCTTGT CTGAGAAAGA GGTCTCAAAT 420

1168

CATCCTTACA TTCTAGTAGA TGATGTTTGG ACAGCCTTTC AATCCTTAGC ATCCTACTAT	480
CTTGAAAAAA CGACTGTTGA TGCTTTGCT GTTACAGGT CAAATGGCAA GACAACGACT	540
AAGGATATGT TGGCGCATT ACTGTCAACA AGATACAAGA CCTACAAAAC ACAAGGCAAT	600
TACAATAATG AGATTGGCCT TCCTTACACA GTTCTTCATA TGCCTGAAG AACAGAAAAG	660
TTGGTTTTGG AGATGGGACA GGATCACTTG GCGATATTC ATCTCTTGTC TGAATTGGCT	720
CGTCCAAAAA CAGCCATCGT GACCTTGGTT GGAGAAGCCC ATTTGGCCTT TTTCAAAGAC	780
CGTTCAGAGA TTGCTAAGGG AAAAATGCAA ATTGCAGACG GAATGGCTTC AGGTTCTTG	840
CTTTTAGCGC CGGCTGACCC TATCGTAGAG GACTATTTGC CAACTGATAA AAAGGTGGTT	900
CGTTTTGGGC AAGGGGCAGA GCTGGAAAT ACTGACTTG TTGAGCGCAA AGATAGTCTG	960
ACCTTCAAGG CCAATTTCTT AGAGCAAGCC CTTGATTTGC CAGTAACTGG CAAGTACAAT	1020
GCGACAAATG CTATGATGTC ATCCTATGTT GCCTTGCAAG AAGGAGTTTC AGAGGAGCAA	1080
ATTCGTTTGG CCTTCCAAGA TCTTGAATG ACGCGTAACC GTACCGAGTG GAAGAAAGCA	1140
GCCAATGGAG CAGATATCCT GTCAGATGTT TACAATGCCA ATCCAACGTC TATGAAACTG	1200
ATTTTAGAGA CTTTCTCTGC CATTCCAGCC AATGAAGGTG GCAAGAAAAT TGCAGTGTG	1260
GCGGATATGA AGGAGCTTGG TGACCAGTCT GTTCAACTTC ATAATCAGAT GATTTTGAGC	1320
CTTCTCCAG ATGTGCTTGA TACCGTGATT TTCTATGGAG AAAATATGTC TGAATTAGCC	1380
CAATTGGCCA GTCAAATGTT CCAATCGGC CACGTTTACT ACTTCAAGAA AACAGAAGAC	1440
CAGGATCAAT TTGAAGACCT AGTCAAGCAG GTCAAGGAAA GCCTTGAGC CCATGACCAA	1500
ATCCTGCTCA AAGGCTCTAA CTCTATGAAT CTAGCCAAGT TGGTAGAAAG TTTAGAAAAT	1560
GAAGACAAGT GATTTTGTCA AGTATTTGCA AAGAATGATT GCCATTACAG ATACTGGCTT	1620
AACCTTTACA AAAGATCCGT TTGACCGTGA GCGCTACGAA GACTTGCGAA GTCTGTTATC	1680
TGAAATGTTG AATCAAGCAT CAGACCTTGA TTCCGAAGAA GTGGCAGAAG TCTTGAAGCC	1740
AACTTCTGCT TATGCGACTC CGTAAATGGA CGTCCGTGCT TGGATTGTTG AGGATGAGAA	1800
GATTTGTCTG GTTAGGGGAC AAGGAGAGGA TAGTTGGGCT TTGCCGG	1847

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1062 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

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CAAGCGAAAA	CATTTTTTAT	TCCAAATAAA	CAGAGCATTT	TAGGAGAACA	AGAGATTTTG	60
AATGCCAAGT	CGATCTTGGC	CTTGCTAGAC	GTTTGGAGT	CACATAGCTA	TGATGTAGTC	120
TATCTCCGTC	AGCCTCTTAA	TCGTCTCGAA	TATATCGAGT	GTGCGATAGT	GGGGCAATCA	180
CAATTTCTCT	TTAAGGTCAG	TTATGCTGAT	GGTCAAAGG	CTTACCGTGT	CGATCTTCCT	240
GACCTACTAA	CAAAGACAGA	CTGGCAGATT	ATCAAGTCAT	TTT'TAGATGC	TTTGCTTGCT	300
TATACAGGGA	CTGATATTGA	AGGGCTAGAT	GGTTTTGATT	TTGAAGCTTA	TTTCCAAGCA	360
AGTATTCAAG	CCTATCTAGC	AGACCCTGTA	GCTCGTTTTA	CGATTTGCCA	AGGAATTTTT	420
AATCCTATTT	TCTTTAGTCG	TGAGAACTTG	AAAAGCTTTT	TAGAGGCAGA	TGGCTTGGCT	480
CAGTTTGAAG	CGCGTGTGCG	TGCGGTCAA	GAGACAGATG	CCTACTTTGC	GAGAGTTTCC	540
TTCTATCAGG	ATGGAGAAGG	AAAAGTGCAT	GGCGTTTACC	ATCTAGCTCA	AGGAGTCAAG	600
ACAGTTTTAC	CGAGAGAACC	GTTTGTTCCT	GCAGCCTATA	TTGAGCAATT	GGTGGATAAG	660
GAAGTCCAGT	GGGAGATTGA	CTTGGTCAA	ATCACAGGAG	ATGGCTCTAA	ACCAGAAGAC	720
TATGAAGCCA	TTGCTCGCTT	GGACTATGCA	AAATCTTAG	AGGTATTACC	CCCATCTTTT	780
TACCACCAAC	TAGACGCCAA	TCAAATAGAA	GTGCAACCCA	TATTAGACAA	AGATTTTAAA	840
ACATTAGCAC	AAGAAAAGTA	AAGCAGAAGC	AGGTCAATCG	ACTTGCTTTT	TTGACATAGA	900
AAAAATCCTG	CCAAGaTGAC	AGGATTGCTA	CTCAATGAAA	ATCAAAGAGC	AAACTAGGAA	960
GCTAGCCGCA	GCTGTACTTG	AGTACGGTAA	GGCGAAGCTG	ACGTGGTTTG	AATTTGATTT	1020
TTGAAGAGTA	TGAAGTTTAA	AGAAAAGCCA	AGATACGAAG	AT		1062

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

TATCTACAAC	CTCAAAAACA	TGTTTTGawG	gCTCGTCAGT	cTATCTACAA	CCTCAAAAAC	60
ATGTTTTgAa	kgCtcGTCAG	tTCTATCTAC	AACCTCAAAA	ACATGTTTTG	AcaGccTcGT	120
CAGTTCTATC	TACAACCTCA	AAAACATGTT	TTGAGCTGAC	TTCGTTAGTT	TCATCTACAA	180
CCTCAAAAAC	ATGTTTTGAG	CTGACTTCGT	TAGTTTCATC	TACAACCTCA	AAAACATGTT	240
TTGangnCnT	CGTCAGTTCT	ATCTGCAACC	TCAAAGCAGT	GCTTTgagcG	CTTCGTCAGT	300

1170

TCTATCTACA	ACCTCAAAAC	AGTGTGTTGC	GCAGCCTTTA	ATCAGCCGCC	TAGTCCGCTC	360
TATGGTATTC	ATTAAGTCAA	CATCTCTTGT	TTAAGAGCAC	CAAATCAGGA	AATCTTCTCG	420
ATTCCCTGAT	TTTTTCTATT	TACGTTTTTCG	TGTTGAGCTA	CGTCTGTGCA	AACCATGAGG	480
TAAGAGAACT	TCACGTCTCT	CCAACTCTTC	CTTATGCATA	ATCTTGGTCA	ACATACGCAT	540
ACTAATGGCA	CCAAGGTCAT	AAAGAGGTTG	GGCAATCGTT	GTC AAGTTTG	GACGGGTAAA	600
GCGTGAGATT	TGTGAATCAT	CACTAGTAAT	AATTTCAAAA	TCTTCTGGCA	CAGAAACACC	660
CTTATCAGCC	AAACCGTCA	AGACTCCTGC	TGCCAACTCA	TCACCTGTCA	CAACTGCTGC	720
AGTTGCATTT	GATGAAATCA	AACGCTCTGC	TAAGGCGTAA	CCATCATCAT	AGCTATATTT	780
AGATTCAAAT	ACCAAACCTT	CACTATAAGT	GATTCCTGCT	TTTTTCAAGG	TTTCCTTGTA	840
GCCAACTAAA	CGAACCTTAC	CATTGATGTC	ATCCACTAGC	GGACCGCTAA	CGAAAGCAAT	900
ACGCTCATTT	TCTTTAGCAA	GGTAACTCAC	TGCATCAATT	GTTGCTTGCT	TATAGTCAAT	960
ATTGACACTT	GGCAACTGGT	GCTCAACATC	GACAGTTCCT	GCGAGAACAA	TCGGAGTACG	1020
TGAACGCGAA	AATCTGAGC	GAATTTTATC	TGTCAAGTGA	TACCCCATAT	AGATAATGCC	1080
ATCTACCTGC	TTTGAAAAGA	GGGTATTGAC	AACAGAAACT	TCTTCTCGT	TATCTTCATC	1140
GCTATTAGCT	AGGACAATAT	TGTACTTGTA	CATTTCTGCA	ATATCATCAA	TCCCCTTAGC	1200
CAAACCTGAA	AAATAACCAT	TGGTAATATT	TGGAATCACG	ACACCGACAG	TGGTTGTCTT	1260
TTTACTTGCA	AGACCACGCG	CAACTGCATT	TGGACGATAA	TCCAAACGAT	CAATTACCTC	1320
TAGCACTTTT	TTACGGGTAT	TCTCTTTTAC	ATTTTTATTG	CCATTGACCA	CACGGCTGAC	1380
CGTCGCCATG	GAAACACCTG	CTTACAGAGC	GACATCATAA	ATGGTTACTG	TATCATCTGC	1440
ATTCATTCCT	TTTCCTGTCC	TTTCTATCTC	ACACATTCCT	TTACAAGTAG	AGGTACTGAT	1500
TGAAGCTCTA	TATCTACTTA	CAAAAGTGAA	GATGTGAAAA	TTTCGTTTTT	ATATTTCTAC	1560
TTATTCCATT	CTATCACTAA	TTGTAAACAC	TTTCAAGTGT	TTTTTGAAGA	TTGATTGAAA	1620
AAATTTCATA	GAAAACCTAG	GTTTAGCTCC	TTGCTACCAC	CTTAGACTAA	ACAAAAAGGA	1680
GGAAACTAAG	CCCTCCTAAA	GTTATAGTAA	AATGAAATAA	GAACAGGATA	AATCGATCAG	1740
GACAGTCAAA	TCGATTTCTA	ACAATGTTTT	AGAAGTAGAG	GTGTACTATT	CTAGTTTCAA	1800
TCTACTATAG	GTATTGTTCC	ATTCACTACC	GTC AATTTTA	GCACATAGTC	TTCATGAAAA	1860
TATTATATCA	TCATAACCAA	CCAGATTCCT	TCGCGATATT	AGCTGCCTCT	GTTTCGATTAC	1920
CTGCATCTAG	TTTCGAAAAGA	ATATTGGTGA	CATAGTTTCG	GACTGTTCCG	TTGGATAGAT	1980
AAAGTTTGTC	TGCAATTTCT	TGGTTAGAGA	AGCCCTGAGC	AATTCCTTTT	AAAACCTGCGA	2040
TTTCTTGCTC	CGTTAATGGA	TTGGGATGCA	TCATCACCAC	TTCCATCAAT	TCAGGCGAAT	2100

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ACTCCTTGCG	TCCTTCGAGG	ACGGTGTGCA	AGGTTTGCAT	GAGGTCTGCA	ATGTTTCTTT	2160
CTTTTAATAC	ATAAGCATCT	ACTCCAGCCT	TGACCGCAGC	TTCAAAATAC	CCAGGACGCT	2220
TGAAGGTCGT	CACCACAACC	ACCTTTGTTT	CAAGCTTTTC	TGCTCGTATC	CACTCCAAGA	2280
CTTCAAGACC	TGTCTTAAAC	GGCATTTCCTA	CGTCAAGGAT	GGCGATATCT	ACAGACTCCT	2340
TTTCTAATAG	TTGGATTGCT	TCTTGCCCAT	TCTTGGCTTG	AAAGACAGAC	TCTACATCCG	2400
GTTGAAGCAT	GAGCAACTGG	CACATGGCAT	CTCGCAACAT	ACTTTGATCT	TCTGCGACTA	2460
ATACTTTCAT	CTACTTCTC	TCCTTATAAA	GTAGTCGAAC	CTGCACCTCA	GTTGGATGTT	2520
TCTGACTGAT	TACACTTACT	TCTCCTGAAA	ATGGAAAAAC	ACGATTTCCG	ACTGTATGGA	2580
GCTCATCCCC	GCTTATAGAG	GCAAAGCCAC	AGCCATCATC	TCTCACTGTT	AGAATGAGTT	2640
CTTCTCTGT	CCGTTCTAAT	TTCAAGTAGA	CTTTAGACGC	TTTAGCATGT	TTGATGATAT	2700
TGGTCACTAA	TTCAAGCAAA	ATCATGGAAG	CCGTTGACTC	CAATTCCTGA	GTTAAGCTAG	2760
ACTTGTCCTA	GTGATTCTCA	ACTTGAACCT	CAATTCACGC	AATTTCTAAC	ATCTTTTCTA	2820
CAGTCTCTAG	TTCCGATGTC	AAAGTCTAG	ACTTAAGATT	TTCCACAATG	GTTCCGACTT	2880
CATTCATGGA	TCCTTGCTGA	TCTGGTGAAT	TTCTTTTAAAT	TCCTTTTCCA	CCTGTGGATA	2940
AGCCTCCATC	TGAAATAACT	GCAAGGCTAA	ATCTGTCTTG	ACACTCAGCA	TAGCAAAGGT	3000
ATGTCCCAGA	CTATCATGCA	AATCCTGACC	GATACGACTA	CGTTCATTTT	CAGCAAGCAA	3060
TAGATTTATC	TGAGCATTTT	GCTTGACCTG	AGCTTCTTTC	AAATCCTCGA	CAATACGAAT	3120
CCGAACCAAT	CCAAAAGTCA	TTAAATCGAC	AAAAGTAAGA	ATTACAAGTA	GATAGAATAG	3180
AAACTCAACT	TCGATTCTCT	GAAAAATCAA	CAGTTGCCCC	ACAACAAGGA	CTTGAGCAAG	3240
AAGAAAAGTC	CAGACATGTA	AAGACTTTAA	ACTACGTACG	CTGAAATGAT	AACTTAAGAG	3300
ATTGGATAGG	AAAAAGAAAA	ACCAGATATA	ATTAACAGCA	ACAAAGGCAG	TATTCCCAAC	3360
TACATAAGTC	AGCATGAGGC	CCCAATATAG	CCAAGATAGG	CGCTGGCTCT	TAGTTGTAA	3420
AACACCCAAA	TATGCCACTA	CAAATAGAAT	ATCAATCAAT	AAATGCCAGG	CAGAAAGCCA	3480
CCCAGTCACT	ACAGACAGGA	TGGGGAAAAAT	CATAAAAATT	AAACTGATCC	AAAACATATA	3540
ATGTATTTCT	TTTCACTTTT	CAAGCATTA	GCATTCTCCT	TATGACCTTG	AAGGTAAATG	3600
GTCAAACCAA	ACAAAACCTAC	TGAAAAAACA	AGTAAATAAA	CTGTGGCTGA	TAGATTGATG	3660
CCACCCTCAT	TTAAGAAGGT	CTTGAGCAAC	TCCATCAACT	GATAGGTCGG	GAGACACTTA	3720
CCTACTACTT	GCATCCAGTC	TGGAAATAAA	GAGATAGGCA	TCCAGAGTCC	ACCTAAACA	3780
GCCAACCCTA	GATAAAGAAG	ATTGCCCCAG	ACAGACATCA	ACTGACTAGT	TGGTAAGAGA	3840

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GTCAAGGTCA AACCAAGCGC TACGAAGGCA ATACTTCCTA CTATCAGCAA AAGTGCAGCC	3900
CCAATCCAAT TTCCAAGAGA CATGTCCACA CCTCTTACAA AATGCCCAAC TGAGAAAACC	3960
ACCAAGATTG AAACCAAATA ATCAACCAGC ATACTTGTTA TCTTTGATAG ATAATATTCT	4020
ACCATATTTA CAGGGCTATG ACGCAATGTT TTCTGCCAGT TGTGATCTT GTCGGTATGT	4080
AAAACAAC TG GGAATGAGAA GATAGCTGTT GACATCATGG AAAATGCAGT CATGGAGATA	4140
AGATAATCAC GCATAAAATF CGCGAGTTCA CCTGGTGTGT CCTGATAGAT ACCAGAAAAA	4200
AATAAATAGA AAGCCGTCGG CATCCCTACT GACAATAGAT AATAGATCAA TTGTCTTTG	4260
GTCAATAAAA ATCTATCTT ACTAAGTGCT AGCCATCGTT TCATCTTAGT TATCTCCCTT	4320
CTGCGTTTCT TCAAAGATTG TATCCAACAA ACTACGATTA TTAACCTCAA TTTCTTGTAT	4380
GCCACATCCT GCTTGAAC TA ACAGTTCCCA AAAAGCATCT GCTTCGCGTG TGACTIONT	4440
TAGAGCATCC TGTTTTTGTG ACCAGTTTTT AACCAAGTTA GACTGCTCAA TGACTTCCTT	4500
GTATGCCAGA GGAAGGATAA AATGCTTTTC AATTCCTCA CTACGCATAG CTAGAGGCGT	4560
CGTATCACGA ATCAACTCTC CCTTATTTAA AACCAAAATC CGGTCAGCCG TATGCTCTAC	4620
CTCTTCAATA TAATGAGACG AATAGAGAAT CGTGACTCCT TCGCTTTTA GGTCCCGAAC	4680
GATTTCCCAA AAGCGTTGAC GAGTTGAAGT ATCCATGGCA GCAGTTGGTT CATCTAAAAA	4740
GACAAGCTTT GGTGCCCCAA TCAAGGTCAA GACAAAAGAG AAGAGACGCT TTTGCCCGCC	4800
TGACAATTTT TCTGCGAATT GCTCTTTTTG TTGCTGGTCA AACTGCAATA GTGATCGAT	4860
TTCTGATCG CTCAAGGAAT TTGGATAGAT ACGTTGAAAG AAAGCAATCA ACTCTTTGAC	4920
CTTTAATTTT TGAACGATGA CATTTTCTTG AGGCAGATAA CCTCTAATAT AGTCTAACTG	4980
AGAACTCGTC ACTGACAAGC CTTGGATGGA TACTTGACCG CTTGTGACCA GTTTATCTCC	5040
AAGCAGACAG TCCAAGAGTG TGGTCTTCCC AGCACCATTG GGCCCAATCA AGGCGACGCA	5100
TTACACTTCA GCTACCTCAA AGGAAATACC CTTCAAAATA GCCTTGCCCT TGATGTTTTT	5160
ATTTAGGCTT TCTACCTTAA TCATATTCAT GATATTCTCC TTCAACCAC TCCATTCTCA	5220
TAAGGAAAAC GACGAAAATC ATAAATCCAA ACCCCAAAGC ACCACGAATG AATTGGCGAA	5280
gCAAGGTTTG GTCAAACCAA CCTGTAAACA TTTCCACTAA CCATACCAAG AGTGACAGGC	5340
CGATAAAGAA ATAGATGATC CCTCTTCTCA TTCTCAAGC TCCTTTTTCA CATCTCCGAC	5400
TAATTTCAA CCTTCTCTAA CAAGCCAAGA CATCATTTCA AAGCCAGCAA AGAGCTCCCA	5460
AGGAAAATGA TAGAACTCT CATCCAATCC CGAAAACATG AGTTAGGTCA TAACTCCTGC	5520
TACTACTAAA CTCACTGCGA TAATCATTTT ATTTCTCATC TCTTCTTCTT CCATTTTATA	5580
CTACAATTAT AGTCTTTTGA AATCAGAGGA GACAGAAGCT TCTGTCACTA GAAAATATGA	5640

1173

CAAATGTCAT AAAAAATCTT GTTCAAAACA AGCAAGATAC ACTATACAAT AAAACACAAT 5700
 TAGAAAAATC TAAGGCAACT TCCTCAAAAG AGATATCAAA CCCAATTAC ACCATAATGT 5760
 AACTAATAC TTATTTAAAA TCAAAAAGAG TAGAAATTTT TATCAGACAA ACACATATAT 5820
 AGTGTATTGA ATCTATAACA GTAGGCCTTA AACTACTAAA TATTTCTATA AATTAATTTA 5880
 ACTTTCCTGA TAGAGCTGTT CATATCTTAT TTCAATTCCTC TAAATTATAC GTTGAACAAA 5940
 ACCCTTCTAT TTCTTTCTTA AAGATTTATA AGAGTTATAA AATCTGTTAA ATTTCAATGT 6000
 GTATACCTAA ACTACGGTAT TTATTGAAA GACTGGAGAC AAAAAGTATA CGCTGCCAAA 6060
 ATGAATTACT GAAAAATCAA AAAGAGAGAA CCAAACCTGAT TCCTCTTAA TGTATATAAT 6120
 ATCTAGTTT AAAAATACAC ACTCACATAT CTCTGTAATG AATCGGGAAG ACAGGATTCG 6180
 AACCTGCGAC ACCTTGGTCC CAAACCAAGC ACTCTACCAA GCTGAGCTAC TTCCCAGTT 6240
 AAATAGAAAA ATGCACCTTA GAGGAGTCGA ACCTCTAACC GCCTGATTCG TAGTCAGGTA 6300
 CTCTATCCAG TTGAGCTAAG GGTGCTCCAT ATTATGCCGA GGACCGGAAT CGAACCGGTA 6360
 CGATCGTTAC CAATCGCAGG ATTTAAGTC CTGTGCGTCT GCCAGTCCG CCACCCCGGC 6420
 CTCTCTAAGC GAACGACGGG ATTCGAACCC GCGACCCCA CCTTGGCAAG GTGGTGTCT 6480
 ACCACTGAAC TACGTTGCA CTGTTTTCTT CTATCTAAA ATGCCGGCTA CATGACTTGA 6540
 ACACGCGACC CTCTGATTAC AAATCAGATG CTCTACCAAC TGAGCTAAGC CGGCTCATTT 6600
 GTTATATCTT AATGCGGGTT AAGGGACTTG AACCCCAACG CCGTTAAGCG CCAGATCCTA 6660
 AATCTGGTGC GTCTGCCAAT TCCGCCAAAC CCGCATATAT GACCCGTACT GGGCTCGAAC 6720
 CAGTGACCCA TTGATTAAAA GTCAATTGCT CTACCAACTG AGCTAACGAG TCTAAAATAA 6780
 cTTGCGTTAC CTTAAACGGT CCCGACGGGA ATCGAACCCG CGATCTcGCC GTGACAAGGC 6840
 GACGTG 6846

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GAATTCATTT TAAATAAAGA TACGGGAGAG GTAAGTGAAT TAAAACCTCA TAGGGTAACT 60
 GTGACCATTC AAAATGGAAA AGAAATGAGT TCAACGATAG TGTCGGAAGA AGATTTTATT 120

1174

TTACCTGTTT	ATAAGGGTGA	ATTAGAAAAA	GGATACCAAT	TTGATGGTTG	GGAAATTTCT	180
GGTTTCGAAG	GTAAAAAGA	CGCTGGCTAT	GTTATTAATC	TATCAAAAGA	TACCTTTATA	240
AAACCTGTAT	TCAAGAAAAT	AGAGGAGAAA	AAGGAGGAAG	AAAATAAACC	TACTTTTGAT	300
GTATCGAAAA	AGAAAGATAA	CCCACAAGTA	AACCATAGTC	AATTTAAATGA	AAGTCACAGA	360
AAAGAGGATT	TACAAAGAGA	AGAGCATTCA	CAAAAATCTG	ATTCAACTAA	GGATGTTACA	420
GCTACAGTTC	TTGATAAAAA	CAATATCAGT	AGTAAATCAA	CTACTAACAA	TCCTAATAAG	480
TTGCCAAAAA	CTGGAACAGC	AAGCGGAGCC	CAGACACTAT	TAGCTGCCGG	AATAATGTTT	540
ATAGTAGGAA	TTTTTCTTGG	ATTGAAGAAA	AAAAATCAAG	ATTAAGATAA	AAGCTATAGA	600
AAAAATGGT	TTATGTACTG	AGATTAGATA	GTGAGGTGAT	GACATAGTTT	TGTGAAAATA	660
GCCATTTATA	ACTCAATTAT	TTAGTTTACT	TTACTTTACT	AGTGATACTA	TTTGGAGTTA	720
TTAATGGACT	TAGTTTATAT	AACTAATGAA	TTGATTGAAA	GGGTAGTAT	TGACAATATT	780
GGTCATATTG	ACTAGAAAAT	AGAGTCTATC	AAAATTTAAA	GGCTAATAGA	GGTGATGAGA	840
CAATTCGGC	TCTTTGTCAA	CTGTAGTGGG	TTGAAGTCAG	CTAAGCTCGA	GAAAGGACAA	900
ATTTTGTCTT	TTCTTTTTTG	ATATTCAGAG	CGATAAAAAT	CCGTTTTTTG	AAGTTTTCAA	960
AGTTTCGAAA	ACCAAAGGCA	TTGCGCTTGA	TAAGTTTGAT	GAGATTATTG	GTCGCTTCCA	1020
GTTTGGCATT	AGAATAGTGT	AGTTGAAGGG	CATGACAAT	CTTCTCTTTA	TCTTTGAGGA	1080
AGGTTTLAGA	GGATGAACCT	GATTCAGATT	GTCCTCAATG	AGTCCGAAAA	ATTTGTCAGG	1140
CTCCTTATTC	TGAAAGTGAA	AAAGCAAGAG	TTGATAGAGA	TTATAGTGGT	GTTTCAAGTC	1200
TTCTGAATAG	CTCAAAAGTT	TATCTATAGT	AGATTGAAAC	TAGAATAGTA	CACCTCTGCT	1260
TCTAAAACAT	TGTTAGAAAAT	CGATTTGACT	GTCCTGAATG	ATTTGTCTTG	TTATTATTTT	1320
ATTTTACTAT	AAATCCACGT	TTACGAATCT	CTTCCACAC	TTGTTCAATG	GGGTTTCATCT	1380
CTGGTGTGTA	TGGAGGAATA	AATGCAAAAC	CAATATTAGT	CGGAATCTTT	AAGGTAAGTTG	1440
ATTTATGCCA	TATAGCATTG	TCCATAACGA	GTAAGAGATA	ATCATCTGGA	TAAGCTTGTG	1500
AAAGCTCCTA	TTCCTAAAGC	CCCTTTATAA	CCTCTGCGA	GAGAGACTAT	TGACTCAGCC	1560
CTTACTTCAT	GCGGATGAAA	CTTCTTATCG	GGTCTAGAG	AGTCATAGCC	ATCTGACCTA	1620
CTATTGGACC	TTTTTGTCTG	GGAAAGTTGA	GAATCAAGCA	ATCACGCTGT	ACCATCATGA	1680
TCAGAGTCGG	AGTGGTTCGG	TAGTACAAGA	ATTCCTAGGA	GATTATTCTG	GCTATGTTCA	1740
TTGTGATATG	TTGCGGCAGT	AACTTAGGAC	TTTAGTCCTC	TAGTTCTGCC	TATGCGATAG	1800
CAGTCCAAGG	TTTAGGAGCA	AGGCGACGCT	AAGCTTGGTA	AACTGCGAAC	CGCTAGAAGC	1860
TTATCGTCAA	CTGGAAGAAG	CTGAACTTGT	TGGATGTTGG	GCGCATGTGA	GAAGGAAATT	1920

1175

TTTTGAAGCG ACCCCCAAGC AAGCAGATAA ATCATCCTTA GGAGCTAAAG GTTTAGCTTA 1980
 TTGTGATCAG TTATTTTCCT TGGAAGkAGA CTGGGAGGCT TTGCCAGCTG ATGAACGACT 2040
 ACAGAAACGT CAAGAACATC TCCAGCCCCT AATGGAAGAC TTCTTTGCTT GGTGCCGCCG 2100
 TCAGTCAGTT TTAGCAGGTT CAAAACCTAGG AAGGGCAATT GAATACAGCC TCAAGTATGA 2160
 AGAAACCTTT AAGACTATTT TGAAAGACGG ACATCTGGTC CTTTCCAATA ATCTAGCTGA 2220
 ACGCGCCATT AAATCATTTGG TTATGGGACG GAGTAAAAGA GTCCAGTGGG CTCTTTTAGC 2280
 CTGAGCTCAG TTTAAAAAAG CGAGGGTGGT TATTTTCTCA AAGTTTTGAA GGAGCTAAAG 2340
 CAAGAGCTAT TGTTATGAGC TTGTTGGAAA CAGCTAAACG TCATCAATTA TAGTGCGTTG 2400
 AATCTATAAC AGTACGCATC GACTGCTAAA ACATTTCTAT AAATCAATTT TCCTTTCCCTA 2460
 ATCGATTTGT TCATATCTTA TTTCAATCCA TTATAAATAG CGAGAAATAT CTATCCTATC 2520
 TTCTAGAATG TCTTCCAAAC GAGGAAACTC TCGTAAACAA AGAGGTTTTA GAGGTTTATT 2580
 TACCATGGAC TAAAGTTGTA CAAGAAAAGT GCAAATAAGA AATCTCCAGA TTAGGAACTA 2640
 TCCGTGAGTT CACTAATCTG GAGATTTTTC AATAGAtTCG TTATTGGGCG GTTACGATAT 2700
 GATcACTACT TCGTCAGTCT TATCTACAAC CTCAAACAG TGTTTTGAGC AACCTGCGAC 2760
 TAGCTTCCTA GTTTACTCTT TGATTTTCAT TGAATATTAG AACAGAAAAA ATGCTTGGAG 2820
 TATTTGTTTG TGTGTTTATT TTTATATAAC AAATATAAAA CAAAATAAAA ATATAAAAAA 2880
 AGAGACAAAA AAGAACAGAA AGTAATTGAC A 2911

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GAAAATAAGT CTTGACAGAA AGCGCTATCA ATGATAGAAT GAATTCAGAT AAAAAGATTT 60
 ATTTTAAAAA CAAAAATGAA ACGTTTCAA AAAAGAAATA AAGAGACAGC GCCAAGCGCT 120
 ATCTTTTCTA GAAAAAATG AAACGTTTCA AAAAAGGAGG TTGCTATGAA TAGCAAAGCG 180
 AAGCAAGTTT CTCTTTGGGA AAGAATCAAG AAACAAAAAC TCTTGTATT GATGACTGTC 240
 CCCGGTTTAG TTTTAACCTT TATCTTTAAA TACATCCCTA TGTATGGGGT TTTAATCGCA 300
 TTTAAAGATT ACAATCCTTT AAAAGGAATT TTAGGGAGTG ATTGGATTGG TTTTCTGAG 360

1176

TTTACAAAAT	TCATATCCTC	TCCCAACTTT	GGTATCTTGT	TAGCCAACAC	ATTAAAATTA	420
AGTATCTATG	GTTTATTGCT	TGGCTTTTTA	CCACCAATCA	TTCTCGCGAT	TATGCTCAAT	480
CAACTCTTGA	GTGAAAAAGT	CAAAAAACGA	ATTCAGCTCA	TTTTATACGC	ACCAAACCTT	540
ATCTCAGTCG	TTGTTATTGT	CGGTATGATT	TTCCTCTTCT	TTTCAGTGGG	AGGACCAATC	600
AACAATTTTC	TTTCTATGTT	TGGAATGAAG	GCTGACTTCT	TGACAAATCC	AGACTTCTTT	660
AGACCTTTAT	ACATCTTTAG	TGGTATCTGG	CAAGGAATGG	GCTGGGCTTC	AACGCTCTAC	720
ACGGCAACAT	TGGTAAATGT	AGATCCAGCC	TTAGTAGAAG	CAGCCCAGCT	GGATGGAGCC	780
AATATCTTCC	AACGAATCTG	GCACATTGAT	ATTCCAGCTC	TTAAGCCTAT	TATGGTTATC	840
CAATTTGTTT	TAGCTGCAGG	TGGAATTATG	AATGTCGGAT	ATGAAAAAGC	ATTCTTGATG	900
CAGACATCGT	TAAATTTGCC	AACTTCTGAA	ATTATCTCGA	CATATGTCTA	TAAAGTTGGT	960
CTTGATPCAG	GAGACTATTC	TTACTCAACA	GCGGTTGGTT	TGTTTAATGC	AGTGATTAAC	1020
GTAGTATTGC	TTGTTGCAGT	TAACCAAATC	GTTAAACGCA	TGAATAATGG	TGAAGGAATT	1080
TAAGGAGGAA	AGTATGAAAA	ATTCGATTAT	GGATACAAAA	TTTGATAGAC	GTATCTTACT	1140
CTTAAATAAA	ATCATTATTG	TCTTTATCGT	TTTGATGACT	TTGCTTCCTT	TACTTTTATAT	1200
CGTCGTAGCA	TCCTTTATGG	ATCCTAAGGT	TCTGGTTAGT	AGAGGGATTA	GCTTTAATCC	1260
AGCCGATTGG	ACTGTAGAAG	GTTACCAGCG	TGTATTCAGT	GACCAATCTA	TTCTAAGAGG	1320
TTTTATCAAT	TCTCTACTAT	ACTCTTTTGG	ATTTGCAGCT	TTAACAGTCT	TGCTATCTGT	1380
GTTTACAGCT	TATCCTCTTT	CTAAGAAAGA	CTTGGTTGGA	CGTCGTTGGA	TTAACTACTT	1440
CTTGATTGTA	ACTATGTCTT	TTGGTGGTGG	TTTAGTCCCA	ACTTACTTGC	TCGTAAAAGA	1500
ATTGGGAATG	CTCAATACTC	CATGGGCTAT	CATTGTTCCA	GGTGCTGTTA	ACGTTTGGAA	1560
TATTATCTTT	GCTAGGGCCT	ATTTCCAAGG	ATTGCCTGAA	GAATTAGTTG	AAGCTGCTGT	1620
CATTGATGGT	GCAAATGATT	TACAGATTTT	CTTCAAAATC	ATGCTTCCTC	TTGCAAAACC	1680
AATTATGTTT	GTTCTCTTCC	TTTATGCTTT	TGTAGGACAG	TGGAACTCAT	ACTTTGATGC	1740
AATGATTTAT	ATCAAGGATC	CAAACCTGGA	ACCATTGCAA	CTTGTACTION	GTAAAAATCT	1800
CATTAGAGC	CAACCAGGTC	AAGACATGAT	TGGAGCACAA	GCGGCTATGA	ATGAAATGAA	1860
ACGTTTAGCT	GAATTGATTA	AATACGCAAC	TATTGTCATT	TCCAGCTTGC	CATTGATTGT	1920
TATGTATCCA	TTCTTCCAAA	AATACTTTGA	TAAAGGAATT	ATGGCTGGTT	CACTTAAAGG	1980
ATAAAAAAAG	AAAAAATAAA	AGGAGTTTTC	TCATGAAATT	CAAAACATTC	TCAAAATCAG	2040
CAGTTTTGTT	GACAGCTAGT	TTAGCAGTAC	TTGCAGCCTG	TGGCTCAAAA	AATACAGCTT	2100
CAAGTCCAGA	TTATAAGTTG	GAAGGTGTAA	CATTCCCCTC	TCAAGAAAAG	AAAACATTGA	2160

1177

AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC AAATGAAAAG TTAATTTTGC 2220
AACGTTTGGG GAAGGAAACT GCGGTCATA TTGACTGGAC CAACTACCAA TCCGACTTTG 2280
CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC AGATGCTATC CACAACGACG 2340
GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG TGTATTATT CCAGTTGAAG 2400
ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT GGATGAGAAA CCAGAGTACA 2460
AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT TCCATGGATT GAAGAGCTTG 2520
GAGATGGTAA AGAGTCTATT CACAGTGTC ACGATATGGC TTGGATTAC AAAGATTGGC 2580
TTAAGAAACT TGGTCTTGAA ATGCCAAAA CTAAGTATGA TTTGATTAAA GTCCCTAGAAG 2640
CTTTCAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA TGAAATTCCA TTTTCATTTA 2700
TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC TGCATTTGGT ATAGGGGATA 2760
ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTGA CTTTCACAGCA GATAACGATA 2820
ACTATAAAGA AGGTGTCAA TTTATCCGTC AATTGCAAGA AAAAGGCCTG ATTGATAAAG 2880
AAGCTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG TCATGATCAG AAATTTGGTG 2940
TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA CGAAAGTTAT GATGTTTAC 3000
CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG TACAAACGGT ATGGGATTTG 3060
CACGTGACAA GATGTTTATT ACCAGTGTA AAAAAACCT AGAATTGACA GCTAAATGGA 3120
TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA CTGGGGAAC TACGGAGATG 3180
ACAAACAACA AAACATCTTT GAATGGATC AAGCGTCAA TAGTCTAAA CACTTACCAC 3240
TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA AGTAGGAGGA CCACTAGCTA 3300
TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA TGATGCCAAA TGGCGTTTGG 3360
ATCTTATCAA AGAATATTAT GTTCCCTACA TGAGCAATGT CAATAACTAT CCAAGAGTCT 3420
TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA AGCAGATATG AATGACTATA 3480
TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT TGATACTGAG TGGGATGATT 3540
ACAAGAAAGA ACTTGAAAA TACGGACTTT CTGATACCT CGCTATTAAA CAAAAACT 3600
ACGACCAATA CCAAGCAAAC AAAAAGTAGA GGTGATTTAT GGGAGATAAG AAATACACAG 3660
TAGAAAAAGC CAATCGTTTT ATAGCAGAAA ATAAACATCT CGTTAATACT CAATATAAGC 3720
CTGAAGAACA TTTTTCAGCT GAGATTGGTT GGATCAATGA TCCAAATGGA TTTGTCTATT 3780
TTCGTGGAGA ATACCATCTC TTTTATCAAT TCTATCCATA TGATAGTGT TGGGGGCTA 3840
TGCACTGGGG ACATGCTAAA AGTAAGGACT TGGTGACTTG GGAGCACTTG CCAGTGGCAC 3900

1178

TTGCTCCTGA CCAAGATTAT GACCGAAATG GTTGTTCCTC AGGCTCTGCC ATTGTCAAGG 3960
 ATGATCGCCT CTGGCTCATG TACTACTGGAC ATATCGAAGA AGAAACCGGT GTCCGCCAAG 4020
 TGCAAAATAT GGTATTTTCA GATGACGGGA TTCACTTTGA AAAGATTTCC CAAAATCCAG 4080
 TTGCAACTGG ATCAGACTTA CCAGATGAGT TGATTGCTGC TGATTTCCGT GATCCAAAAC 4140
 TCTTTGAAAA AGATGGACGC TATTACTCCG TAGTAGCTGC CAAACACAAG GATAATGTGG 4200
 GCTGTATCGT TCTACTAGGG TCCGATAACC TAGTAGAATG GCAGTTCGAA TCCATCTTTT 4260
 TAAAAGGGGG AGAACACCAA GGTTTTATGT GGGAAATGCC AGATTACTTC GAGTTAGATG 4320
 GGAAAGATTG CCTTATTATG TCACCCATGC GTTATCAGCG TGAGGGAGAC TCATATCATA 4380
 ACATCAACTC ATCGCTTTTG TTCACGGGTA AGGTAGATTG GAGAGAAAA CGTTTTATCC 4440
 CAGAATCAGT TCAAGAAATT GATCATGGCC AAGACTTCTA TGCGCCTCAA ACATTGTTGG 4500
 ACGATCAAAA TCGTCGTATC CTGATTGCTT GGATGCAGAC ATGGGGGCGT ACCCTTCCAA 4560
 CCCATGACCA AGAACACAAG TGGGCATGTG CCATGACTCT ACCTAGAATT CTAAGATTGG 4620
 AAGATGGCAA ACTAAGACAA TTCCCTGTTA AAAAAGGCCA ATATCAAATC CAAATAGATA 4680
 AAGATTGTCA TTACCACTTA GGAAATGATA TAGATTATCT TGAATTTGGT TATGACAGTA 4740
 ATGCGCAGCA AGTTTACATT GATCGTAGCC ATCTTATPCA AAAAATCTA GGTGAAGAAG 4800
 AACAGGACAC TAGTCGACGG TATGTAGATA TTGAAGCTAA AGAATTGGAA GTTGTCTTAG 4860
 ATAAAAATC CATCGAGATT TTTGTCAATC AAGGTGAAGC AAGCTTGACT GCAACTTATT 4920
 ACTTAACGGT GCCAGCTGAG CTATCACGAA TTGATTAATA ATTAAGTTAT TTCTCCTAAA 4980
 GAAAAAGTTC TCTTCTAAA ATAGTGGAAA GAGGACTTTT TGTGTTTTGG GTATATAAGC 5040
 TTAGTTTATG GTATTTGTAA AATTGGTGTT GGATTATGAT TTAAGCTAGT TTTCTAAAGA 5100
 ATTTGAAAAA AATTTTATTT AAGCAAAAAA ACCTTGGTTC CAAGGCTTTT CCTGTTGTAT 5160
 TTAGATGCC CCTACAGGA TTGTAGGAGA TATGTTGCTT AGATGTTCTT GATTTTCTGG 5220
 TGTTTTGTAA CGTTTAAATG AGTTTTTTGA GTTGTGTTGGT GGGGCGTTGC CCGCAATG 5280
 CCCGACTTAT TGCTTGAAAA AGAATTTAAA ATATAGTATA GTTAATTATA GATTAACACT 5340
 TGCTTGAGG AACTGATGAA GAACAATGAA AGATTAGGTA TTAAATTAAG TAGAGATAGC 5400
 GTTTTAGGAT TGAGGGAAGT TAGAAGGCTT TATTTAGGCA GTTCAGATAT CCCAGTTTCT 5460
 GATGGCTATG TGATTGAAGT TGCTTATAAC CAGATATCAC ATGAGATGTA TATTTATGAT 5520
 TGGGTAGAGT TGAACAAGTC AAAAATTAAG ATAAGTAAA TTAGTGAAAG CGTGGATATA 5580
 GATGCCACTA GCTTGAGAAC AACTTTGACT TTAGACACAT TAGTATATGA AGGTATGAGA 5640
 GATATACAGT TAAAGTTGAG AGAGCTTACA AAGGGGAGAG TATTCTTTTC ATTTGTACTG 5700

1179

AAGTTAGTTT TGTTTGCTTC TATTTTAAAG AAAAAAGATT TACTAGAAAA ATTTCAAGAA 5760
 AAGTGTTAAT CAAGTATTGA CACTTTATCT GGATTTCCGT ATAATATGCT TAGAAAGGAA 5820
 TCTTTCTAAA TTTTTTTCGT CCTTATGTGT TAATCAAAGA CGAATACAAA AACATATTTT 5880
 TTTACTCTAA AAAGTGTTAA TCAATGATGT ATTTGTTAGA GAGGTAGATA AATGGAATTG 5940
 AGAGCACCAC CAGTTATAAT AGTATAAAAC GTATAATAAA AATATTTTAA CTTGAATTAT 6000
 AGAAAAGGAG AAACAAATCA TGAAACAAAA ACAACCGATT GTTTCTAGAA CGAAACAACA 6060
 TACATTTGAA GAGCTTATTC AAGACCAAAA GTTAGAAAGA TTGGCTAAGT TGTCGCCCGA 6120
 TTTGGTTGGA AGGTATGGTT TFACTGCTAG CTGTGCGTCT TCATTTGCGA ACTTGATTAA 6180
 AGAAGCGTAT GGGGGTAAAA ATCTAAACGT AGTTTATGCG AGTCGGATGT TGGCTCTCTG 6240
 GAATATTGCT TGCAGTTGTT ATCATAAGGC TGATGGGTAT TCTTTAGCAG ATGCGCTTTT 6300
 TAGTGATAAA AAAATTTGTC TAGATTCTTA CTATTACCAC AAGAATACCT CTAATACCAT 6360
 AACTAGTGAT GTGATAAAG ATGTTTACGA TAATTATAAT AATTATATGG TTTTAACTCG 6420
 AGAAGCGACA CCTGAATACA TTTATGTTGT ACAAACGAA ATGCCAAAAG ATTCAGATTT 6480
 ATATTTTAT ATTAGAGAAG TTCTGGGATT ATCGTTTAGT ACCATGCATT ATGCATTTT 6540
 AGTCAAGGTT CTTGCAGGAG CGCTTGCTAG AAAATATAAG CCATATCGAA ATTGAATTAT 6600
 TTAAATTTAT ACTCTTCGAA AATCAAATTC AAACCAAGTC AGCTTCGCCT TGCTGTACTC 6660
 AAGTGCTGTC TGTGGCTAGC TTCTTAGTTT GCTTTTGGAT TTTTATGAG TATTACTCTT 6720
 ATGGTAGTTA TTTATGGCAT AATAATATTG ATTTGGGAGT TATAGCGAAA ATTTTAGGTT 6780
 CTATAATATT TGTAGTGGGT AAACCACTAT AGATATTATG GAGCCTATTT ATTGTAGAAA 6840
 AAAGTCCCAT ATGA 6854

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3895 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

TCCTTGCTAA GTTTTACTC AATGAAAATC AAAGAACAAA CTAGGAAGCT AGCCACAGGT 60
 TGCTCAAAGC ACCGCTTGA GGTTCAGAT AAAACTGACA CGGTTTGAAG AGATTTTCGA 120
 AGAGTATTAA TTTACATAAA TAGCCAGTGT TTGATAGGTT TTGAGTAGAA TTTTCTCAGA 180

1180

CACTTCTGCA	TCTTCATAGT	TTGATATCAA	AATCTGTCCA	TTTTGGTAGA	CTGCTGGCAA	240
GTCGATTTcA	CTTCTTTAGC	ATAAAAAGTTA	TTGAGCACTA	GTAACCTTTG	ATCCTCAAAC	300
TGGCGTTCAA	AAGCGTAGAC	TTGTTTGCTA	TCTTCAAAGG	CTGGTTTGTA	ACTTCCTTCT	360
GAAATGATTG	GCATTTCCCT	ACGCATCGAA	TCAAGTCTTG	ATAGAAGGTA	AAAATCGGAC	420
CCTGGATTTT	ATTTTCTACA	TTGATGTATT	TATAGGATTT	ACCAGCTTTC	AACCAAGGAG	480
TGCCTGTGTA	AAATCCTGCA	TTTTCCGAAG	CATCCCCTG	CATGGGAATG	CGTGAATTAT	540
CACGCGACTT	AGCTTGAATA	ATCTGGAAGG	CTTCTTGCTG	ACTCTTTCCT	TCTTCTAAGA	600
GCATCTGATA	GGCATTAAAG	GATTCGACAT	CCACATAATC	AGCCATAGAA	TCATAGTCTG	660
GGTCAATCAT	CCCATTTC	TCACCCATGT	AGATATAAGG	TGTCACCGT	GACAGGTGAA	720
TGCTGGCTGC	TAGCATGGTG	GCTCCTTCCT	TGCGGAAGTT	TTGAATATCG	ACAAAACGGT	780
TCAAGGCACG	TGGTTGATCG	TGATTATTCC	AAAAGAGGGC	ACTCCAACCG	TCTTTATCAC	840
TCATTTCCCT	ACCCCAACTA	TGGTAAAGAC	TCTTCAACTC	TTCAAAATCA	AAGGGAGCCA	900
AGGTCCACTT	TTGTCCATCC	TTATAGTCCA	CCTTGAGGTG	ATGAAAATTA	AAGGTCATGG	960
ATAATTCCTG	ACGATCAGGC	GACGAATAGA	GGACACAGTT	TTCCATGGTG	GTAGAAGACA	1020
TTTCCCCAAC	TGTCATAAAG	CTATCGTCGG	ATCCAAAAGT	GGCTTGGTTC	ATCATAACGCA	1080
AATAGTTATG	AACGATGGGT	TTGTCTGTAT	AAGCTGGCTT	CCCTTCATTT	TCAGGACAGT	1140
CCACTGAAAC	CTCGTCCTTA	CCGATCAAAT	TGATCACATC	AAATCGGAAA	CCTTTGACAC	1200
CCTTGTTCGCG	CCAGAAATTA	ACAACCTTGA	AAAGCTCCTT	ACGGACATTG	GAATTGCGCC	1260
AGTTAAGGTC	AGCCTGGGTC	TCATCAAATA	GGTGAAGATA	GTATTTCCCA	GTATCCCCGA	1320
AAGGCGTCCA	TGCAGAACCA	CCAAACTTAG	ACTGCCAATC	TGTTGGTTGG	TCTTGGATGA	1380
AGAAAAAGTC	TTGATAATAC	TTATCACCAG	CTAGGGCTTT	CTGAAACCAT	TCATGCTCTG	1440
TCGAACAATG	ATTAAGTACC	ATGTCCAGCA	TAAAGTCAAT	CTTGTGCTCT	TTACCGACAC	1500
ACACCATTTT	CTCAAAATCA	GCCATATCAC	CAAAAAGAGG	ATCCACTGCC	ATATAACTCTG	1560
AAATATCGTA	ACCATTATCC	CGTTGAGGGC	TTGGATAGAA	TGGATTGAGC	CAGACCATAT	1620
CCACACCTAG	TTTGGCTAAA	TAGGGAATTT	TTTCGATAAT	CCCACGGAAA	TCCCCAATAC	1680
CGTTTTCAGT	GGTGTCTTTG	TAAGATTTTG	GATAGATTTG	ATAGACTACT	TTTCCTTTAT	1740
CAAGTGTCAT	CTGTTTCTCC	TTTTCTGATA	AAAGGGAGGA	AGCAGTCTTC	CGTCCCTATT	1800
TGTGCTATTT	CAATTATACT	CAATGAAAAT	CAAAGAACAA	ACTAGGAAGC	TAGCCACAGG	1860
TTGCTCAAAA	CACTATTTTG	AGGTTGCAGA	TAGAGCTGAC	GTGGTTTGAA	GAGATTTTCG	1920
AAGAGTATTA	GATTCGTGTA	GCGACCATGA	GAGATGCTCC	AGCTTGGATC	GTTGTCGGAT	1980

1181

AAGTTCGGG AATAGTCGCT GTATAAGCAT CTTGGTTGGT GATGATAACA GGAGTTTCTG	2040
TCACCAGACC TGCAGCCTTA ATGACATCCA TATCAAAACG AATCAGTTGC TGACCAACTG	2100
TAACGTGATC TCCTTGACT ACAAGACTTT CAAAACCTTT GCCATCAAGA CCTACTGTAT	2160
CCATACCGAT GTGGATGAGC AATTCAACTC CCTCGTCAGA GACAATGCCG ATGGCATGCT	2220
TGGTAGGGAA AAGAACCGTC ACTGTCCCAT TAACTGGAGA GGTCAACTCA CCTTGGCTTG	2280
GTTCAATGAC TAGACCTTGC CCCATGACAC CTGATGCAAA AATAGGATCC GTCGCTTGAC	2340
TCAATTCCTT CACTTGGCCA GTTAGTGGC TGATAATTTT TACCGAAGTA AGTTCTACTG	2400
GTTCATGGTT CACAAATCTT GCTTCTTCTT GAGCAACGAA TTCTGCCTGC AAGTTCGTAT	2460
CGCCCTCTGT TTTTGTAAG AGACCAGCCT TCGGAAGAA GAAAGTCAAG AGCATTGGAA	2520
CAACAATCGC AACTAGCATA GTTCCTGCAA ATGGCAGCAT GTATTGAGGT TGAATAGAGA	2580
GAATACCTGG CAAACCACCG ATACCAATAG AAGCCGCAGT TACATTAAAA GTAACGGATA	2640
ACATGCCTGC AAGGGCTGAA CCAGTCATCC CAGCAACAAA TGGATAAATA TATTTTACGT	2700
TAACCCAAA AAGAGCTGGT TCTGTAACAC CGAGATAGGC TGAATGGTT GCAGGAAGTG	2760
AAACCTGAGC CTCACGCTCA TCATGGCGAT GCATGAAATA ATAGGCAAAC ACGGCTGAGC	2820
CTTGAGCAAT ATTAGAAAGA GCAATCATTG GCCATAGGGC AGTGCCACCA GCATCCGCAA	2880
TCAATTGTGT ATCAATGGCA TTGGTCATAT GGTGCAGACC TGTGATGACA AATGGAGCGT	2940
AGAGGGCGCC AAAAAATGCA CCGAAGAGCC ATTTAACTGG ACCAGTTAAA CCTGCCAAGA	3000
CAACTGATGA AAGTCCTTGT CCAATTGTCC AACCGATTGG TCCCAAAACA GTATGAGCCA	3060
AAATCAAGGC TGAATCAAT GACAAGAAAG GTACAAAAAT CATAGAAATG ACTTCTGGGA	3120
TATGCTTGTG CCAGAAGATT TCAAGATAAG ACAGACTCAA ACCTGCAAGC AAGGCTGGGA	3180
TAACTTGGGC TTGGTAACCG ATACGATTAA CAGTAAAATA GCCAAAATTC CAAACCCAGT	3240
TTGCCGCGAT ATCAGCTGCT GCGGTTGAAG CAACCGCATA GGCATTGAGC AACTGAGGCG	3300
ATACCAAACA GATTCGAGA ACAATCCCA AAATTTGGCT GGTCCCATC TTACGAGAAA	3360
CAGACCAAGT AATCCCTACT GGTAAGAACT GGAAGATAGC TTCACCAGGC AACCAGAGGA	3420
AGTGATTGAC ACCTGCCCAA AACTGAGAGG ATCTGTGAT GGTCTTGCCA TCCAACATCG	3480
ACCAATGGAC ACCTTCCAAG ACATTACGGA AACCGAGGAT CAATCCTCCG ACTATCAAGG	3540
CTGGAATAAT CGGAGTAAAA ATCTCCGCCA GAGTGGTCAT AACACCTTGG ACCACGTTTT	3600
GATTACTCTT AGTGCAGAC TTGGCTGCTT CTTTGAAAC ACCCTCAATA CCTGAAACGG	3660
CTGTAAAATC ATTATAAAAG ATGGGCACGT CATTTCCAAT GATTACCTGA AATGACCTG	3720

1182

CATTTGTAAA GGTTCCTTTA ACAGCTGGAA TTGACTCGAT AGCTTTAACA TTAGCCTTCT	3780
TATCATCTCC TAAAACAAAC CGCATCCGTG TCGCACAGTG AGTTACGGCA GTCACATTTT	3840
CTTGCCTCC GATTGCCTGA AGCAGATCTT TGGCTTCTTG TTCAAATTTT CCCGG	3895

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGGATCGCCG CTCCAGCTAC TAAGTCTCGT GCAGTGCCGA TTTATCAAAC AACATTTTTT	60
GTTTTTGATG ACACGTAGGA AGGTGCCGAT CTGTTTGCCT TGAGGAAACC AGGGAACATT	120
TATACTCGTA TCACCAATCC TACAACAGCT GCCCTGAAG GTGGTGTGA AGCGCTAgcA	180
ACAGCATCAG GTATGACTGC AGTGACTTAT ACGATTTTGG CGATTGCCCA TGCTGGTGAC	240
CATGTAGTGG CTGCTFCGAC TATTTACGGT GGAACCTTCA ATCTTTTGAA AGAACCCCTT	300
CCTCGTTATG GTATCACAAC AACCTTTTTT GATATTGATA ATTTGGAGGA AGTAGAAGCA	360
GCTATCAAAG ACAATACCAA GCTTGTCTTG ATTGAAACCT TGGGTAACCC CTTGATPAAT	420
ATTCCAGACC TGGAAAACT GGCAGAGATT GCTCATAAAC ATCAAATCCC ACTTGTGTCA	480
GACAATACTT TTGCAACACC TTATTTGATT AACGTCTTCT CTCATGGCGT TGACATTGCC	540
ATTCACCTCG TGACTAAGTT TATCGGTGGG CATGGTACAA CTATTGGAGG AATAATGTGTC	600
GATAGTGGTC GTTTTGACTG GACGGCTTCA GGGAAATTC CTCAATTTGT TGACGAGGGT	660
CCAAGCTGCC ACAATTTGAG CTATACTCGT GATGTGGGTG CAGCAGCCTT TATTATAGCT	720
GTTCGAGTTC AATTGCTTCG TGATACAGGT GCAGCCTTGT CACCATTCAA TGCTTTCCCTC	780
TTGCTACAAA GACTTGAAAC CTCTTCACTT CGTGTGGAAC GCCATGTACA AAATGCTGAG	840
ACAATFGTTG ATTTTCTTGT CAACCATCCT AAGGTAGAAA AGGTAAATTA TCCAAAACCT	900
GCAGATAGTC CTTATCATGC CTTGGCTGAG AAATACTTGC CAAAAGGTGT CGGTTCATC	960
TTTACCTTCC ACGTCAAAGG TGGCGAGGAA GAAGCACGCA AGGTCATTGA TAATTTAGAA	1020
ATCTTTTCTG ACCTTGCAA CGCGGCAGAT GCTAAATCGC TTGTTGTCCA TCCAGCAACA	1080
ACCACTCACG GTCAATGTG AGAAAAAGAC CTAGAAGCAG CAGGTGTCAC ACCAAACTAA	1140
ATTCGTTTGT CAATCGGTCT TGAAAATGTA GAAGATTTGA TTGAAGACTT GCGCTTGGCC	1200
TTGGAAAAAA TTTAAAGTAA AAGAAGATAA ACAGTGGGCT TCGACTCACT GTTTTTGATT	1260

1183

TTCCCTCAGG	CATGATATAA	TGGTTACAGA	AGTCTAGAAA	GAGGAACGAT	ATGAACGAAA	1320
TCAAATGTCC	CAACTGTGGG	GAAGTCTTTA	CAGTAAATGA	GAGTCAGTAT	GCCGAACCTCT	1380
TGTCCCAAGT	GAGAACGGCA	GAGTTTGATA	AGGAACTACA	CGATAGGATG	AAGCAGGAAC	1440
TGGCCTTGGC	TGAGCAAAAG	GCCATGAATG	AGCAACAGAC	TAAACTGGCT	CAGAAGGATC	1500
AAGAAATTCG	GCAATTACAG	AGTCAGATCC	AAAACCTTGA	TACAGAAAAA	GAATTGGCCA	1560
AGAAAGAGGT	TGAACAGACA	AGCCATGAGG	CTCTCTTGGC	TAAGGACAAG	GAAGTACAGC	1620
TCTTAGAAAA	TCAGTTGGCT	ACCTTGCGTT	TGGAGCATGA	AAATCAACTA	CAAAGACCC	1680
TTTCTGACCT	AGAAAAAGAA	CGGGATCAGG	TTAAAAACCA	ACTACTTTTG	CAGGAAAAGG	1740
AAAATGAATT	ATCTTTGGCT	TCTGTTAAGC	AAAACCTACG	AGCCCAGCTC	AAGGCAGCTA	1800
GTGAACAAGT	CGAGTTTAT	AAGAATTTA	AGGCTCAACA	ATCTACAAA	GCGATTGGGG	1860
AAAGCCTAGA	ACAGTATGCA	GAGAGTGAGT	TTAACAAGGT	TCGTAGTTTC	GCCTTTCCAA	1920
ATGCTTACTT	TGAGAAGGAT	AACAAGGTCT	CTTCGCGTGG	GTCTAAAGGG	GACTTTATCT	1980
TCCGTGAGTG	TGATGAAAAT	GGAGTTGAAA	TCATTTCTAT	CATGTTTGAG	ATGAAAAACG	2040
AAGCGGACGG	AACAGAGAAG	AAGCACAAGA	ATGCAGATTT	TTACAAGGAA	TTGGACAAGG	2100
ACCGTCGGGA	GAAGAACTGT	GAGTATGCCG	TTTTGGTGAC	CATGCTTGAG	GCTGATAATG	2160
ACTACTTTAA	CACAGGGATT	GTTGACGTCA	GTCACGAGTA	TGAAAAAATG	TATGTTGTTC	2220
GTCCTCAATT	CTTTATCCAA	TTGATGGTC	TCTTACGTAA	TGCGGCGCTA	AATTCCTTAA	2280
AATACAAGCA	GGAGTTGGCC	TTGGTTCGCG	AGCAAAATAT	TGACATTACG	CATTTTGAGG	2340
AAGATTTGGA	TGCCTTTAAG	CTAGCTTTTG	CTAAGAACTA	TAATTCAGCT	TCGACTAACT	2400
TTGGAAAAGC	TATTGATGAA	ATCGACAAGG	CCATCAAACG	CATGGAAGAG	GTTAAGAAAT	2460
TCCTGACCAC	ATCTGAAAAC	CAACTCCGTT	TAGCTAACAA	CAAATTGGA	GATGTCTCTG	2520
TTAAAAAATT	GACCCGAAA	AATCCAACAA	TGAAAGCGAA	GTTCGAAGCA	CTGAAGGGG	2580
AGTAGAAAAGC	AAAAATGAAC	GGTATTATTA	ACTTAAAAAA	GGAAGCAGGA	ATGACCTCGC	2640
ATGATGCGGT	TTTTAAACTG	CGTAAGATTT	TGGGAACCAA	GAAAATTGGT	CATGGTGGAA	2700
CCTTGGATCC	GGATGTGGTG	GGTGTTTTGC	CGATTGCGGT	TGGCAAGGCG	ACACGCATGG	2760
TCGAGTTTAT	GCAGGACGAG	GGTAAGATCT	ATGAGGGGGA	AATCACTCTG	GGCTATTCCA	2820
CGAAGACTGA	GGATGCTAGT	GGGGAAGTGG	TCGCAGAAAC	CCCTGTTTTG	TCTCTCTTGG	2880
ATGAAAAGCT	TGTTGATGAA	GCGATGCTA	GCTTGACTGG	GCCTATTACT	CAGATFCCCC	2940
CTATGTATTC	GGCAGTTAAG	GTTAATGGTC	GCAAGCTCTA	TGAGTATGCG	CGTGCTGGTC	3000

1184

AGGAAGTGGA GCGTCCAGAA CGTCAGGTGA CCATTTATCA ATTTGAGCGA ACAAGTCCGA 3060
 TTTCTTATGA TGGCCAACTT GCCCGATTCA CTTTTCGTGT AAAATGCAGT AAAGGGACGT 3120
 ACATCCGTAC TTTGTCACTT GATTTGGGTG AAAAGCTTGG TTATGCGGCT CATATGTCCC 3180
 ATTTGACTCG TACTAGTGCT GCTGGCTTAC AATTAGAAGA CGCTCTTGCC TTGGAGGAAA 3240
 TTGCTGAAAA AGTAGAGGCT GGGCAATTAG ATTTTCTCCA TCCTTTAGAG ATTGGGACAG 3300
 GTGACCTTGT CAAAGTTTTC CTAAGTCCAG AAGAGGCTAC AGAAGTTCGC TTTGGTTCGTT 3360
 TTATTGAGCT AGACCAAACG GACAAAGAAC TGGCTGCCTT TGAAGATGAT AAATTGTTAG 3420
 CCATTCTAGA AAAACGGGGC AATCTCTATA AGCCAAGGAA GGTTTTTAGC TAGATCGTTT 3480
 AGGAATAAAA ATCGGGTGAT AGATAACAAT TGCTTGATAA AACCCCATAC TAATAGTAGA 3540
 ATGGTTTTGG GAATTATAAT ATTCCAATTG TFGCGAGTTG TAGGTACTCA AATAATCTAT 3600
 ATAGAAATTT AGAGGTGTGA AATGAAGCAA TTTAAAATTC TTTCAGATAA ATATTTAGAG 3660
 TCCATTACAG GTTCTGATGG GAACTTAGGC CCAGGATTTG GTGTGATAAT TCCATGATGC 3720
 GAAATGAGTT TCGAGAAAGG GTGGAGCAAC TTCTTCAACA AAAAGAAATA AATGAAAATA 3780
 GTGAGTTGAG TCACCTGTTT CGTCTTGCTA TACAAAATTT AGACAGAAAT GAAAAATACC 3840
 AATCGGTCAT GGCCAATTTG AGTCAAGGGT TGTCACTTTA CCTCATGACG CATCATTACC 3900
 AGGCACCTAA GTCTGTCATT GATTTTGTTT TATGGA 3936

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

CATCCAGCAA CTGCTCCTCT GAGCGTTTCA AAATTGATGT AATTTTCTA GTTTTTCTA 60
 ATAAATGTGC CATTTTTCAC CTCGAATTTA ATCGCTATCA TTATAACATA AAAACGTCTC 120
 TTTTTCAATA ATTATCTGAA AATTCCTTAT TGACTTGCAT TGACTTACAA TTTAATTA 180
 AACCAGAATA TTTTAAATTA AATTGTTCC TTTCTATTGA CAAGTTGCCT ATTTTGTGT 240
 ATCATAATAT TATAAAAGAT AATATAATAA TTTTATTTGT CTTTTCACAT TCGGTCTCCT 300
 TATATAAAAA AGCGATTCAT TTTGAACCG TTTTCTTAT TTATCGCCTT TGTTACGAAT 360
 AACAAAGCCT GTTTGCTTTT CGCTTAAAGT ATTGCGTGGT TTTTATTAT CCTTACGGTA 420
 ACGTTTTTCC TTATCAAAC GATCGTTGCC ACGACTTCCT TTTTGAAC TATCACGGC 480

1185

ACCATTGCCA	CGGCGATCAC	GCTCTCGACG	GTCGTCCCCA	CGACGGCCTC	CACGACCTCC	540
CTTAGCTTTA	CCACCGAAAC	CATTACCTGA	TGGTTTAAAC	GGTAGTGGtT	TTTCACGTGC	600
AATCTCCACT	TCTGGAAGGC	TATCTGGGTC	TTGGACTGTC	AGACTCAAGA	TATACATTGC	660
CAATTCTTCT	GGAGTAAACT	CAGCAGCCAA	TTTGCGAGCA	TCCTTACCAA	ATTCTCAAA	720
GTTGGCACGA	ATGGTTTCAT	CTGCAAAATC	ACGTTTCGAT	TTCTTGAGAG	CTACCTGTFT	780
TTTTGATTGG	AAGGATTCTT	CTACACTTGC	AGGTTTGAGA	CCTTTCATGC	GTTTCTTAGT	840
CAAGTTTTC	ATGATTTGAA	GGTAACCCAT	TTCGTTTGG	GCAACAAAAG	TAATAGATTG	900
ACCTGACTTA	CCAGCACGAC	CTGTACGACC	GATACGGTGA	ACATAACTCT	CAGGATCTTG	960
TGGAATATCG	TAGTTGTAGA	CATGGGTCAC	ACCTGAAATA	TCCAAACCAC	GCGCTGCAAC	1020
GTCTGTGCGA	ACCAAAACAT	CAAGATTGCC	ATTTTTAAAG	TCACGAAGGA	CACGAAGACG	1080
TTTGTFTTGG	TCTAGGTCGC	CATGAATTC	TTCTGCACGG	AAGCCACGAA	TTTTCAAACC	1140
ACGAGTCAAT	TCATCCACAC	GGCGTTTGGT	ACGACCAAAT	ACAATAGCGA	GTTCTGGTTG	1200
TGCCACATCC	ATGAGACGAG	TCATGGTGTC	AAATTTTCT	TGTTCCCTAA	CACGGATATA	1260
GTACTGGTCA	ACCAATTCTG	TTGTCAATTC	CTTAGCCGCA	ATCTTGACAT	GTTCAGGGGC	1320
TTTCATAAAC	TGAACACCGA	TACGTTTGAT	GGCATCTGGC	ATAGTTGCTG	AGAAAAGCAA	1380
AGTTTGACGG	TTCTCAGGTA	CACGGGAAAT	AATGGCTTCG	ATGTCTTCAA	GGAAGCCCAT	1440
GTTAAGCATT	TCATCCGCTT	CGTCAAGGAT	AAGGGTTTCA	ATGTCTTGTA	ATTTCAAGGC	1500
CTTGCGTTTA	ATCAAGTCCA	AGAGGCGACC	TGGAGTCCC	ACCACAATAT	GGGCACCAGA	1560
TTTAAGAGCC	TTAATTTGTT	TTTCAATGCT	TGATCCGCCA	TATACTGAAC	GGAATTTGAC	1620
TCCCTTACTA	CGACCAAAGC	GGAAGAGTTC	TTCTTGACTT	TGGACAGCTA	GTTACAGAGT	1680
TGGAGCGATG	ACCAAGGCTT	GGATAGTCGC	TTCTTCTGTA	CGGATTTTTT	CAAGGGTAGG	1740
CAAGCCAAAG	GCTGCAGTTT	TTCTGTACC	AGTCTGAGCT	TGACCGATAA	CATCCTTGCC	1800
TTCAAGGGCC	AAAGGAATAG	TTTGTCTTG	GATAGGACTA	GCTTCTACAA	AACCAGCTTT	1860
TTCAATTTCT	GCTAGCAAAT	CAGCAGACAA	GTTTAATTCA	TTAAATTTCA	CGTTATTCTT	1920
CTTTCTAAAG	GTGGTGCGAA	GCCACCCTAT	AGGGCTTAGT	TTATACTTTT	CTTTTTATGA	1980
CGTATTTTCA	TATAACTAGA	TATAAAATCG	TGTTGCTTCT	TTCCACAAA	AGAAAAGTAC	2040
TGTTTTCTTT	GCAACCTATC	TAGTATAACA	CAAGACCAGA	GCAAAAGATA	GCCCCATTT	2100
TACAGAAAAT	CATGTAAGCG	CTTTTTGACT	TTCTTTTTTG	ATTGAACGAC	CTAGATAATA	2160
AGACAAAGCC	AAGGCGATAC	TGTATAAAAT	GAGAAAACG	AACAAGGTTT	GTGTGTACGA	2220

1186

ATGAGCCATT TTATAAGTCT CTGCTAATAA AATAGGTCCC GCTAAACCAG CCATTGCCCA 2280
 AGCTGTTAAA ATATAACCAT GCAGAGCGGC CAATTCCTTG GTTCCAAAAA TATCACTGAG 2340
 ATAAGCTGGA ATCAAAGAAA AACCAGCTCC ATAGCAAGTC ATCAAATAG ACATAGCAAC 2400
 TACAAATAAA ACGGAATCTG TAAAGAGCCA AAGTGAGAGA GAAAAGAAAA GATTGACAAG 2460
 CAGTAATATA CTAAAGGTTA GAGGGCGACC GATATAGTCA GACAAACTCG CCCAGAGCAA 2520
 GCGACCAAAT CCATTGAAAA TCCCCAAAAC ACCCACCATT ACTGCTGCAT GACTTGTTAGA 2580
 CAAGCCAGCC ATCTCCTGTG CCATTGGCGA TGCCGCTGAA ATTAAGCCTA AACCACAAGC 2640
 TATGTTGATA AAGAAAATAA TCCAAAGCAT ATAAAACCGA TTGCTTTTTA GAGCCTGATT 2700
 TGCAGCCATT CCTTGCCTCA AAGAGGCTGT TTTTCTTTC CCTGAAGAAG ATAAAATTGC 2760
 AAGCTCTTGC TCATTTGGAC GCTTAATGAA TTGTGAAGCT AGGAGCATGA TAATAAAGTA 2820
 ACTTGCTCCT AAAATATAAA AAGTTTCTAC AAGCCCTACC CCTGCGATGA GGTGTTGCGC 2880
 TATGGGACTA GTCAATAAAG AAGCAAAACC AAACCCATA ATCGCTAAAC CTGTTGCGAG 2940
 ACCACGTTTA TCAGGAAACC ATTTTATAAT CGTCGACACA GGGGTAATAT AGCCTGCTCC 3000
 CAAACCAAGC CCACCTAAAA TGCCATAAGC GAGATACAAC AACCACAGCT CTGACGGTCT 3060
 ATTGCAAATC CTGTTAAGAT ATTTCCACCT GCGTATAGAA AAGCAGATAG ACTTCCCATG 3120
 ACTTTCGGAC CAAATTTTTC TACCAAACGC CCCATAAATG CAGCCGATAA GCCCAAACAA 3180
 AAGATTGCTA GACTAAAGGC GAAGGCAACA GAAGCCTGAT CCCATCCCGT 3230

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5096 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CCTATGAAGA CTGTCCCAAC TGGGTGTCCT TCTAGGCTAT CTGGTCCTGC CACTCCAGTC 60
 AAATAATTTC CAAAATCAGA CTGGGTCTTG CTTCGTGCCT GCTCAGCCAT CTCTGAGCT 120
 GTAAATTCAG ACACCACACC ATGTTCTTCC AAATTCCTTG CAGGAATATC CAACATCCTT 180
 GATTTTTCCT CCAAGCTATA GGTCACAAA CCACCCTAA ATATACTTGA AACTCCAGAA 240
 AAATTCGCCA CGGTAGCTTG GAAAAGACCT GCCGTCAAAC TCTCTGCAGC CGCGATGGTT 300
 TTCCCTTGCC TTTTCAGTTC TTCTACCACA ATGCTGGCTA AACTAGTTTC TTCCCCATAA 360
 CCATAGCAA AGTCTCGTAA AGAAATTCCT TCGAAAGTCT GGCAGTCAA GATTTGATTT 420

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TCCAAGATAT	CCAGCGCTTG	ATTCGCCTCT	TCTTGACTGC	TAGCCTTTGT	TGACAGACGT	480
AGAGTGACTT	CTCCTGTCTT	GGCATAAGGG	GCCAAGGTAG	GATCGATCTG	ATTATCAATT	540
AAATCAGCCA	AAATCGTAAC	CAACTGGCTC	TCGCCAATCC	CAAAGAAACG	AAGAACTCGG	600
GAATACAGCT	TGCTCCCTGT	CATCAACTTG	GGTAGAAGTT	GGTTAAGAC	CATGGGTTTC	660
AATTCACTTG	GCGGACCTGG	AAGGACGACA	TAGGTCACTC	CGTCTACTTC	TAATTTTCCCT	720
CCAACAGCCA	GTCCTGTTTC	GTTTGGCAGT	GGAATCGCTC	CTTCTACAAT	TTGAGCTTGT	780
CTTTCGTTAT	TCGGTGTTCG	GGCATAAGTT	GGTTCGAGGG	TAAAAAAGAT	ATCCAACCTC	840
TCCTGAGCCT	GAGGATCAAA	GACTAATGCT	TTCCCTAAAA	ATTTAGCTAG	GGTTTGTTCG	900
GTTAGGTCGT	CCTCAGTTGG	CCCCAAACCG	CCTGTCAAAA	TCACCAGACT	GCTACGTTGA	960
CTGGCAATCT	CAAGCAAAGA	CAAGAGACGA	ACTTCATTGT	CTCCTACAGC	CGTCTGAAAA	1020
TATACATCTA	CCCCAATCTC	AGCTAGTTTT	TCCGACAAAA	ACTGGGCATT	GGTGTGACA	1080
ATCTGCCCTG	TCAAATCTC	TGTTCCAACA	GCAATGATTT	CTGCTTTCAT	GTTTCCTCCT	1140
ACCTATCTAT	TCGTATTTTT	TTGAAAAAAT	CGCAGGAATF	TTCTACGAT	TGATTTTTTT	1200
ATTTGTATCA	AAAGTTAATT	ATCTTCATCA	CCAACAGGTG	CTCTGCCAAA	TAAATCTTCA	1260
AATAAAACCG	CATTGGTTTC	AAGCTGAGTA	ACTTCTTCTT	GTCCCAAAGA	ACGTCGGAGT	1320
AGATTTTGCA	TTTCCAACAT	ATGTGCTCTC	GAAACAATCT	GGTAAGAAAC	ACCTTGAAGT	1380
ATCTCTCCTT	CACCCTGCAA	CTGCTGAGTT	TCAATGGTTT	TAAATGAATC	TTTATAGCCT	1440
AGCAAGTTAG	GGATACTTTT	TGCAGACAAA	TCAATATTGG	TCTGCATATT	GTCACTCAAA	1500
GCTTTTAGAA	TCTCTTGATA	ATGACCAATG	CTATTTAAAC	TGAGAGCTTT	TTCCATGACT	1560
TTTTGAATAA	CTTCACGTTG	ACGTTTTTGA	CGACCATAAT	CCCCCTCAGG	ATCTTGGTAA	1620
CGCATTCGTG	CATAGACTAG	GGCTTCTTCT	CCCCCAATAT	GTTGCTCCCC	AACACCGATA	1680
GAAATAGTAT	TAAATCTTTC	TTGGTCACTG	ATAGAAATTG	GGAAACCTAG	GATATTATTG	1740
ACTGTAATAC	CTCCTACTGC	ATCCACTAGT	TTTTGCAATC	CTCTCATATT	GACCATCACA	1800
TAGCGATCAA	TATGGATATT	CATCATTTTT	TGAATGGTTT	CTATAGCAAG	CTCTGCTCCA	1860
CCATCTGCAT	ATGCTGAGTT	CAGTTTCGCT	TCATGAGCCT	GACCATTCCC	TGATTCAAATG	1920
CGCGTCAGAA	TATCCCGCTC	TAAACTCATC	ATTGTTGTTT	TTTTCGTTTT	AGGATTCACT	1980
GTCATCAAGA	TCATGCTATC	ACTTCTACCG	ACCCAAGTTT	CAGTTCGTTC	AACATTTCCG	2040
GTGTCCACTC	CCATTAACAG	AATGGTTAGA	GGTTCAGTCG	CTTCAATAAC	CTTGGTTTCT	2100
TCACCGATTT	TTTTATAGGT	TTTAGCTAAG	GTTTCTGTCC	CTTGTGATA	AATAGTATAA	2160

1188

GCAAAAACAC	CTACTCCTAC	TACAGTTACA	GAAAGTAAAG	CTAGCACCAT	TCCAATAATT	2220
TTTTTAACCA	TATTTCTACT	AACCTATCAG	TTTACCCATC	AAGTAAACAT	CGATAAATTT	2280
CCCTTCTTCT	ATATATGCCC	CACGCTCTTG	GCTACCTTCA	ATGACAAAGC	CATGCTTTTG	2340
ATAAAGATGG	ACTGCTGCTT	GATTACGAGT	TTGGACAGTC	AGTTGGAGAC	GACGCAGAAT	2400
GCCACTTGCT	TGTGCCCACT	CTATCGCTTC	TTCTAGCAAC	AAACTTCCCA	AGCCATTATT	2460
CCAATATCTT	TTTCCAATCA	CAATGAAGAG	ATCTCCAATA	TGACGGACTC	TCTTACGCTG	2520
ATCAGCTGTA	ATATTTACAA	TACCAGCAAT	TTTGCCATTT	AAGAATGCAA	GTAAGGTTAT	2580
CTGATTGTCC	GAAC TAGCTT	GCTTGTGAG	GAATATTTCC	ATCTCCTCAC	TAGTCAAGAG	2640
AATACCATCT	CCGTCTAGGC	TGGTAAAGTC	TGTCTCCAAA	CTCACACGAT	TTAAAAAGGC	2700
CACTAATTCA	GCTGCATCTT	TGGGCTCTGC	TTCCCTAATG	AGCAATTCAT	ACTCCATATT	2760
GAAGCTCCTC	TAACAATTTT	TCAGCACGCA	AACCTTTTGC	CTGAAAATTT	AAACGGCGTC	2820
CATCTGCTTC	TTTTAGAATT	TCCAATTCTA	AATAAGCATC	TGGCAAGGCA	TCTCCTAAGA	2880
GATTTCCCCA	CTCAATAACA	GTCAGCCCGC	CACCAAAGAT	AAACTCATCC	AAGTCGATAG	2940
AATCAGCATC	TCCTTCAATA	CGATAAACAT	CTAGGTGATA	AAGTGAAGT	CGACCTTCAT	3000
ACTCTCTCAC	GATAGTATAG	GTGGGACTTT	TAATCATTTG	AGAAATCTGT	AATCCTTTTG	3060
CAAGTCCTTT	AGTAAAGGTC	GTTTTACCTG	CACCCAGTTC	TCCAGTTAAG	ATTAAAAACAT	3120
CATTCTTTGC	TAATAGATGG	CCCAAACGCT	CCCCTAAGGC	TTGCAACTCT	TCTTCATTTT	3180
TTGTGTACAT	ACTCTTATTA	TACCAAAAAC	TTTTCTTTTG	TGTCTATTTT	CCTACTAAAC	3240
TTATCATCAT	AACATCCATA	AAAAACAGGC	TTTCTCTAAA	AGAAAATGAG	CGTAACAATG	3300
ACCAATACAA	GATCTCGGAA	AATATGACCA	TAAAAGGAAA	CTTCCTTCTT	AACCGAATTT	3360
GGGACAAGAT	AGGCTGCAAA	AAACAAGCCC	AGTCCAATAT	AAATCAGAAG	TGAGACAATG	3420
GTCATTGGAT	TTCTTAAGAA	AAGAAGTGTT	GCTAAAATAG	TCACCAACAC	TGTCTTTTTT	3480
CTGTCCAGCA	TAGCAAGAAA	ATCGCGCACG	TATTTTTTCA	AGGGTAAAAA	AATCAGCAAA	3540
TCTAGCCCAA	ATAGGAAAAA	GAAGGATGGC	AATAAAAAGT	CAACTAATTC	TTGCTGCAGC	3600
GTATTTTTGA	TGAACAAGTT	ATCTGACAAA	ACAAGAACAG	CTCCTAACAA	ATTAATTAAG	3660
AGTAACATAC	TGTAAAAAAG	CTTCAACGAC	TTCTTACTGG	CTAGGACACT	ATGGACTTCT	3720
TGCTTACGGG	TATAAAGATA	ATTTACTCCA	GCACAGATTC	CTGAAACGAA	AACCATGCTT	3780
CCGATGAAAA	AAGCTGTACT	TTGTTTAAAG	GACAAGATGC	ATTCCTTCCA	TAGGAAACAG	3840
CTACTCAAAC	TGATTTGAAT	TAAAGCTAAC	AAAAATAAGA	TTCTCATTGA	TTTCATCTTC	3900
TCTCTCCCTT	CCTACCAATC	ATTATACTAG	GAGAAAAGAG	AGAAGTGTTC	CTAATCTTCT	3960

1189

CAAATGTCTC TTTAAGACGC TAAACAAACA CTAGAGACTA ATACTCAATG AAAATCAAAG	4020
ATCAAACACTAG GTAGCTAGCC ACAGGTTGCT CAAAACAGTG TTTTGAGATT GCAGATAGAG	4080
CTGACGTGAT TTGAAGAGAT TTTCGAAGAA TATAAATTTG AAATCATGAA AATCCGTCAA	4140
ACGGGTGGTT GTTTTGTCTC GCACCTCACG GAGCGAGACG GACTCAGAGT CACATAATTA	4200
TAAGGCTGAT AGTATTAATC TAACTATCAG CtTmCAGGTT ATTTAACGTT TCAGAAAAAC	4260
TATAATGTCA AGATTAACATA AACAGTATCT AGTTCCTTCA AATAATTTTC TATCTTCATC	4320
AACATTAAG GATTGTTATA AATCTTACAT AACTCTCTTG CTTCTATATA ATAATTTTTG	4380
ACTTGTTCTC TGTCTAGAAA TTTGGCTCCA GCATTTCCCTA CAAGAATAAG TAGAGGAGCC	4440
AATTGGTAGC TTGTCTGTCT TTGTTTACAG AGTTC AATCG TTTCAAGAGC TTCTTGGATG	4500
GCTTCATTAT ATTTTTCCTT TGATACTAGG TAGTGAGCGT AGTGTAACG AACTCTGATG	4560
TAGCCAAATA AAAACTCTTG ATGGTCCAAA TTTTTGTCT GATACAACCT TATTAAATGA	4620
GAGTAGTTTG CCTCATATTC TTGTTACGA CCCACTAAGG AATAGAAAT AGATAGAGTA	4680
TTCAACGCCT TTAATAAAT CAGAGTATTT GAAGAGACTT TTAATAATAT ATTTTCCAAT	4740
GACGAAATTG CCTCACACTT ACTGTCATAT TGATAGAAGT CAATTATAGA TTTAATCCAT	4800
TCAAGGTAAG TTCGGTCTTC TAATGTTAGA AAAGTGCTTC GTTCTACTTC TATTTTATAA	4860
AGATATTCTA AATCGTCATA ATTTCTGTCA TCTAATAGGC GAGCAGATAG ATGTTTGAAA	4920
TTAGAGAGGT TAGACTTAAC TTCGATTTGT TCATTGAAAA AGTAATCCAA AGGGACTTCA	4980
AGTCGTTGAG AGAGTTTGAA TAACAAGTCT GCGGAGGGAA TAAAATGACC TCTTCAATT	5040
TTACTAATCT GGCTTTGTTT ACAAATTCCT TCTGCAAGAG TTTGTTGGGA GAGTCT	5096

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ACAAGATAAA AATAAAGGAT TACAATGGGG AATATAAAGT AAACCGGTAA ACCTAAAAAG	60
AAAGGAGAAA AGATGAAAAT TGTACTTGTA GGCATGGAC ATTTTGCTAC AGGGATTTAT	120
AGTTCCTTAC AATTGATTGC AGGTAATCAA GAAAATGTGG AGGCGATTGA CTTTGTGGAA	180
GGAAATGTCAG CAGATGAACT CAAGCAAAAA ATCTTACTTG CAATTTCAAA TGAAGAAGAA	240

1190

GTTTTAATCC TAAGTGATCT CTGGGAGGA TCGCCATTCA AGGTTTCTTC TACCATAATG	300
GGAGAAAATC CAGCCAAGAC AATGAATGTT CTCTCGGGTT TGAACCTAGC CATGTTAATG	360
GAAGCAGTCT TTGCTAGAAT GGCTCATAGC TTTGATGAGG TTGTTAATAA ATCAGTAGTG	420
GCGGCCCAGG GCGGAGTCGT AAATGGTAAA GAATTGTTTT CAACGGATGC AGAGGAAGAG	480
GAAGAAGATT TCGAATCGGG TATTTAAAGG GTAAAAGAAT GATAAAAAAG GTTACGATTG	540
AAAAAATAAA ATCGCCTGAG CGCTTCTTAG AAGTACCCT TCTGACGAAA GAAGAAGTCG	600
GCCAGGCAAT CGATAAGGTT ATTCGGCAGT TAGAACTCAA CCTTGACTAT TTCAAGGAAG	660
ATTTCCCGAC GCCAGCTACC TTTGATAATG TCTATCCAAT CATGGATAAC ACGGAATGGA	720
CCAATGGTTT CTGGACAGGA GAACTGTGGT TGGCTTATGA ATACAGTCAA CAGGATGCAT	780
TTAAAAACAT CGCTCATAAA AATGTCTTTT CTTTCCTGGA TCGTGTCAAT AAGAGAGTAG	840
AATTGGATCA CCATGATCTC GGCTTCTTGT ACACACCGTC TTGTATGGCT GAATATAAGA	900
TAAATGGAGA TGGAGAGGCT AGAGAAGCAA CCTTGAAGC TGCAGATAAG TTGATTGAAC	960
GCTATCAAGA AAAAGGTGGT TTTATCAAG CTTGGGGAGA CTTGGGCAAG AAAGAGCATT	1020
ACCGTTTGAT TATCGACTGC TTGCTCAATA TCCAACCTT ATTCTTGCT TATCAAGAAA	1080
CAGGCGATCA AAAATACTAC GATATGCAG AAAGCCATTT CTATGCTCA GCTAATAATG	1140
TAATCCGTGA TGACGCTTCG TCCTTCCACA CCTTCTATTT TGATCCTGAG ACAGGTCAAC	1200
CCTTTAAAGG TGTAACGAGA CAAGGTATA GTGATGATTC ATGCTGGGCA CGTGGTCAAT	1260
cATGGGGAGT CTATGGTATT CCTTTGACTT ATCGTCACTT AAAAGACGAG tCCTGCTTTG	1320
ACTTGTTTAA GGGTGTGACC AATTATTTCT TGAATCGTCT GCCAAAAGAT CATGTGCCT	1380
ATTGGGATTT GATTTTAAAT GATGGTAGTG ATCAATCACG AGATTCTTCA GCAACAGCTA	1440
TCGCCGTCTG TGGGATTCAT GAAATGCTAA AACATCTCCC AGAGGTGGAT GCTGACAAAG	1500
ATATTTATAA ACATGCTATG CATGCCATGC TTCGTTCCCTT GATCGAACAT TATGCAAATG	1560
ATCAATTTAC CCCTGGTGGG ACAAGTCTCC TCCACGGTGT GTACTCATGG CATTACAGTA	1620
AAGGAGTGGA TGAAGGCAAT ATCTGGGGTG ACTACTATTA CCTAGAAGCC CTTATCCGTT	1680
TCTACAAAGA CTGGAACCTA TATTGGTAGG AGGAGAAATA TGACAATGCC AAATATTATT	1740
ATGACCCGTA TCGATGAACG GTTGATTCAT GGACAAGGAC AACTTTGGGT AAAATACCTA	1800
GGTTGTAATA CGGTCATTGT TGCCAATGAC GAAGTAAGCA CGGACAAGAT GCAACAAACT	1860
CTGATGAAAA CAGTTGTGCC AGACTCAGTT GCCATGCGTT TCTTCCCTTT GCAAAAAGGTG	1920
ATTGATATCA TTCACAAGGC TAATCCTGCT CAAACGATCT TTATCGTTGT AAAGGATGTG	1980
AAGGACGCTT TAACCTTGGT AGAAGGTGGT GTCATATCA AAGAAATCAA TATTGGGAAC	2040

1191

ATTCACAATG CCCCTGGTAA AGAGCAAGTG ACACGCTCCA TCTTCCTGGG TGAAGAGGAC	2100
AAGGCGGCC TCAAGGAATT GAGCCAACT CATCAAGTAA CATTTAATAC GAAAACAAC	2160
CCAACAGGAA ATGATGGAGC TGTTCAAGTC AACATTATGG ACTATATTTA ACAGAGGAGA	2220
TCGTTATGTC GATTAATGTA TTCAAGCGA TTTAATTGG ATTATGGACA GCTTCTGTT	2280
TTAGTGGAAT GCTGTTAGGA ATTTACACCA ATAGATGTAT TGTTCTGTCA TTTGGTGTGC	2340
GAATTATTCT AGGTGATCTG TCATGCTCTT GCAATGGGAG CCAATGGTGA ATTGG	2395

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCTTCTTTAG AGGTTAATTT TGCAAAATCG TCGATTGTTA TATAAGGATT ATTATAGAGA	60
CTGTTTCGCAA AGAATCTCTG ATATGTTTTT GAATCTTTTG AATACAAAAC TATCTCTCTA	120
ATAGCATTGC CATCTGTTCC ATCAATTGGT AAACATACCG TAACTAGAAA AAGAATTATA	180
TTCAAAATAA AAAATCTCTGA TCGGTACGGC ACAAATCCCA AAAGTGCTAA TATTGCGACA	240
ATTAGGTTAG CTCCACCTCC CCCAAAGAAG TAGAACACCA AATTCCTATC ACTATTTTTT	300
TCATTAGTAA TGTTTCTATT ACTCATTTGA CAATAACCGA ATGCTAATAA CACTGGAAAT	360
TTGAAATATA TTTTTTTTCT GAAATAGAAG AAAAAGGGAG TAGCAAGCAT CTCTAGTTTA	420
TAAGATAAAC ATCTTCCCAC TAAAAATGA CCTAGTTCAT GTAATGTAAT TGATATTAAC	480
GAAATTAATA TCAATCGAAA ATAATAGATT AATGAATCAT TTGGAAAAAT TATCAATAAT	540
AGGAACAATA ACGGAATCAA ACATAAATAT ATGACAGAGT TATTTAATAT TTTCAACATA	600
ATACCATTCC TCTAAACTAT TAGCTTCAA AAGCGTTTTT TTCTCCCAAT ACATCTTCTC	660
AAAATGTTTCG GAATCATAAT TTTCTAAAAT TAATTTTAtG TCTGGTAAGC TCTTTCTTGA	720
TAATCCGTTG TTTTGTACTT AATTTTCCCT TCAAGTACAT CTTCAATTTT ATAAGTTGCC	780
TCCATCAACT GAGCCTCTGC AATATCTTTG AGTGAATTGG TAATGAAAC TTGGTGTAAT	840
ATCTGTCTCts CCATATATGA AAATATATCT CTAAGATATT CTGACACATT ATCAGAGCCG	900
TTACTCTCAG CAACATCTAA TGTTACAACA AACTTTCAG CTAATCGAAA AAGATGGCTC	960
CACCCCCCAA TCCTTTCAAT AAAGTTTTTT GTGTCCACAG ATACGTTTTG TAAATATACA	1020

1192

GGAGAAGAGA	TAATTATAAT	ATCAGACTCT	AATAACTCTT	TTTTTATAAC	ACCTCCATCA	1080
TCAGCATTAC	TTTGCCTATC	AATTCCTTTC	TAAACAACCT	CTTCTGAATC	AGAATTAGAT	1140
ATTTCTAGCT	CTGAATTGAA	AGGTGTCCTG	AAAGATATAT	CAACATTATT	TCTACTAGAA	1200
ATGATACTTG	AAAGTCTCTT	AGTATACTCT	AAAGTCTTAG	AGTTATGATT	TCGCACCTCT	1260
GCATATATAA	ATATTTTATT	CATTTTAATT	CATCCTCTCA	ATTTGAATTT	AGTAGATTTT	1320
TCAAGATAGT	ATGGTACAAA	AACAGACTTT	TGTTGACTCA	CATTATTACA	TATGTTTTGT	1380
ATTAAACCAA	AATCAATACT	ATTTTGGAG	TAATTTTGAT	TTTAGTTTAA	AATCATTTCT	1440
ATAACAGTAG	CATATACCTC	AAGCCGTTTA	GCAATTAGAA	TAGAATTTT	CTTTATTATA	1500
TTATTATCTC	AACGAAAAGC	TACACTATTA	AAAATATTTT	ATAGAATTAC	ATATTAAACT	1560
AGTCAATCTT	GGTATTTTTA	TATTGCTTAA	TGAGTGGACA	CCTCTATTTT	AGAAACAAAA	1620
CTATAAATTA	AGCTAGATTT	CAAGTAATGA	GGGGATAACT	ATCTTTTGT	CATTCTGATT	1680
CAGTGCATA	TACCTTAAAA	AAGTATAAGC	AATACCAGTC	ACACCTGTAT	ACAAAGAAAA	1740
ATCTGGGAAA	TTGCTTGTTT	GGACGATACG	ATACTCTCCT	TCTTTTGATT	TATTCATTAC	1800
AACACTACAC	AATAAAGACT	CCAATCCAT	ACTAGTATCC	ATTTCTTTCA	TGTAGTCGAT	1860
GTAATAAATTT	ATTATGGCCA	TACTTCCATG	GCAAAATGTA	TCATTATCTA	AACTAGCTAC	1920
AATTCCTCT	GGAACACTTT	GGGGATGATT	AACTAATGTC	CCAAATCTC	CACTACACCA	1980
CTTCAAAGAA	TGAATTTTGA	TTTTCTCCCT	AGGAAGTAGT	TGTAATAATA	ATTCTTTATA	2040
TTTTTTAAGT	CTTGCTCACTT	TATAAATATT	TTTTAATGTA	AAAATTACAC	CTGATAGTCC	2100
ATGGCCAAAA	CTATATCCAA	AATTACTATT	ATCTCTCTCG	CTTACATCAT	TATATAGCGT	2160
ATCACCTAAA	CTTAATACTA	GCCTTAGAAC	ACGTCCTTC	TCTATTCCTC	TCCTATAATA	2220
TCTTACCAGT	GTATTAATTA	AAGGTAGAAG	ACCATTAATA	TAGTCAGACT	TGTTTGAAAC	2280
ACTTGCAAAA	TCAGTCTTTT	CAAGCTCAGT	TAAAACACTC	TTTATATAAT	TTAAGCATGC	2340
GAGAGTATTT	GTATCGTAAT	CCTCTATAAT	GGATAGAACA	ATGAAATATC	CTATATCCCC	2400
AGTTAAACCA	AATGTGGTCT	TAGATAAAGA	AACAGATGGC	GGAATTGCAG	ATAACATTTT	2460
ATTGTACAGT	TGAGTATATG	ATGATTTATC	TTTCAATAAT	TTTACATAGT	ACATAAACAG	2520
TAATATPCCA	GCTCTACCCC	TATACATATC	ATTmCCCGTT	TGTTCAAGAC	ACCATTTAGA	2580
ACCTTTAAAA	TTAACAGGTA	TACTCCAAAT	TGGATATTCG	TCATAAATAT	TATTAATAAC	2640
CAAAGAGTCT	GCAATATTTT	CTACTTCATT	ATGCAGAATA	GTAACATAAC	TTTCATTTGG	2700
GAGTTTTTTT	CTATTAGATA	AGTTTAATTT	ATATCCTTTT	TTTCGCTGAT	CAAAGCTTGG	2760
AAAATAAATTT	TCAATGATAT	CAAGTTGCTT	TTCTAAATTT	TCCAAATTAT	TATTAGGTAA	2820

1193

ATATTTTCATA AAATAGTCAT ATCCAGAAAA TTGATGTAGG GAAATAAAAT GATTTCCAAA 2880
 ATCATCGTAG ATTTTCATTGA TATTTGTATC TGTATAAAAA ATCGGAATAT CTAATAACCT 2940
 CATTGTGTTCA CATTGCTTG CTACAATACC TTGATTAGAA AACTTATTGC TCCAGAGATT 3000
 TTCCAATGCT TTTTCTCTAT CTAACATTTT TCATAAAAA TCAGGATGAT ATAAAAAGA 3060
 TAGTACTGAA GCATAGCTAT TTGTGTCTCT AAAAAGTACC CTGTCTTTA AACCATACAA 3120
 GTTTGCTTTT AATAGCATTT TAAATCTTC TGTTTTATTT AACTCTTCAA ATATCAGATA 3180
 AAAATCCCTA AAACCTTTTT TGAAATCTTT TATATACTTA TCAAATCTA TATCACCATC 3240
 CCGAACAGGC AGGTTTTTCC CACCTTCAA ATCAATTTTC CCAATATCAA ACTTTACCTT 3300
 ATCAGTATTT AAATTAATTA AAACCTTGACC AGGGATCCTC TA 3342

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GAGAAAAGAA TGTAAAGAA AAATGATATT GTAGAAGTTG AAATTGTTGA TTTGACCCAT 60
 GAAGGGGCAG GAGTTGCCAA GGTAGATGGT TTGGTCTTTT TTGTAGAGAA TGCTTTACCG 120
 AGTGAAAAA TTCTCATGCG TGTCCTCAAG GTCAATAAAA AGATTGGCTT TGGAAAAGTT 180
 GAAAAATACC TTGTCCAGTC ACCACACCGT AATCAAGATC TAGATTTGGC TTACCTGCGT 240
 TCAGGAATCG CGGATTTAGG ACACCTTTCT TATCCAGAAC AGCTCAAGTT TAAAACCAAG 300
 CAAGTCAAGG ACAGTCTCTA CAAGATTGCT GGAATTGCAG ATGTAGAAGT TGCTGAAACG 360
 CTTGGTATGG AACATCCAGT CAAGTATCGC AATAAGGCGC AGGTGCCCGT TCGTCGAGTG 420
 AATGGTGTCT TGGAAACAGG ATTTTCCCGT AAGAATTCGC ATAACCTCAT GCCCCTTGAA 480
 GATTTCTTTA TCCAGGATCC TGTCATTGAC CAAGTCGTAG TAGCTCTTCG AGACCTGCTC 540
 CGTCGTTTGT ATTTAAAACC TTATGACGAA AAGGAACAGT CTGGATTGAT TCGGAATCTT 600
 GTGGTGCGTC GTGGTCACTA TTCAGGACAA ATCATGGTCG TTTTGGTGAC AACTCGTCCA 660
 AAAGTTTTTC GTGTTGACCA ATGATTGAA CAAGTTATCA AGCAGTCCC AGAGATTGTG 720
 TCTGTATGC AAAATATCAA CGACCAGAAT ACCAATGCGA TTTTGGTAA GGAGTGGCGC 780
 ACTCTTTATG GTCAAGACTA TATTACGGAC CAGATGTTGG GAAATGACTT CCAAATCGCT 840

1194

GGCCAGCCT TTTACCAAGT CAATACTGAA ATGGCGGAGA AACTCTATCA AACAGCCATT 900
 GACTTTGCAG AGTTAAAAA AGATGATGTG ATTATTGATG CCTATTCTGG TATTGGAACC 960
 ATTTGGTTTAT CAGTCGCCAA GCATGTCAAA GAAGTCTACG GTGTTGAACT GATTCCAGAA 1020
 GCAGTAGAGA ATAGCCAGAA GAATGCTTCT TTGAACAAGA TTACTAATGC CCACTATGTC 1080
 TGTGACACGG CTGAAAATGC CATGAAGAAA TGGCTCAAGG AAGGTATTCA ACCAACCGTT 1140
 ATCTTGCTG ATCCTCCACG CAAGGGCTTG ACAGAAAGCT TTATCAAAGC AAGCGCCAA 1200
 ACAGGAGCCG ATCGCATCGC CTATATCTCC TGCAATGTGC CAACCATGGC GCGTGATATT 1260
 AAATAATACC AAGAGTTGGG ATATGAATTG AAGAAAGTCC AGCCGGTGGG TCTATTTCTT 1320
 CAAACGCATC ACGTCGAGAC GGTAGCACCT TTGTCCAAAC TCGATGTCTG TAAGCACATA 1380
 AGTGTGAAA TTAGCTGGA TGAGATGGAT TTGACAAGTG CGGAGAGCAA AGCAACATAT 1440
 GCTCAAATCA AAGAATATGT TTGGAATAA TTTGAATTAA AAGTTTCGAC ATTATATATT 1500
 GCACAGATAA AAAAGAAATG TGGAAATAGAA TTACGAGAAC ATTACAACAA GTCTAAAAAG 1560
 GATAAACAAA TTATTCCACA GTGTACACCT GAAAAAGAAG AAGCCATCAT GGATGCTTTG 1620
 AGACACTTCA AAATGATTTA ATAGAAAAGA ATGACAGTAT ATGACTTTCT GCATTTATTA 1680
 CATTCCTACT TGGTATAGGA ACAGCTATTA TTCCTTTCTT GCAAGGTATC AATTAGAAAA 1740
 TAGGCTCAAT ATAAAGATTG ATAGGATCAT TTTTATATTT AAAGGAGCGT TGAATGATT 1800
 GATAAAGGCA AAAAAAATT TTAGATAAA TTTGCTAAGT TGTATGCCTC TTTTATGAAA 1860
 AAAGATAAAG AGGTTTATGA TAAAGTTTGT GAATATCTTA GTCCTCATTT GAATAAAGAT 1920
 ATGGAGGTGC TTGAACTTGC TTGTTGGTTT CGTGCATAA CAGTTATAGA GGCAAATAGT 1980
 TATGTAATA TAAGGAGTTC AAGACTTCTA CCAAAGTTTA AACTCAAAA AATAAATAGT 2040
 TGGTGTGCTG CTTACAATAT CCATTTAAT AATGGATATT GTAAGCAGCA CCCCcAtGAA 2100
 TTTAAAGATT CTTTAAAGAG TCTTATTTTG TGATGAAAAT TTAATATGTA AATCTCAGAC 2160
 GATAGAAATT AAAAATCTA TCGTCTTTT TATACTCAA ATTAGGAGGT AAAAATGGTA 2220
 AGGATAAGAG GTCCCACTTA AAACAATTTA TGGCAAAATA AGGACGGAAT AACACAACAA 2280
 ATTCTCTAAA ACAAATCACT AAATCAATGT AAGATTGAAT GAAATCAATA TTTATGCTAT 2340
 AATTAAATA ATTTAATGAA GAAAAAAGA GGGATATTAT GGCACCTAAC TATAAACCAT 2400
 TATGGATACA GTTAGCAAAA AAAGGACTAA AGAAAACAGA TGTAATAGCT ATGGCAGGAC 2460
 TTACAACAAA TGTATGGCA CAAATGGGAA AGGATAAACC AATTACATTT AAGAATTTAG 2520
 AAAGAATATG TAAGGCTTTA TCTTGCCTC CTAATGATAT TATTAGTTT GAAGATAATT 2580
 TTAGTGACGA GGAATAGAAA ATGACTTTAA GGACAGAAGA TCAAGTTAGG GATTATGCAA 2640

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GAGAAGTATA GGCTTTAATG AAGTTGAAGA AAACATCAAT CAAGGTACTG GTCAAATAAC	2700
TACTTTTAAT CAATTAGGCT TCAAGGGATA TTCAAATAAG CCAGATGGTT GGTATTTACC	2760
TAAAAATATG AATGATGTAG CAATAATCCT TGAACAAAA TCAGAAGAAA GAGATATTAG	2820
CAAACAAAT TTTATTGATG AGTTAATGAA AAATATAGAC ATAATTTAAC TAAAAATAAA	2880
AACTAGATCC TTTTTTGAAA AAATTATATT ATTAAATTTG TAACGTGATC TATTGACAAT	2940
GATAATTATT ATCGATACAA TAGACTTGAA ATATGTTTAA GGAGTTTTTA TGAAAaCAA	3000
TTTTTCTAA TmGCTATTTT AGCTATGTGT ATAGTTTTTA GCGCTTGTTT TCTAATTCT	3060
GTAAAAATG AAGAAAATAC TTCTAAAGAG CATGCGCCTG ATAAAATAGT TTTAGATCAT	3120
GCTTTCGGTC AACTATATT AGATAAAAAA CCTGAAAGAG TTGCAACTAT TGCTTGGGGA	3180
AATCATGATG TAGCATTAGC TTTAGGAATA GTTCTGTGTT GATTTTCAA AGCAAATTAC	3240
GGTGTAAGTG CTGATAAAGG AGTTTACCA TGGACAGAAG AAAAAATCAA AGAACTAAAT	3300
GGTAAAGCTA ACCTATTTGA CGATTTGGAT GGACTTAACT TTGAAGCAAT ATCAAATTCT	3360
AAACCAGATG TTATCTTAGC AGGTATTCT GGTATAACTA AAGAAGATTA TGACACTCTA	3420
TCAAAAATTG CTCCTGTAGC AGCATACAAA TCTG	3454

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CGGGAGTATA CTTAATATAA TTATAGTCTA AAAATGACTA TCAGAAAAGA GGTAATTTA	60
GATGAATAAG AAAAAATGA TTTTAACAAG TCTAGCCAGC GTCGCTATCT TAGGGGCTGG	120
TTTGTGTTACG TCTCAGCCTA CTTTGTGTAAG AGCAGAAGAA TCTCCACAAG TTGTCGAAAA	180
ATCTTCATTA GAGAAGAAAT ATGAGGAAGC AAAAGCAAAA GCTGATACTG CCAAGAAAGA	240
TTACGAAACG GCTAAAAAGA AAGCAGAAGA CGCTCAGAAA AAGTATGAAG ATGATCAGAA	300
GAGAAGTGA GAGAAAGCTC GAAAAGAAGC AGAAGCATCT CAAAAATTGA ATGATGTGGC	360
GCTTGTGTTT CAAAATGCAT ATAAAGAGTA CCGAGAAGTT CAAAATCAAC GTAGTAAATA	420
TAAATCTGAC GCTGAATATC AGAAAAAATT AACAGAGGTC GACTCTAAAA TAGAGAAGGC	480
TAGGAAAGAG CAACAGGACT TGCAAAAATA ATTTAATGAA GTAAGAGCAG TTGTAGTTCC	540

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TGAACCAAAT	GCGTTGGCTG	AGACTAAGAA	AAAAGCAGAA	GAAGCTAAAG	CAGAAGAAAA	600
AGTAGCTAAG	AGAAAATATG	ATTATGCAAC	TCTAAAGGTA	GCACTAGCCA	AGAAAGAAGT	660
AGAGGCTAAG	GAACCTGAAA	TTGAAAAACT	TCAATATGAA	ATTTCTACTT	TGGAACAAGA	720
AGTTGCTACT	GCTCAACATC	AAGTAGATAA	TTTGAAAAAA	CTTCTTGCTG	GTGCGGATCC	780
TGATGATGGC	ACAGAAGTTA	TAGAAGCTAA	ATTAAAAAAA	GGAGAAGCTG	AGCTAAACGC	840
TAAACAAGCT	GAGTTAGCAA	AAAAACAAAC	AGAACTTGAA	AAACTTCTTG	ACAGCCTTGA	900
TCCTGAAGGT	AAGACTCAGG	ATGAATTAGA	TAAAGAAGCA	GAAGAAGCTG	AGTTGGATAA	960
AAAAGCTGAT	GAACTTCAA	ATAAAGTTGC	TGATTTAGAA	AAAGAAATTA	GTAACCTTGA	1020
AATATTACTT	GGAGGGGCTG	ATCCTGAAGA	TGATACTGCT	GCTCTTCAA	ATAAATTAGC	1080
TGCTAAAAAA	GCTGAGTTAG	CAAAAAACA	AACAGAAGCTT	GAAAAACTTC	TTGACAGCCT	1140
TGATCCTGAA	GGTAAGACTC	AGGATGAATT	AGATAAGAA	GCAGAAGAAG	CTGAGTTGGA	1200
TAAAAAAGCT	GATGAAGTTC	AAAATAAAGT	TGCTGATTTA	GAAAAAGAAA	TTAGTAACCT	1260
TGAAATATTA	CTTGGAGGGG	CTGATTCTGA	AGATGATACT	GCTGCTCTTC	AAAATAAATT	1320
AGCTACTAAA	AAAGCTGAAT	TGGAAAAAAC	TCAAAAAGAA	TTAGATGCAG	CTCTTAATGA	1380
GTTAGGCCCT	GATGGAGATG	AAGAAGAAAC	TCCAGCGCCG	GCTCCTCAAC	CAGAGCAACC	1440
AGCTCCTGCA	CCAAAACCAG	AGCAACCAGC	TCCAGCTCCA	AAACCAGAGC	AACCAGCTCC	1500
TGCACAAAAA	CCAGAGCAAC	CAGCTCCAGC	TCCAAAACCA	GAGCAACCAG	CTCCAGCTCC	1560
AAAACCAGAG	CAACCAGCTA	AGCCGGAGAA	ACCAGCTGAA	GAGCCTACTC	AACCAGAAAA	1620
ACCAGCCACT	CCAAAAACAG	GCTGGAAACA	AGAAAACGGT	ATGTGGTATT	TCTACAATAC	1680
TGATGGTTCA	ATGGCAATAG	GTTGGCTCCA	AAACAACGGT	TCATGGTACT	ACCTAAACGC	1740
TAACGGCGCT	ATGGCAACAG	GTTGGGTGAA	AGATGGAGAT	ACCTGGTACT	ATCTTGAAGC	1800
ATCAGGTGCT	ATGAAAGCAA	GCCAATGGTT	CAAAGTATCA	GATAAATGGT	ACTATGTCAA	1860
CAGCAATGGC	GCTATGGCGA	CAGGCTGGCT	CCAATACAAT	GGCTCATGGT	ACTACCTCAA	1920
CGCTAATGGT	GATATGGCGA	CAGGATGGCT	CCAATACAAC	GGTTCATGGT	ATTACCTCAA	1980
CGCTAATGGT	GATATGGCGA	CAGGATGGGC	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2040
CGCTAACGGT	GCTATGGCTA	CAGGTGGGC	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2100
CGCTAACGGT	TCAATGGCAA	CAGGTGGGT	GAAAGATGGA	GATACCTGGT	ACTATCTTGA	2160
AGCATCAGGT	GCTATGAAAG	CAAGCCAATG	GTTCAAAGTA	TCAGATAAAT	GGTACTATGT	2220
CAATGGCTTA	GGTGCCCTTG	CAGTCAACAC	AACTGTAGAT	GGCTATAAAG	TCAATGCCAA	2280
TGGTGAATGG	GTTTAAGCCG	ATTAATTTAA	ATCATGTTAA	GAACATTTGA	CATTTTAATT	2340

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TTGAAACAAA GATAAGGTTC GATTGAATAG ATTTATGTTC GTATTCTTTA GGTACCTATC 2400
 TTATGATTTTC AGGAAATGTC ATTAAAAAAA CGACTCATTT TCTCTAACCT GAAAAATAGA 2460
 TTAGAGAAAA TGGGTTGTFTT TATCTATTAT AGTTATTTGA ATGAAGmTAA GAAGAAGGTA 2520
 TACTCACATC ATTCACATAA TCTGTATATT GACTATAAGT TTTAAAAAAC AATTTTTAAG 2580
 CTCTTCCTTG TCTTCTCTAA CCAAGCGTGT TATAATGAAT ACTGCTCAAG CGACCTTCAA 2640
 TCGTGAAGCA CACACGACCT TCAATCGTGA ATAAACGAAT AGATGGGAGA CTTACCATGA 2700
 GTGATAACTC TAAAACACGT GTTGTCTGGG GGATGAGTGG TGGTGTGAT TCGTCGGTGA 2760
 CGGCTCTTTT GCTCAAGGAG CAGGGCTACG ATGTGATCGG TATCTTCATG AAGAACTGGG 2820
 ATGACACAGA TGAAAACGGC GTCTGTACGG CGACCGAAGA TTACAAGGAT GTGGTTGCCG 2880
 TGGCAGACCA GATTGGCATT CCCTACTACT CTGTCAATTT TGAAAAGAG TACTGGGACC 2940
 GCGTTTTTGA GTATTTCTTA GCGGAATACC GTGCAGGGCG CACGCCAAAT CCGGACGTTA 3000
 TGTGCAACAA GGAAATCAAG TTCAAGGCCT TTTTGGACTA TGCCATAACC TTGGGGGCG 3060
 ACTATGTAGC GACTGGGCAT TATGCTCGAG TGGCGCGTGA TGAGGATGGT ACCGTTTACA 3120
 TGCTTCGTGG CGTGGACAAT GGCAAGGATC AGACCTATTT CCTCAGCCAA CTTTCGCAAG 3180
 AACAACTTCA AAAAACCATG TTCCCACTAG GACATTTGGA AAAGCCTGAA GTACGCAGAC 3240
 TAGCAGAAGA AGCAGGCCTT TCGACTGCTA AGAAGAAAGA CTCGACAGGG ATTTGCTTTA 3300
 TCGGAGAAAA GAACTTTAAA AACTTTCTCA GCAACTACCT GCCAGCTCAG CCTGGTCGCA 3360
 TGATGACTGT GGATGGTCGC GATATGGGCG AGCATGCAGG TCTTATGTAC TATACAATCG 3420
 GTCAGCGTGG CGGACTCGGT ATCGGTGGGC AACACGGCGG TGACAATGCC CCTTGGTTTCG 3480
 TTGTTCGAAA AGATCTAAGC AAGAATATTC TCTATGTAGG ACAAGGATTC TACCATGATT 3540
 CGCTCATGTC AACTAGCCTA GAAGCCAGTC AAGTCCACTT TACTCGTGAA ATGCCAGAAG 3600
 AGTTTACGCT AGAATGTACG GCTAAATTC GTTACCGTCA GCCTGACTCT AAGGTGACCG 3660
 TTCATGTCAA AGGAGAAAAG ACAGAGGTCA TCTTTGCGGA ACCACAACGC GCGATTACAC 3720
 CAGGACAGGC AGTTGTCTTT TACGATGGCG GG 3752

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TATTTATATT	TTTTTATCTC	TGGCATACTT	TGATACCTTT	TTAGACTTAA	AGTCTTTAAT	60
AGTGCCTTTC	CACCTCTTTT	TATCTATAAA	GATTCTCCTA	CATCATAAAT	CATTTTTTTA	120
TTTAAACCTT	TCTGCTCTAG	TTTGTCTTTA	TCTTCTTCAT	ACCATTTTAA	GATTGTCACA	180
TAGTGGTTTT	GATAGGTCTT	ACCACTGCTT	TCCATGTATC	TGGATAGTTT	ATTTATCATT	240
ATATCTGTGT	GTGAGTTTAA	TTTTTCTTTT	AGATTTTTAT	ATCTTCTTTT	GCTTAACCTT	300
ACATTTTTGA	ATCTCCATA	AAAAATGGGG	GTGGACTTTT	TATCTATCTC	TCCCTCTCTC	360
TCTTTATCTA	TCTCTATATC	TTCCATGTA	ATTCCAATCT	GGAGTACCTC	TACTGTCTAT	420
CGGTAATTTA	ATTTTGATAT	CTGGCAATAC	TGTGCTAGAT	ATTTGATCTT	TATATTCAGT	480
ATTTTTTAAA	GCTTGCCFAA	TAATGAAGT	TAAATAGAAT	GCTACTTCTT	TATTCAATTC	540
TTTATTTTTT	AATTTTAAAC	AATGAATTTT	CATATCTAGG	CTTGCTTTAT	ATTTATGATA	600
AAAGACTGCT	CCTAAAAATG	AAACAGATAT	AAAATTTTCA	AAAACCTCTAT	AATTTTTTATC	660
ATCTATATCT	TCGTAGTAAC	CTAAGATACC	ATTGTCAATA	TTTGTAGCAC	TAATTCAGG	720
AGTTTTTCCA	TCGAGTAAAT	ATCTTTTGG	AATAGATGAG	CCTGTTGGTA	CCTAACTCGA	780
TTTCCCCTTT	TTTTCGGTAA	TAAATATTTT	TTTTTATTTT	GTGTCTGAT	ATTTTTCTTA	840
CCTGTCCTTT	GTAGGATGAG	TATTTTCTAG	ATTTTCYFGA	ATAACTTTTT	ACTTGAAGTT	900
TTAGCTTTTG	AACTAGTCGT	TGTACTTTCT	TTTTGTTTAT	TATCAGTCCT	GATCTTTTTA	960
ATATTGCTGT	TATTCTCTAT	ATCCTATTTT	TCATTCATGA	TATTCTTTTA	CTAATTTTAT	1020
CTTAAATPCT	GTGCTGTATT	TGCCATTAAT	AAACTGACCT	CCTTTAGTTA	GTTTTTGGC	1080
CTAACTTTTG	AGGGTCAGTT	CAAAATTTGC	GACTTTTTAAA	TGAATCCAA	TATTCAATTA	1140
TTAAGAGTTA	ACATGGTGCT	TGCCAATAGG	AATCATTAGA	GGCGAATTGG	AAATAGGGTC	1200
ACGTATAAAT	TTTGCTTCAA	GATTAAAGAT	ATCTTTAACT	AGTTTATCAT	TTAGTATATC	1260
TTCAGGCTTT	CCCTCTGCAA	CAAGTTTACC	TTCTTTAATT	GCAAATAGGT	AATCAGCGTA	1320
TCTTGCTGTT	AGATTTATAT	CGTGCAAAAT	CATGCAAAATG	GTTGTCTTAT	ATTTTTGGTT	1380
TAGATCAGTC	AAGAGGTCTA	ATAGTTCAT	TTGATATGAG	ATATCCAAGT	AAGTAGTTGG	1440
CTCATCTAAA	AGTAGGATAC	TTGTATCTTG	GGCTAGGGCT	AGAGCTATCC	ATACTCTTTG	1500
CCTTTGACCC	CCAGAAAGTT	CTTCAACTAG	GTTATTTGCT	AGATCTTCAA	CATTGGCCTT	1560
AACCATTGAT	CTGTTTATTA	TTTCAAGGTC	ATCTTTTCCA	AGACTCTTAA	AAGGCTTTCT	1620
GTAGGGGAAA	CGACCACGGC	TTACAAGATC	AGCTACTGTT	ATTGATTCAG	GGATTATTTG	1680
AGATTGAGGT	AATATAGCTA	TGTGTTTTC	TAAATCTTTT	TCTTTATAAG	AATTAATTGA	1740

TTTATTATCA AGCAATACTT CTCCCTCTAA TGGCTTTATA AGTCGAGACA AGGTTTTAAT 1800
 GAGTGTGAT TTCCCACAAC CATTTGACCC AATAATAACT GATATTTTTT CTCAGGTAT 1860
 TTTTATATTT ATATTTTCCA AGATTATTTT TTCATCATAA CCGCAGGTAA GATTATTTGA 1920
 CCACAGACCT TTCATTATAT ATTCCCTCTG TTCATTTTTA TTAGTAAGTA TATTAAGTAT 1980
 GGTGAACCTA ACAAGCCAGT TACAACACCT ACTGGATATC TAGCTGGTAA AATATTTTGA 2040
 GAGAATATGT CTGATAACAA AACTAGTAAA ATTCCAACCA ATCCAGCTAA TATTGGGCTT 2100
 CTTTTCTTGC CAATATTTAA GGCTATGGGA CCAGCTAAAA AAGATATACA AGCTATTGGT 2160
 CCTGTAAATG AAGTAGAAAA AGCAGTTAAA GATACAGCGC AAAAAATTA AACAAGCCTT 2220
 GAAAGCTCGG GATTTGCTCC AAGTCCGATT GCTATTTCTT CACCAAGTTC AATAATTTCT 2280
 AGTCTTTTAT TAAAAAATAA AACTAATATA GTAGCAATAA TACTTACTAT TAGAACAAGA 2340
 GGTATGTCAT CTAAC TTTGT AAAAGATAAA GAGCCACTGA GCCATCTCAT AACTTCTTGT 2400
 AATTCATATC TTGCTACTTT CAACAATAAA AATGAGGTGC CTGCTCTTGT GACAGCTTGA 2460
 AAACCAATAC CTAATATTAT CAGTCTTGCT GCTGAAAAAC CATCTTTTTT AGCTAGTAAA 2520
 AATAATATTA AAGATGATGT TAGTCCACAA GTTATTGAAA TAATTCAGT AGTTAAACTA 2580
 TTTGTTTTTA ATACCAATAT GCAAAAGACC GCTGCAATAG ATGAAGAAGT TGTGACACCG 2640
 ATTATATCAG GACTTGCAAG AGGATTTCTT AACATAGTTT GAAAGATAAA TCCTGCCAAT 2700
 CCAAAGACC AGCCAGCTAT AATCCCTGCT AATAATTTTG GTAATCTAAT TTCCATAATC 2760
 GAAAACTAG CTCCAGGAAC AGTTTCACTA TTTAAGACTT TAATCAAAGT TGAAAAAGAA 2820
 TAACTTTCAT CTCCGATAAG TAAAATGAAA AATGATAGAC TGATTATTAT TAATAAAAAT 2880
 AGTGAGGAAA ATAGTGTTAT TCTATTTTTT CTTTTTTGAA TACCTATAAT TAAATTTTGC 2940
 ATTAGTTATT AACCCCTCTA TTTTTCATAG TTACATAAAT AAGTACTGGA CCCCCGATTA 3000
 TTGCAGTAAT TATCCCTACT TCAATTTTAC CTGGTTTACC TAACATACGG CCGATTATAT 3060
 CACATATAAG CAAGAGCTCT GCACCTATAA AAGATGAAGA AATGGTCATT GTGCGTATAT 3120
 CTTTGCTTAT AAATAAGCCA CAAAAGTGAG GAACTATAAG ACCTACGAAG CCAATAGGTC 3180
 CACCAATTGC AGTAATACTT GAACATAAAA GCACACTTGC AATTATGCA AGTGATCTTA 3240
 TCCTATTAAC ATTAACCTCA AGACCAACAG CCATTTTCATC ACCCATAGcT AAAGCGTTTA 3300
 AATCTGATGA AATAAATATA GCTATCAAGT GACCTAAAAT TATAAAAGGT AGTAGTGTAG 3360
 ATATAGAAGA TAATGTAGCT GCTCCAAGGC TACCTATTTG CCAAATCTA AATTTGTCTA 3420
 AGACGTTATT ATTCGGTAAA ATTAATAAAC TTACAAAACCT GCTTAAAGCC ATACTAACAC 3480

1200

AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC 3540
 GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATGCG 3580

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGGCA GATGGGCGTG ATATGTGTGC 60
 TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT 120
 CAATATTTTA ACCCGTCTTC ATCGCTCACG TCCGTTGATG ACACAATTGA GTCGTTTGGG 180
 CTATGCCATG GAAACACCTG TAGATTTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC 240
 TTTGCGTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCCAGG 300
 ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA 360
 GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT 420
 GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTAGAAA CATCAGTGGA AGGAATGGTT 480
 GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATTGTATT GGTATGGTCA 540
 ATTTGCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTTAG AAAATGTCAA 600
 TCGGGAGATT CATGGTTTGC GTCATTTCCG AGACAAGTAT GGAAAGAGAA GATGAGAGTT 660
 AGAAATCGTA AAGGGGCAAC AGAATTAATA GAGGCAAATC CCCAGTATGT GGTCCCTCAAT 720
 CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGGCA ATGATAATCC CATTGATGTG 780
 GAAGTTGGAA GTGGAAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC 840
 AACTATATCG GGATTGATAT TCAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT 900
 GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGGTAGATG GTTCTGACTT AACTGACTAC 960
 TTTGAAGACG GTGAGATTGA TCGCTTGTAT CTGAACTTTT CAGATCCATG GCCGAAAAAA 1020
 CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTCAA ACGTATCTTG 1080
 CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTTTGA GTACAGTTTA 1140
 GTGAGCTTTT CTCAATATGG CATGAAACTC AATGGTGTCT GGTTAGATTT GCATGCCAGT 1200
 GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GGGGCAAGTT 1260
 ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT 1320

1201

TTGCTTTACA	TAAGTTGGCA	AACGTGCTAT	ACTGATAGTA	AGAATATGAA	AAGTGAGGCG	1380
GGGAAATATC	TTGCCTCTT	GCTTATGAGG	AGGTGGACGC	AATCGCAACA	ATCGTAGAAT	1440
TAGTCAGAGA	AGTTGTAGAA	CCTGTCATAG	AAGTCCTTT	TGAACTCGTG	GATATCGAGT	1500
ATGGAAAGAT	TGGCAGTGAC	ATGATTCTCA	GTATTTTTGT	AGATAAACCC	GAAGAATTAC	1560
CTTGAACGAC	ACGGCAGACT	TGACAGAAAT	TATCAGTCCT	GTCCCTAGACA	CCATCAAGCC	1620
AGATCCCTTC	CCAGAACAAT	ATTCCTAGA	AATTACCAGT	CCAGGTTTGG	AACGTCCTTT	1680
GAAAACCAAG	GATGCCGTCG	CTGGAGCGGT	TGGAAAATAC	ATCCATGTCG	GGCTCTACCA	1740
AGCCATCGAT	AAGCAAAAGG	TCTTTGAAGG	AACCTTGTTG	GCCTTCGAAG	AGGACGAGTT	1800
GACTATGGAA	TATATGGACA	AGACGCGTAA	GAAAACCGTC	CAAATTCAT	ACAGTTTAGT	1860
ATCAAAGCA	CGTTTAGCAG	TTAAATTATA	GAAAAGAAA	GGATAGCTTT	TGAGGATTCA	1920
AAAGTGAAGA	AAACATGAGT	AAAGAAATGC	TAGAGGCCTT	CCGCATTTTG	GAAGAAGACA	1980
AGGGAATCAA	AAAAGAAGAT	ATCATCGACG	CAGTAGTAGA	GTCGCTTCGT	TCCGCTTATC	2040
GCAGACGCTA	TGGTCAGTCA	GACAGCGTAG	CTATTGACTT	CAACGAAAAA	ACAGGTGACT	2100
TTACAGTTTA	TACTGTCCGT	GAAGTTGTTG	ATGAAGTATT	TGATAGCCGT	TTGGAAATCA	2160
GCTTGAAAGA	TGCTCTTGCC	ATTAATTCAG	CTTATGAACT	TGGAGACAAA	ATCAAGTTTG	2220
AAGAAGCACC	AGCTGAGTTF	GGTCGTGTAG	CAGCCCAATC	TGCCAAACAA	ACCATCATGG	2280
AAAAAATGCG	CAAGCAAACA	CGTGCCATCA	CTTACAATAC	TTACAAAGAA	CATGAGCAAG	2340
AAATCATGTC	TGGTACAGTA	GAACGCTTTG	ACAACCGCTT	TATCTATGTC	AACCTTGGTA	2400
GCATCGAAGC	CCAATTGTCA	AAACAAGACC	AAATTCCTGG	AGAAGTTTTT	GCTTCTCATG	2460
ATCGTATCGA	AGTTTATGTT	TACAAGGTTG	AAGACAACCC	TCGTGGTGTG	AACGTCTTTG	2520
TTAGCCGTAG	TCATCCAGAA	ATGATCAAAC	GTTTAATGGA	GCAAGAAATF	CCAGAAGTTT	2580
ATGATGGAAC	TGTTGAAATC	ATGAGCGTGG	CTCGTGAAGC	AGGTGACCGT	ACGAAGGTTG	2640
CTGTTCTGAG	CCACAATCCA	AACGTGGATG	CTATCGGTAC	AATCGTTGGA	CGTGGTGGTG	2700
CTAATATCAA	GAAGATTACT	AGCAAATTC	ACCCAGCTCG	TTACGATGCT	AAAAATGACC	2760
GCATGGTACC	AATCGAAGAA	AATATCGATG	TTATCGAGTG	GGTAGCAGAT	CCAGCTGAAT	2820
TTATCTACAA	TGCCATCGCT	CCTGCTGAGG	TTGACCAAGT	TATCTTTGAT	GAAAACGACA	2880
GCAAACGTGC	CTTGGTGGTT	GTTCCAGATA	ACAAGCTTTC	TCTTGCCATT	GGTCGTCGTG	2940
GACAAAACGT	GCGCTTGGCG	GCTCACTTGA	CTGGTTACCG	TATCGATATC	AAGTCTGCTA	3000
GCGAATTTGA	AGCCATGGAA	GACGCTGCTT	CAGTAGAGTT	GGAAGTAGAA	AACGATACTG	3060

1202

TAGAAGAATA	AAAGCTGCTA	GAGGAGGGAA	AGATGAAAAC	AAGAAAAATC	CCTTTGCGCA	3120
AGTCTGTTGT	GTCTAACGAA	GTGATTGATA	AGCGTGATTT	GCTCCGCATT	GTCAAGAACA	3180
AGGAAGGACA	AGTCTTTATT	GATcCTACGG	GCAAGGCCAA	TGGCCGCGGC	GCTTATATCA	3240
AACTAGACAA	TGCAGAAGCC	CTAGAGGCGA	AAAAGAAGAA	GGTCTTTAAC	CGCAGCTTTA	3300
GCATGGAAGT	GGAAGAAAGC	TTTTATGACG	AGTTGATCGC	TTATGTGGAT	CACAAAGTGA	3360
AAAGAAGAGA	GTGCGGACTT	GAATAAGCAA	AAGATAAGTA	ATCTCTTGGG	GCTTGCTCAG	3420
CGAGCAGGGC	GCATCATATC	GGGTGAAGAA	TTGGTGGTCA	AGGCCATTCA	AGACGGCAAG	3480
GCCAAGTTGG	TCTTTCTAGC	TCATGATGCT	GGACCCAATC	TGACCAAGAA	GATTCAAGAT	3540
AAAAGTCATT	ATTATCAAGT	AGAAATTGTA	ACCGTGTTTT	CAACACTGGA	ATTAAGCATA	3600
GCAGTCGGGA	AATCGAGAAA	GGTTTTGGCT	GTAACAGATG	CTGGATTTAC	AAAGAAAATG	3660
AGGTCTCTTA	TGGAATAGAA	GAGGAGGACA	TGATTTGTCT	AAGAAAAGAT	TGTACGAAAT	3720
CGCAAAAGAA	CTTGGAAGAA	AAAGTAAAGA	AGTTGTAGCG	CGTGCAAAAG	AGTTGGGCTT	3780
GGATGTGAAA	AGCCACTCAT	CAAGTGTTGA	AGAAGCTGTC	GCTGCAAAAA	TTGCTGCCAG	3840
CTTTAAGCCT	GCAGCTGCTC	CGAAAAGTAGA	AGCAAAACCT	GCAGCCCAA	AAGTAAGTGC	3900
AGAAAAGAAA	GCCGAAAAAT	CTGAGCCAGC	TAAACCAGCT	GTAGCTAAGG	AAGAGGCAAA	3960
ACCTGCAGCC	CCAAAAGCAA	GTGCAGAAAA	GAAAGCCGAA	AAGTCTGAAC	CAGTAAAACC	4020
AGCTGTAGCC	AAGGAAGAGG	CAAACCAGC	TGAGCCAGTC	ACTCCGAAAA	CAGAAAAAGT	4080
AGCGGCTAAA	CCGCAAAGTC	GTAATTTCAA	GGCTGAGCGT	GAAGCACGTG	CTAAAGAGCA	4140
GGCAGAGCGA	CGCAAGCAAA	ATAAGGGCAA	TAACCGTGAC	CAACAACAAA	ACGGAAACCG	4200
TCAGAAAAAC	GACGGCCGTA	ATGGTGGAAA	ACAAGGTCAA	AGCAACCGCG	ACAATCGTCG	4260
CTTTAATGAC	CAAGCTAAGA	AGCAGCAAGG	TCAGCAAAAA	CGTAGAAATG	AGCGCCGTCA	4320
GCAAGAGGAT	AAACGTTCAA	ATCAAGCGGC	TCCACGTATT	GACTTTAAAG	CCCCTGCAGC	4380
AGCCCTAAAA	GCAGAGCAAA	ATGCAGAGTA	CGCTCGTTCA	AGTGAGGAAC	GCTTCAAGCA	4440
GTATCAGGCT	GCTAAAGAAG	CCTTGGCTCA	AGCTAACAAA	CGCAAGGAAC	CAGAGGAAAT	4500
CTTTGAAGAA	GCGGCTAAGT	TAGCTGAACA	AGCACAGCAA	GTTCAAGCAG	TGGTTGAAGT	4560
CGTCCCTGAG	AAAAAAGAAC	CTGCAGTGGG	TACACGTCGT	AAAAACAAG	CTCGACCAGA	4620
CAAAAATCGT	GACGATTATG	ATCATGAAGA	AGATGGTCCT	AGAAAACAAC	AAAAGAATCG	4680
AAGTAGTCAA	AATCAAGTGA	GAAATCAAAA	GAATAGTAAC	TGGAATAACA	ACAAAAAGAA	4740
CAAAAAAGGC	AATAACAAGA	ACAACCGTAA	TCAGACTCCA	AAACCTGTTA	CGGAGCGTAA	4800
ATTCCATGAA	TTGCCAACAG	AATTTGAATA	TACAGATGGT	ATGACCGTTG	CGGAAATCGC	4860

1203

AAAACGTATC AACCGTGAAC CAGCTGAAAT TGTAAAGAAA CTTTTCATGA TGGGTGTCAT	4920
GGCCACACAA AACCAATCCT TGGATGGGGA AACAATTGAA CTCCTCATGG TGGATTACGG	4980
TATCGAAGCC AAACAAAAGG TTGAAGTGGA TAATGCTGAC ATCGAACGTT TCTTTGTCGA	5040
AGATGGTTAT CTCAATGAAG ATGAATTGGT TGAGCGTCCA CCAGTTGTTA CTATCATGGG	5100
ACACGTTGAC CACGGTAAAA CAACCTTTT GGATACTCTT CGTAACTCAC GTGTTGCGAC	5160
AGGTGAAGCA GGTGGTATTA CTCAGCATAT CGGTGCCTAC CAAATCGTGG AAAATGGTAA	5220
GAAGATTACC TTCCTTGATA CACCAGGACA CGCGGCCCTT ACATCAATGC GTGCGCGTGG	5280
TGCTTCTGTT ACCGATATTA CGATCTTGGT CGTAGCGGCA GATGACGGGG TTATGCCTCA	5340
GACTIONTAA GCCATCAACC ACTCAAAAAGC AGCTAACGTT CCAATCATCG TAGCTATTAA	5400
CAAGATTGAT AAACCAGGTG CTAACCCAGA ACGCGTTATC GGTGAATTGG CAGAGCATGG	5460
TGTGATGTC ACTGCTTGGG GTGGAGATTC TGAATTTGTT GAAATTTCCG CTAAATTCAA	5520
CCAAAATATC GAAGAATTGT TGGAAACAGT CCTTCTTGTG GCTGAAATCC AAGAACTCAA	5580
AGCAGACCCA ACAGTTTCGTG CGATCGGTAC GGTATCGAA GCGCGCTTGG ATAAAGGAAA	5640
AGGTGCGGTC GCAACCTTC TTGTACAACA AGGTACCTTG AATGTTCAAG ACCCAATCGT	5700
TGTCGGAAT ACCTTCGGTC GTGTCCGTGC TATGACCAAC GACCTTGGTC GTCGTGTAA	5760
AGTTGCTGGA CCATCAACAC CAGTCTCTAT CACAGGTTTG AACGAAGCAC CGATGGCGGG	5820
TGACCACTTT GCCGTTTACG AGGATGAAAA ATCTGCGCGT GCAGCAGGTG AAGAGCGTGC	5880
CAAACGTGCC CTCATGAAAC AACGTCAAGC TACCCAACGT GTTAGCCTTG AAAACCTCTT	5940
TGATACCCTT AAAGCTGGG AACTCAAATC TGTTAATGTT ATCATCAAGG CTGATGTACA	6000
AGGTTCTGTT GAAGCCCTTT CTGCCTCACT TCAAAAAGATT GACGTGGAAG GTGTCAAAGT	6060
GACTATCGTC CACTCAGCGG TCGGTGCTAT CAACGAATCA GACGTGACCC TTGCCGAAGC	6120
TTCAAATGCC TTTATCGTTG GTTTCAACGT ACGCCCTACA CCACAAGCTC GTCAACAAGC	6180
AGAAGCTGAC GATGTGAAA TCCGTCTTCA CAGCATTATC TACAAGGTTA TCGAAGAGAT	6240
GGAAGAAGCT ATGAAAGGGA TGCTTGATCC AGAATTTGAA GAAAAAGTTA TTGGTGAAGC	6300
GGTTATCCGT GAAACCTTCA AGGTGTCTAA AGTGGGAACT ATCGGTGGAT TTATGGTTAT	6360
CAACGGTAAG GTTGCCCGTG ACTCTAAAGT CCGTGTATC CGTGATGGTG TCGTTATCTA	6420
TGATGGTGAA CTCGCAAGCT TGAAACTA TAAAGACGAC GTGAAAGAAG TGACAAACGG	6480
TCGTGAAGGT GGATTGATGA TCGACGGCTA CAATGATATT AAGATGGATG ATGTGATTGA	6540
GGCGTATGTC ATGGAAGAAA TCAAGAGATA AGATTTTGTG CTCCTTCTT AGGTGGTGAG	6600

1204

GGACGCAAGC	AAACCGATGG	TTCATTGCT	TATTTTTGAG	CCTAGGGTCT	CAAAAATCCC	6660
CTGTGATGGG	ACTGATAAAT	CAGTTCCATC	ACTTTCACCA	CGGCGAAAGA	AGCAGATGAC	6720
TTCAAATTGA	ACTTCGT TTC	AATTTAAACT	GAAAATCAAG	AAGTTTAAAA	TAGCTAGGTC	6780
TGCTGGCCTA	GCTTTTG GTT	CAAAGTAGAG	AAAGGAATAT	CATGGCAAAT	CATTTCCGTA	6840
CAGATCGTGT	GGGCATGGAA	ATCAAGCGTG	AAGTCAATGA	GATTTTGCAA	AAGAAAGTCC	6900
GTGATCCACG	TGTCCAAGGT	GTGACCATCA	TAGATGTTCA	GATGCTGGGT	GACTTGCTGTG	6960
TTGCCAAGGT	TTATTACACC	ATTTTGAGTA	ACCTTGCTTC	GGATAACCAA	AAAGCCCAAA	7020
TCGGGCTTGA	AAAAGCAACT	GGTACCATCA	AACGTGAACT	TGGTCGCAAT	TTGAAATTGT	7080
ACAAAATCCC	AGATTTGACC	TTCGTCAAAG	ACGAGTCCAT	CGAGTATGGA	AACAAGATTG	7140
ACGAGATGCT	ACGCAATCTG	GATAAGAACT	AAAGAAGAGG	GGTTGCCCTT	CTTTTTTGGT	7200
GGAGGAAAAAT	AGGTTGAATT	TGAAATGGAA	AAATATTCTT	TTATAATAGA	TTGAAACTAG	7260
AATAGTACGC	CTCTACTTCT	AAAATATTGT	TAGAAATCGA	TTTACTGTC	CTGATCGATT	7320
TGTCCTGTTC	TTGTTTCATT	TTAATATAAA	AAAGGGATTC	TGTATTTTTT	AATGTTATCT	7380
AATTAGAAAA	TGCTTTTTTT	GTAGGAAATA	TAATATGATA	AGGTGCAAAA	AAGAAATAAG	7440
GAGTTTGTAT	ATGGCTGAAC	AAGACTTAGC	TATGCAAGTA	TTGCAACAAG	TGGTGAAACT	7500
ACCTGTGTGT	AAGGTTGATC	GTTTCGAAAT	TTTAGTGGAT	AAGTTTTCCA	AAGAATTGGA	7560
TCCAAAAGAT	ATTCCTACCT	TATTGGAACA	AGGTCCAACG	ACTCTTCTAT	CTCAAGAAAT	7620
ATTAGATCGT	GTAGCTAATG	CTTGTATTCG	GGACAATGTA	TTATTAGCGA	GTGGGACTTC	7680
TGTTTTGGCA	GGATTACCTG	GAGGGCTTGC	TATGGCAATT	ACCATTCCAG	CTGATGTGGC	7740
TCAATTTTAT	GCTTCTCTC	TGAAATTGGC	TCAAGAATTA	GGTTATATTT	ATGGTTATGA	7800
GGATCTTTGG	GCTTCACGAG	AGGAGTTGAG	TGAAGATGCT	CAAAAATACC	TCTTGCTTTA	7860
TCTAGGCGTA	ATGTTAGGGG	TGAATGGAAC	CGCTGCTTTG	CTACGTGTTG	GTAGTATAAC	7920
AATTGCCAAA	CAGGTAATGA	AAATAGTGCC	TAATAAAGCT	TTAACAAAAGA	CGCTTTGGTA	7980
CCCTATTTTG	AAAAAAGTCT	TAAAAATATT	TGGTGTGAAT	CTTACCAAGG	GAGGGTTGGC	8040
CAAAGGAATG	GGGAAATTTA	TTCCTATCTT	GGGTGGTATC	ATTTTCAGGTG	GTTTAACCTT	8100
TGCAACTATG	AAACCAATGG	GGGAAAGCTT	GCAGAAAGAA	TTATCCAAGC	TAGTCAACTA	8160
TAGTGAAGTT	CAATATCAAG	AAGATGTTGA	AACAATCCGA	AAAGAGGCTG	AAATCATCAA	8220
AGGAGAGTAA	TATGAATCCT	ATCAAAGCTT	TTGCTAAAAAT	TTATGGTAAT	TACTTTTTGA	8280
CCGTGCAAGG	TGTA AAAAGTG	ATGAAAACGA	TAAAGAAAGC	TGACCATGTC	GTTGTTGGTC	8340
TGGGGAAACT	TTTTATTGCC	GACAAGTTAA	TGGATACGGC	TCGGTGGCTC	ATTAAGCCAG	8400

1205

AGGAGAGAGA	ATGAAATTTT	TTTGGTCTTC	TTGCTATTCT	TTTTATCAAA	CCGATTATTG	8460
GGATTGTGAA	ATTCTTTTGG	ATGATCATCT	CTTTTGCAGT	CCAATTGCTG	TTTTACAAGA	8520
TAGTGTTTAA	GATATTGGAT	TGGCTCTTTA	AACTTATCTA	GATGGTAATC	CAAGTTGCAG	8580
AGAACTAGCA	GGAACTCCAC	TGCTAGTTTT	TTATTCTCTT	TCCATATGGT	ATAATATAAG	8640
CAGTAAAATC	ATTTTATACT	CTTCGAAAAT	CTCTTCAAAC	CACGTCAGCT	TCACCTTGCA	8700
GTATATATGT	TACTGACTTC	GTCAGTTCTA	TCCACAACCT	CAAAACGGTG	TTTTGAGCTG	8760
ACTTCGTCAG	TTCTATCTAC	AACCTCAAAA	CACTGTTTTG	AGCAACCTGC	GGCTAGCTTC	8820
CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAGAACATAC	AATGGAGGTC	GTCATGGACA	8880
ATATCATCGA	TGTGTCAATT	CCTGTGCAG	AAGTGGTGA	CAAGCATCCA	GAAGTCTTGG	8940
AAATCTTAGT	GGAGTTGGGT	TTTAAACCCC	TTGCCAATCC	CTTAATGCGC	AATACAGTTG	9000
GTCGTAAAGT	ATCACTTAAA	CAGGGTCTA	AGCTAGCAGG	AACTCCTATG	GACAAGATTG	9060
TACGCACACT	GGAAGCGAAT	GGCTACGAAG	TGATTGGATT	AGACTAATGA	CAGATGAACG	9120
GATTCATATC	CTACGGGATA	TTTTGTTAGA	ATTGCACAAT	GGCGCCTCTC	CTGAGTCGGT	9180
TCAAGATCGC	TTTGATGCGA	CCTTTACGGG	CGTGTGAGCC	ATCGAGATTT	CCCTTATGGA	9240
GCACGAGCTG	ATGAACTCGG	ATTCGGGCGT	CACTTTTGAA	GATGTTATGG	AACTCTGTGA	9300
TGTCCATGCC	AATCTTTTTA	AAAATGCTAT	CAAAGGTGTC	GAAGTTTCAG	ATACTGAGCA	9360
TCCAGGTCAC	CCAGTTCGTG	TCTTCAAAGA	AGAAAATCTG	GCTCTCCGTG	CGGCCTTGAT	9420
TCGCATTCGT	AGATTGTTAG	ATACCTATGA	GTCTATGGAA	GACGAGGAAA	TGCTGGCGGA	9480
GATGCGTAAG	GGTTTGGTGC	GTCAGATGGG	ACTTGTGGGT	CAATTTGACA	TCCATTACCA	9540
ACGTAAGGAA	GAACTCTTCT	TTCCATATCAT	GGAGCGCTAT	GGACACGATT	CACCTCCCAA	9600
AGTTATGTGG	GGAGTGGATG	ATCAGATTAG	GGAACTCTTT	CAAACAGCTC	TAACGACAGC	9660
CAAGTCACTA	CCAGAAGTGT	CAATTAGCAG	TGTAAAGGAA	GCTTTTGAAG	CTTTTGCGAC	9720
AGAGTTTGAA	AGTATGATTT	TCAAGGAAGA	GTCCATCCTC	CTCATGATTC	TCCTTGAGTC	9780
TTTTACTCAG	GATGACTGGC	TTCAGATTGC	GGAGGAGAGC	GATGCCTATG	GCTATGCCAT	9840
CATCCGTCCG	TCAGAGAAAT	GGGTGCCAGA	ACGACAGAGC	TTTATGAGG	AAAAGATTGC	9900
AGAGGAGCCT	GTACAGCTAG	ATACGGCAGA	AGGTCAAGTT	CAACAAGTCA	TAGATACGCC	9960
AGAAGGCCAT	TTTACCATTA	CCTTTACCCC	TAAGGAAAAG	GAAGCTGTGC	TGGACCGCCA	10020
TAGTCAACAG	GCTTTTGGTA	ATGGCTATCT	TTCAGTCGAG	CAGGCCAATC	TCATCTCAA	10080
TCATCTCCCT	ATGGAGATTA	CCTTTGTCAA	TAAAGAAGAT	ATTTTCCAGT	ATTACAATGA	10140

1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GGCGCAATGT 10200
 CGAACTCTGC CATCCGCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG 10260
 TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT 10320
 CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTGAGTA 10380
 TGTTTCAGGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA 10440
 AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGGTCAATAC 10500
 CCAAATCATG ATTAACGACA TGGCGCACAA GGAAAGCCAA AAAGTTTACG AAGAAGACCA 10560
 GGACGAGCGT GCCAAAGATG CCATGATTCG CTACGAGAGT CGCTTGGATG CTTATCAGTT 10620
 CTGCTTGGT AAGTTTGAAA ACTTCAAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG 10680
 CTTGTTTGGT GAGCGAAAATT ATTAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG 10740
 ATAGAATGTT TATGTTAAAT CCTGTGCAGA GCAGGGATT TTTATTGAAA GGATTTTATC 10800
 ATGTCAAAGA AACTCAATCG TAAAAAACA TTAGCAAATG GCCTCCGTCG CGCAGGTGCC 10860
 TTTTCAAGTA CGGTGACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA GCGTGCAGAA 10920
 CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAAG TTGAACAAGC AGTAGAAGCT 10980
 ACCAAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTTGGGT 11040
 GGACTIONCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT 11100
 TTCAAAAAGT GGACTIONAAA AGAACTCCTT GCCTTGAAAAG GAATCGGCC AGCTACCATC 11160
 AAGAAATGTA AAGAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTTCCG 11220
 AAAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTTGA ATCCACATT TTACAGAAAG 11280
 TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGGTT GCTAATGGAT GAAAAATTGA 11340
 AATAAAAGTG TCTTTTGTCT TTAAAGACGA GAGTTGCC 11378

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGGCGAATTT GCTGCGGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG 60
 AACAAGAAAA GGTTCAGTGT GTGACCTTTA TGCCAAATGA AGGTCCTGAT GATCTATACG 120
 CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG 180

1207

ACCTTTGGAG TGGTTCTCCA TTTAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTTATCGGA GACGGTAAAT	480
TGAAAATCAA TCTTGCCCGT CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTTTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTTCATG GCTCACTCAA CAGGTAAAAC ATTGGTCAAT ACCGTTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGAATTGGT GTTGAATTTG	900
ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTTGTT TGAATTGATT AACAAAGCCA	960
ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTTGCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTTT	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACCTG GAAGCAGGGA	1140
TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGGTTG GTCAAATATC GGTGCTGCTA	1200
TCGCTCCTGA TGCTGCACTT GCTTCTGTGC CTGCTGCCAT TATCATGGTT CTTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCC AAGCGTTGC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGG TTTGGTTCAT ACTGCAGATG	1380
CTGCCCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTCATC GCGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCTGCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG	1500
TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG	1560
GTATGGTCGT TGCCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTCTAAA ACTGGTGGAA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAAACTT CAATTAAC TAATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGTCT TGAACCTTTG AACGGATGCA	1920

1208

AAACTTGGGC	TGGGCTTATA	CACTCATTCC	AGCTATCAAA	AAACTCTATA	CTAAAAAAGA	1980
AGATCAAATC	GCTGCTCTTG	AGCGTCACCT	TGAGTTCTTC	AACACTCATC	CATACGTAGC	2040
TGCTCCAGTC	ATGGGGGTTA	CTCTTGCGCT	TGAAGAAGAA	CGTGCTAACG	GTGTGGAAAT	2100
CGATGACGCT	GCTATCCAAG	GGTTAAAAAT	CGGTATGATG	GGACCTCTTG	CTGGTATCGG	2160
TGACCCAGTA	TTCTGGTTTA	CAGTACGCCC	AATCCTTGGA	TCTCTCGGTG	CTTCACTTGC	2220
CCTTACTGGC	AATATCTTGG	GGCCACTCCT	CTTCTTTGTT	GCATGGAACT	TGATTCGTAT	2280
GTCATTCTTG	TGGTATGTTC	AAGAGATTGG	ATACAAGGCT	GGATCAGAAA	TCACTAAAGA	2340
TATGTCTGGT	GGTATCCTTC	AAGATATCAC	TAAAGGAGCT	TCTATCCTTG	GGATGTTTCA	2400
TCTTGCTGTC	CTTGTTCAAC	GCTGGGTAAA	TATTAATTTT	GCTTTCGATG	TTTCTAAAGT	2460
TCAACTAGAT	GAAAAGGCTT	ATATCCATTG	GGATAAATG	CCAGAAGGGT	CTAAAGGTAT	2520
CCAAGAAGCA	TTCGCACAAG	TAGGACAAGG	ATTGTCTCAA	ACTCCTGAAA	AAGTTACTAC	2580
TTTCCAACAA	AACCTGGATA	TGTTGATTCC	TGGATTATCA	GGACTACTCC	TTACTTTACT	2640
TTGCATGTAC	TTACTTAAGA	AAAAAGTATC	TCCAATCACT	ATTATCCTTG	CCCTCTTCGC	2700
AGTGGGTATT	GTGGCACATG	TTCTTCACAT	CATGTAATCA	AGCAACTAAA	AAGGAACCAG	2760
GTTCATAAAT	CTGATTCCTT	TTTTCTATGC	TTTTATTTCAG	CCAAGGCTCC	CATTGGATCC	2820
CATGGTGCAA	GTACGATTGG	TTCTGCTCCA	TAGGCAGCTT	GTTCTTCTGC	TGTCAGCAAT	2880
TCCTTACGAA	CAACGATTTG	GTATGTGTAT	TCGTCCATCC	AAGCGTCTGA	GGCAACAAAG	2940
TAACCATCTG	TACCGACCTT	GTCTCCCCAT	GAGTTTTCAA	CCTTCCACTT	GTTTGATTTA	3000
CCATTTTCGT	CCAAGTCAAC	ACCTGTCAAG	ACCATGGCGT	GGGTCATCAA	GCTTTCACTA	3060
TAGTCCAAAC	GTCCAGCCTT	GTCTTGAGTA	AGTTTAATGT	CCATGCTTGA	TTCAAAGTCA	3120
TAAACATCTG	TCGCAAGGAT	GCCAGCTTAC	GGTTGCTGAG	CTGGCCGACA	TCAGAACCAA	3180
ACCAAACAGT	CTCACCTGCT	TGCATTTGGG	CAATCGCCAA	TTCTTTCAAG	CGCTCCATTG	3240
GAACGTTGAT	GTAGCGAACT	GCACGGCTAC	CAACCACATT	CCCCAACATC	TCAACTGTGT	3300
AAGATTTTCC	GTAAGGTTTA	TCAGCAGTTG	GAGCATTGAT	AACAGAAACG	TAGTCTTCTA	3360
AAGGAAGATT	GACATATTTT	TTGTAAAACT	CTTGTGGTGT	GATTCCTTTT	TCACTTTTGT	3420
AGTTGTTATC	TTTATCGCGA	TAAGCAAAGT	CAAACCTGCG	TGGTGGAAGT	CCTAATGACA	3480
TAGCAAGAAA	GTAAAGATT	TCTTGCAAGA	GGTCTTCTTT	CTTAGCTTGA	ACAGTCGCTT	3540
GATCTGCACC	AGAAACAAGC	AAGTCACGCA	AGATTTGAGC	ATCTTGACGA	AGCAATTTAT	3600
TAAGGATCGC	ATTTAGCTCA	CGACTGCTGC	TAGATGAAAC	AGACTCAGGA	TAAACTGACT	3660
TAGGCACGAC	ACCGTATTTT	TCAAAGAGGG	AAACGACCAT	ATCCCATTGA	CGCCATCTT	3720

1209

GTTGAGGTGT TTGGAGTAAG AAGCTAACTT GCGGCTAGTC AATCTTGGT CTGAAGTCGC 3780
 AATGACTTGC TCCAAGAACC AGTTTGATTT CTCATACTTA TCCCAGAAGA AAGTGTGGGC 3840
 TTGTGACAAC TCAAAGTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT 3900
 GAGAGCCGCA AACATCCAGC AACGACCAGA CGCTTTCTGG TTAGTGACCT TGTCCTTGGT 3960
 TAAATCCAAT GAGAAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC 4020
 AAAAATTCCG TTGTGGCTGG CAGCATTTTC AATCGCTTGG TATTTTACAT TTGCTTCATA 4080
 GTTGGCAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCATAGATT CCTCCTTTTA 4140
 GTCTACAGTG TATTGG 4156

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3902 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AAATAAACA AAAACAAAAA TATCGAGGTT TATTTTCAAA ACTTTCGATA 60
 TTTTATTAA GTTATTATTT TGTGTTTCT AGTTACTTT TTGATGGTTA AGAGTGGTGG 120
 AGAATTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG CTAGCCGAG GCTGTAATTG 180
 AGTACGGCAA GCGAAGCTG ACGTGGTTG AATTTGATTT TCGAAGAGTA TTAGTGCAAA 240
 CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCCG 300
 ACTTGAGAGA AGAAGTCATG GTTGAAGTT CTGTTGAAA TACCGTTCAT AACGATTGGG 360
 TTGACATCTT CAGCTGAATC TGGGAAAAGT GGATCTTGTC CCATGTTTAT GAGAGCTTTA 420
 TTGGCATTGT AGCGAAGGAA GTTTTAACC TCTTCAGTCC AACCAACACC GTCATAAAGA 480
 CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGGTCGTA CATCCATTCT 540
 TTGAGTTTTT CTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA 600
 ATGTAGGTTC CGTGAACAGA CTCGTCACGA ATAATCAATT TAATGATTTT TGCAACGTTG 660
 GCAAGTTTGT TGTACCAGG ATAGTAGAGG GGAGTGAAGA AACCAGAGTA GAAGAGGAAG 720
 GTTTCGAGGA AGACGCTGGC AACTTCTTT TCAAGTGGGC TGCCGTTTAG GTAGATTTCC 780
 TTGACAATCT CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAAATTTCT 840
 TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATTT AGCGTGGACA 900

1210

GATTCCATAA	ATTGGATGTT	ATTGAAGACA	GCTTCCTCAT	GTGGTGTACG	GATGTCTGCG	960
CGAAGGGCTT	GAACCCCACT	TTCAGATTGC	ATAGTGTCAA	GAAGGGTTAA	ACCACCAAAA	1020
ACTTTTCCGA	CCAAGTCTTT	CTCTTTGTTA	GATAGCTTTC	TCCAGTCATC	CAAGTCGTTT	1080
GATAAGGGAA	TACGTGTATC	GAGCCAAAAT	TGCTCCGTCA	GTTTTTCCCA	AGTTGATTTG	1140
TCGATGACAT	CTTCGATGGC	ATCCAGTTA	ATGGCTTTGT	AGTAAGTTTC	CATTTAAAAT	1200
CTCTTTCTGT	GTTTAGTATT	GCGAACTCAC	AATTATTTCT	ACTTTACCAT	AATTCTATAG	1260
GAGTATCGCA	CAAAAAGTCG	GAAGCCCGAC	TTTTAAAATG	TTACATAAAT	TATGTTATGA	1320
CATAGTAGAT	TTGATTTTAT	CAGTGCTGCT	TAGGGAAAAA	TAGTGTTTCT	ATGCTAGAAA	1380
CTAAATCACA	CAGCTTTCAC	ATTGGTTGGC	GCCGACTTCT	CCACCGTCAT	CTGTAAAGGT	1440
ACGGACGTAG	TAGATAGACT	TGATTCCCTT	GTAAAGGCA	TAGTTACGAA	GGATGGACAA	1500
GTCACGTGTC	GTTTGTTTAT	TTCCCTCTT	CCATTCGTAA	AGGCCTTTTG	GAATGTCACT	1560
GCGCATGAAG	AGGGTGAGTG	AAAGTCCTTG	ATCCACGTGT	TCAGTCGCAG	CAGCGTAAAC	1620
ATCGATGACT	TTACGCATAT	CCATATCGTA	GGCAGAAGTG	TAGTAAGGAA	TGGTTTCTGT	1680
AGACAAGCCA	GCAGCAGGGT	AATAGATTTT	ACCAATTTTC	TTCTCTTGGC	GTCTTTCGAT	1740
ACGTTGCGTA	ATCGGGTGA	TAGAAGCAGA	AACGTCGTG	ATATAGCTGA	TAGAACCATT	1800
TGGCGCTACA	GCAAGGCGAT	TTTGGTGGTA	AAGACCATCT	TCTTGAACCT	TGTCGCGAAG	1860
TTCAGCCCAA	TCAGCAACAC	CAGGGATAAA	GACATTTTTC	AAGAGTTCTT	TAACACGGTC	1920
TGATGTTGGA	ACAAATTCAC	CAGTTACATA	CTTGTCAAAG	TAACCTCCGT	TAGCATAGTC	1980
TGATTTTTC	AAGTTGTGGA	AGGTAATACC	ACGTTACCGT	GCAATATTGT	TTGACTCTAC	2040
CAAGGTCCAG	TAGTTCATAA	GCATAAAGTA	GATGCTTGTA	AATTCAACAG	ACTCAGGTGA	2100
ACCATATTCA	ATGAGTTGTT	GGGCAAGGTA	GCTGTGCAGT	CCCATGGCAC	CGAGACCAAA	2160
GGTGTGGGCT	TGGCTATTTT	CATGGTCAAT	CGTTGGTACA	GCTACGATAT	GTGAACATATC	2220
TGTAACGAAA	GTAAGGGCAC	GAACCATAGC	ACGGATAGAA	CGACCAAAAT	CAGGTGAAGT	2280
CATCATGTTA	ACCACGTTGG	TTGAACCCAG	GTTACATGAA	ACATCTGTTC	CCATTTGAAG	2340
GAATTCCTGA	GCATCGTTGA	TCAAGCTTGG	TTCTTGAACT	TGAAGAATCT	CAGAACACAA	2400
GTTACTCATG	ATAATCTTTC	CATCAACAGG	ATTTGCACGG	TTAGCCGTAT	CGATGTTGAC	2460
TACATAAGGA	TAGCCAGACT	CTTGTGCAA	TTTAGAGATT	TCAGTTTCCA	AATCCCAGCGC	2520
CTTGATTTTT	GTCTTGCAG	TATTTGGATT	TGCGACCAAT	TCATCGTATT	TTTCAGTAAT	2580
GTCGATGTAA	TTGAATGGCA	CACCGTATTC	TTTTTCTACA	GAGTAAGGGC	TGAAGAGGTA	2640
CATTTCTTCA	TTTTTACGAG	CCAATTCGTA	GAATTTATCA	GGTACTACAA	CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGTA CTTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT 2760
 GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCCAATTG 2820
 GTTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC 2880
 TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC 2940
 ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT 3000
 ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC 3060
 ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTTCAT TGGCAATATC 3120
 GATTGCAACA GCTTCATTC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC 3180
 CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT 3240
 ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC 3300
 TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTTCAAT 3360
 GAGGTAATTG ATTTTGTCTT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC 3420
 TTTAAAGAAA GCATCCAAGG CTTCTTGTG TTTATGAAGC ATGATTTGTC CATTAACAGG 3480
 ACGGTAAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT 3540
 AAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC 3600
 TTCTGGATGA TGTACTAAGA TTATGCTAAT TGTTTCAGTT TTCCTGGTTG GAAACCTGAA 3660
 AAGACTTCAG TTGGTGTTTG GATAACAGGA GCTGCGCTAA AACCGAGCTC TTTAACTTGA 3720
 TCGACGFACT CAGGTGTGTC ATCAAGATTG ATTTACAGAT AAGAGACATT ATTACTGTCC 3780
 AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTTACCATT 3840
 GTGTAACCTC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTTCG 3900
 GG 3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTTGCAG TTAGTAGGCG GTGAGACTCA 60
 CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAAC TATGCTAAAT 120

1212

CAATTGAGGT TGTTTACATA AAACCTCTATA TCAGAGAAGC CTGATATAGA GTTTTTCTT	180
GCTAGTTTTTA GGATTTTTTT GTAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG	240
AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT	300
TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTTATCG GAGAAATTGC CGAATTAGAC	360
GGACAATTTG CCATTATAAA GAATGGGAAT GTCGATAGTT TTTATAAAAA ATTGGAAAAA	420
GCTGTGGAAA TTTTGATTGA AAATTATAAT TTAGCAAAAT AAGTCTTGT TTTTGAAAT	480
TTTCATGATA TAATAGTCCA TGTGTATTGT AGGAGAGATA GCGAAGAGGC TAAACGCGGC	540
GGACTGTAAA TCCGCCCTT CGGGTTCGGG GGTTCGAATC CCTCTCTCTC CATTTTATTA	600
ATGGGGTATA GCCAAGCGGT AAGCAAGGG ACTTTGACTC CCTCATGCGT TGGTTCGAAT	660
CCAGCTACCC CAGTCTTAG GTAATAATCA AGATAGAAAG CAAAATATCT TAGGGTATTT	720
TATTTTTATA ATTGAAAGAC GTGAATGATA TGAACATGTC CTGCGGGTG CTTAGGAAAA	780
AAATTATAAG TATGTCAACT TTAAGAAAAA CTTGATTGTT GGAGGATTTT TTAGATGAAC	840
GAATTTGAAG ATTTGCTAAA TAGCGTTAGT CAAGTTGAGA CTGGTGATGT TGTAGTGCT	900
GAAGTATGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTGAA	960
GGTGTCTTGA CTCTCGCGA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT	1020
AAAGTAGGAG AAGTATTGGA TGTCTTGTA CTTGTCGCAAG TAGTTGGTAA AGATACTGAT	1080
ACAGTTACAT ACCTTGTATC TAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAACTT	1140
GTTGGTCGCG AAGAAGAAGT TGTACTGTT AAAGGAACGC GTGCCGTTAA AGGTGGACTT	1200
TCAGTAGAAT TTGAAGGTGT TCGTGGATT ATCCCAGCTT CAATGTTGGA TACTCGTTTC	1260
GTACGTAACG CTGAGCGTTT TGTAGGTCAA GAATTTGATA CTAAAATCAA AGAAGTTAAC	1320
GCTAAAGAAA ACCGCTTCAT CCTTTCACGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA	1380
GCTCGCGCTG AAGTATTCGG TAAATTGGCT GTTGGTGATG TTGTAAGTGG TAAAGTTGCT	1440
CGTATCACAA GCTTCGCGC TTTCGTCGAC CTTGGTGGTG TTGACGGATT GGTTCACTTG	1500
ACTGAATTGT CACATGAACG TAATGTATCA CCAAATCAG TTGTAAGTGT TGGTGAAGAA	1560
ATTGAAGTGA AAATCCTTGA TCTTAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA	1620
GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGATGTAGTA	1680
GAAGGAACAG TTAACGTTT GACTGACTTC GGTGCATTG TTGAAGTATT GCCAGGTATC	1740
GATGGACTTG TTCACGTATC ACAAATTTCA CACAAACGGA TTGAAAATCC AAAAGAAGCT	1800
CTTAAAGTTG GTCAAGAAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC	1860
GTGTCACTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAAGG AAAAAAGAA	1920

1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT 1980
 CCAGAAACAC AAACAGGATT TTCAATGGCT GATTTGTTTG GTGATATCGA ACTTTAATCA 2040
 AATTGAAAAT TCACAAAATC CTTTGTTTAC TAAACAAGGG ATTTTCTGG CTCTTTGTCA 2100
 ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTTGTC CTTTCTTTTT 2160
 TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAAGTTTTC AAAGTTCCGA AAACCAAAGG 2220
 CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT 2280
 GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTA AAGACAGTCT 2340
 GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT 2400
 CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG 2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10974 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTtWACA AAGTCCAATT ATATGCGGAT 60
 CTATACCTCC ACAATGTCCA TTATTATmCC TAACTATAAT ATGAGCCGAA AACACTATAT 120
 CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATTGCA 180
 TTGTAACCAT CTCCTTAAAC GACGCATAT GATATTTGAT AGAGAAATTT TTATGAATAA 240
 CTCAATAATT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGCTCTC 300
 GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT 360
 TTTAGCACTG TATAAAAACG TTTCATACA CTAACCTCAA GAAAACCTCC ACTATTAATT 420
 GAAAAAATTG ATAGAGATAA ATTAAAAATC TATATTGAAA CTCATCCCGA TGCTTATTTG 480
 ACTGAAATAG CTGCTGAATT CAACTGTCCCT CCAACAAC TAATTACGC TCTAAAGGCT 540
 ATGGGATATA GTCTAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT 600
 CGGTTCCCTTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA 660
 GGGGTTGAGA CCTATTTTFA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT 720
 CTGGAAGAAG ATATAATTAT TTGAATTAAG ATCGAGACAA CGCACACCAG AGATTGCGAT 780
 ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTCAATAT ACTATGGCTC CGATGACCTA 840

1214

TAAAGATACG	ATGACGAGTG	ACTTTTTCGA	AGCTTGCTTC	CAAAAATFCT	TACTACCTAC	900
TTTAGATACA	CCATCCCTTA	TCATTATGGA	CAATGCAAGG	TTTCACAGAA	TGAACATGTG	960
TAAGGAGCAG	GGCATAGACT	GTTACCACTT	CCTACCTATT	CACCCGAGTA	TAATCCCATT	1020
GAGAAAATAT	GGGCTTACAT	CAAAAACATC	TCAGAATAAT	ATTGTCAAAT	TACGATGCCT	1080
TTCTTGAGGC	ACTTTTGTCC	TATTC'TGT'T	TCAGCCGACT	ATACTCCGTT	ATTGGGCAGC	1140
TACGGAACAG	TCGATGGGAC	GATGGGGGGA	CATAAAAAAA	TCCTCCAGTT	TGTTTTTTTA	1200
TAACAGTATA	CTGGAGAATT	GACAATCTCG	GTAGATACCT	CGTTATAGCG	CGGTTACTTA	1260
TTAGGCAGTT	ACAAAACAAC	TGTGAACAGA	AAACATTCCA	GAGTCAGACA	AGACTTTGGA	1320
ATGTTTTGGC	TCTATAATTT	CTGTAGTGGG	TAATCCCACC	CCAGGAATTA	TAGGGTCGTT	1380
TCTTGTAGAA	AAAAAGCCCC	ATATGACCTA	TAATGAAAAG	CGTCTAACCA	ACTCATTAGA	1440
AAGGGTTCAT	ATGGAACAAC	TTAAGAATAC	CACAGATTTG	CTCGGATTGG	AAGACAAAAA	1500
TATCAAAATC	TTGTCTGTTC	TGAAATACCA	AACCCATCTA	GTCGTTCAGG	CAAAGTTGGA	1560
TTCCCCGCT	CCTCCTGTGC	CTCATTGTCA	AGGGAAGATG	ATCAAATACG	ACTTCCAGAA	1620
AGCCTCTAAA	ATTCGGCTTC	TCGACTGTCA	GGGTTTACCC	ACGGTACTGC	ATCTCAAAAA	1680
GCGCCGCTTT	CAGTGCAAGA	ATTGCCTTAA	GGTGGTCGTT	TCTCAAACAT	CCATTGTCAA	1740
GAAAAATTGC	CAGATTTCCA	ACATGGTGAG	ACAAAAAATC	GCTCAGCTCC	TCCTTGAAAA	1800
GCAGTCTATG	ACTGAGATTG	CCCACAGATT	GGCGGTCTCA	ACTTCCACCG	TCATCCGAAA	1860
ACTGAGGGAA	TTTAAGTTTG	AAACCGATTG	GACCAAGTTG	CCAAAAGTTA	TGAGTTGGGA	1920
TGAGTATAGC	TTCAAAAAGA	GCAAAATGAG	CTTCATTGCC	CAAGATTTTG	AGTCCAAATC	1980
CATCCTCGCA	ATTTTAGACG	GGCGAACTCA	TGCGGTGATT	CGAAACCATT	TCCAACGCTA	2040
TCAGAGAGAG	GTTCGGGAGC	TGGTCGAGGT	CATCACCATG	GACATGTACA	GCCCTTATTA	2100
TCGGCTCGCT	AAGCAACTCT	TTCCAAAGGC	GAAGATTGTT	CTTGACCGCT	TCCACATTGT	2160
CCAACATCTG	AGCCGAGCTA	TGAACCGAGT	ACGAATCCAA	ATCATGAACC	AATTTGACCG	2220
AAAATCCTTG	GAGTATCGGG	CGCTCAAGCG	CTTTTGGAAC	CCTCGCTTTT	TCGTTTCTAG	2280
GCTCGGGCTA	AATCAGTCCA	CTGGACTGAT	TTACTACACC	AGTATAGCTT	CAAGCTCTGT	2340
CAGAAACGAT	TCTATCAGCC	CACGTTTCGA	ATGCACTTAA	CCCATCGGGA	AGTACGAGAT	2400
AAGCTGCTTT	CTTACTCTGA	GGGATTACAG	GTTCACTACG	AACTCTATCA	ACTCCTGCTC	2460
TTTCATTTTC	AAGAGAAGAA	TGCCGACCAT	TTCTTTGGAT	TGATTGAGCA	AGAACTGCCA	2520
ACGGTTCATC	CGCTTTTCA	AACGGTCTTT	TGGACTTTTT	TAAGGGATAG	AGATAAGATT	2580
ATCAACGCAC	TTAAGCTGCC	TTATTCCAAC	GCTAAACTTG	AAGCGACCAA	TAATTTGATT	2640

1215

AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACTTTA ACAATTTTAA AAAACGGATT 2700
TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTTCG TACTCTCCAG ATTGCAGCTT 2760
TTCGCCTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG 2820
ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTTCT TTGTTCCTACT CGCTGACGCT 2880
GGCATAGGCA ATCATACTTG CATTGTCTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT 2940
GACATCTGTG ATTTCCGGCTG CTAGGCGTTC TCTGAGACCT TTATTGGCTG CCACACCACC 3000
TGCCACAACCT AGGATTTTAA CAGGATATTT CTCCAAGCC TTCTTGGTTT TTGCCATGAG 3060
AATGTCCATA ACTGCTGCTT GGAAGGAAGC ACACAAATCT TCTGTAGACA GGCTTTCTCC 3120
CTTTTGCTCG GCATTGTGAT GAAGATTGAT AAAGGCAGAT TTCAAACCTG AGAAGGAGAA 3180
CTCCAGATTA TCTTCCTTAA TCATGGCAG GGGGAAATCA TAAATATCCT GCCCCTGATG 3240
AGCCAGCTCG TCAATCTCAC GACCTGCAGG ATAGGTCAAG CCCATGACAC GGCCGACCTT 3300
ATCATAAGCC TCACCAACCG CATCATCACG GGTTCCTCCA ACAATCTTAT AATCTCCTGC 3360
CTCCGAAACA TAAACCAACT CTGTGTGTCC GCCGCTGACC AAGAGGGCTA GCAAGGGAAA 3420
CTCCAAAGGC TCCACACTCT GAGCTGCCAT GAGGTGCCCA GCCATGTGAT TAACAGGAAT 3480
CAGTGGAAAGT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC 3540
TCCGACCAAG CCTGGTCCGT AGGTAACCGC AACAGCTGTC ACGTCCTCTT CGGTAATCCC 3600
TGCTTCTGCC AATGCCTCCT CGATACAGGC TGTAATGACC TCGACATGGT GACGACTGGC 3660
TACTTCGGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT 3720
GGACAAGAGC TCATCGTCGT TTTTCAAGAC GCGGACACTG GTCTCATCAC AGGATGTCTC 3780
AAATGCTAAA ATATATCTAT CCTTCATCTA TTTCTCTCTT CATGATAATG GCGTCCTCGA 3840
CTGGGTCATG GTAGTAGGCC TTTCGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAATA 3900
ATGCTTGCGC TCGTTGATTT GACTGTCTGA CTTGAGGAA AATTTCCCTG TCTGTCCGCA 3960
ATTGAGCAAA CAAGGCTGAC GCAATCCCCT GACCCTGATA AGCTCCTTTG ACAGCGATTT 4020
GCAGGACTTC TGCTTCAAAA AGATTCTCCT GCACAGCTAG AAATCCAATC ACTTCTGCCC 4080
CATCATAAGC CAATGCATAC CAAGTCTGGT CTTGGGACAG ATCTGCTTGG ATTTGCTCCA 4140
GAGTCCAAGG ACTGACTAGG TAAACAGCTG CCATAACAGC GTAGATGGCT TGAGCTAGGT 4200
CAGGCTGTTG TTGAATTGCG TTGATTTCTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA 4260
CTCGGTATGG TTCTTGAGCC AGTTTTCTC AGCCTCGACT CGTTTGAGGT AATTCGGCAC 4320
AAAATCATGC AAGGAGTCTG CTTCTTGTC CCAGGCCAAA AGAGCTAGAT TAGCTGCATT 4380

1216

GGGCAATGTT	TCTTTGTAAT	CAGTCCTTGG	CAAGTGTTTT	TGAATCTGCT	CAACAAAGGG	4440
GCCAACTTCT	CCGACAAAGG	TTACCTGACT	AGTACCCTTG	ACTTTTCTA	GCACCTCTTC	4500
AAAAGATAGG	TGCGCTTCTG	CCATGACAGG	TTTGGCATT	TCATAAAATC	CTGCATAAAC	4560
ATTATTGCGA	CGCGCATCCA	TCAAGGGGAC	AAACAAACCT	TCTTGTGAT	GGGGCACCAG	4620
AGCCAAGAGA	CTCGACATAC	CAACCAACTC	GATGTTGAGG	GTGTGAGCTA	AGGTCTTAGC	4680
AGTTGCTACC	GCAATTCGCA	AGCCTGTATA	GCTACCCGGC	CCTTCAGCTA	CCACGATTCG	4740
GTCCAAATCC	TTGGGTGTCC	AATCCAAACT	TGCCATCAAA	AAATCGATGG	CAGGCATAAG	4800
AGTAATACTG	TGATTTTTCT	TAATATTAAT	CGTCGTCTCG	GCAAGAACCT	GCTTATCCTC	4860
TAAAATAGCC	AGAGAAAGAG	CCTTGCTGGA	CGTATCAAAA	GCTAATACTT	TCATAACACA	4920
TTCTATCTT	TTTGTCTGCT	TACTATTATA	CTACAAAAGC	TGGCACATGG	GAATTTCTT	4980
TGCCCCAGA	CAAGAGTGCC	CTCACTTAAC	TAAAAATAAT	TTAAAAAAT	GCTCACTTTT	5040
CCTTTCTTT	TCCGAATATA	AAAGTGAACA	AGAAAAAGG	AGGAAAAGTC	AATGACAAAT	5100
TTTGACATTC	TTGACAATCA	ATTTTATCC	TTATCTGAAA	ATGAATTATC	AGATATTGAT	5160
GGCGGTCTCG	CTCCCTTGGT	TATCTTTGGA	GTAGCAGTAT	CTTGGAAGGC	TATTGCAGGT	5220
GGAACAGCAC	TTATAGGTC	TGGTTGGCA	GCTGGTTAT	TTTTAGGAGG	AGATTAATAT	5280
GATGAAAGAT	TTGAACAAT	ATCGTGAAT	TTCTAATAAG	GAATTGCAAG	AAATCAAGGG	5340
TGGCTTTGGT	GTCGGTGTG	GTATCGCTT	ATTTATGGCA	GGTTATACCA	TTGAAAAGA	5400
CCTTCGTAAA	AAGTTTGTA	AGTCATGCTA	GATAAGAAAC	ACATTTTATAG	AAGGATAAAT	5460
TTTATTGTCT	TCATCTCTTA	CAGTTTGCTC	AGCATTCTCA	ATGATTTGAA	CATTACTACC	5520
ATCCCTTAC	CATTGATTT	ATCTGTTTGT	ATGTTTTTAT	TTTTATGCTT	CAACTCTATT	5580
TTTGATCAGA	ACAATGACTC	CCATAAAAAT	AATAAGCTTT	GAAAATTCCA	TTGTCATGTC	5640
ATGTTAGAAA	AATGCAAAGA	CCACCTCATC	TTGATAGATG	GGGTGGAAT	TTGCTGCTGT	5700
AAATCTACTA	TCTCTACATT	CCCCAACAAA	AAACCCAGC	ATAAGCAGGG	CATCTAAGCA	5760
TTTAATTCAA	AGTAAAATAC	AAACCAAACG	ACATAGGTCA	CGAGGAGGAG	AAAAAGCGAG	5820
TAGAGAGTCA	CAAAGGTCAT	TTCCACAAG	AACTTGGTTT	GTCGTCGTTT	CAGTTTGCA	5880
AATAGAAGAT	TCCCCGCATA	AACGCAAGCA	ACAAAAACAA	TAAAAGCTAC	CAAGCGAGCT	5940
CCGATAGCAA	AAGCAAATAA	GTTATACATA	GGGCAACCTC	CTTGACTTAA	AATCTATATG	6000
GAATTATGAC	AAGCAATAAA	TTTCACTTCC	GTTATCAACA	TAATACATTT	TCTTTATTTT	6060
TGAAAACGCT	TACCAAAGAA	ATCGTCCCCT	AACTTCTCG	TTCCGCTTT	TTACTAATTT	6120
TTTATTTTGT	GGTATAATG	AAATAATTGT	AACGAATCAA	GGTCAATCTA	GACACAAAAT	6180

1217

GGAATGAAAT CAAGCAAATA TCTGCTAAAA GTTTGGAATA AGCTGACCTG TAAATAGAAA	6240
GGAACTATAT GATTTACAAA GTTTTTTATC AAGAAACAAA AGAACGTAGC CCACGCCGTG	6300
AAACAACACG CACGCTTTAC CTAGACATCG ATGCCAGCTC AGAACTTGAG GGCCGTATCA	6360
CTGCTCGCCA ACTTGTCGAA GAAAATCGCC CAGAGTACAA TATCGAGTAT ATCGAACTCT	6420
TGTCTGACAA ATTGCTCGAT TACGAAAAAG AACTGGCGC CTTCGAAATF ACGGAGTTCT	6480
AATATGGCCT ACACTCTTAA ACCTGAAGAA GTCGGCGTTT TTGCCATCGG TGGTCTAGGA	6540
GAAATCGGGA AAAACACTTA CGGAATTGAA TACCAAGACG AGATTATCAT CGTCGATGCT	6600
GGGATTAAT TCCCAGAAGA TGACTTGCTT GGTATCGACT ATGTCATTCC TGACTIONCT	6660
TACATCGTGG ACAATATCGA CCGCGTCAAG GCTGTTTTAA TCACACACGG ACACGAGGAC	6720
CACATTGGTG GGATTCGGT CTTACTCAAG CAAGCAAATG TCCCTATTTA TGCTGGACCG	6780
CTTGCCTTGG CTTGATCCG TGGGAACTC GAAGAACAGC GCCTCTTGGC CAACGCCAAA	6840
CTTTACGAAA TCAACCACAA CACCGAGTTG ACCTTTAAAA ATCTCAAGGC AACTTTCTTT	6900
AGAACGACTC ACTCTATTC AGAGCCTTTG GGGATTGTCA TTCATACTCC TCAAGGGAAA	6960
ATCGTCTGTA CGGGTGACTT TAAGTTCGAC TTTACTCCAG TTGGAGAACC TGCGGACTTG	7020
CATCGTATGG CTGCGCTTGG TGAAGAAGGC GTGCTCTGTC TCCTGTCTGA CTCGACAAAT	7080
GCGGAAGTAC CAACCTTTAC CAACTCTGAA AAAGTCGTG GTCAGTCCAT TATGAAGATT	7140
ATCCAAGGTA TTGAAGGACG TATCATCTTT GCATCCTTTG CCTCAAATAT CTTCCGTCTC	7200
CAGCAGGCAA CAGAAGCTGC TGTTAAGACT GGACGCAAGA TTGCGGTCTT TGGTCTTCT	7260
ATGGAAAAGG CCATTGTCAA CGGAATCGAT CTTGGCTACA TCAAAGCTCC TAAGGGAACC	7320
TTTATCGAGC CAAATGAAAT CAAAGATTAT CCTGCAGGAG AAGTTCTTAT CCTCTGTACA	7380
GGTAGTCAGG GTGAGCCTAT GGCAGCCCTC TCTCGTATCG CCAACGGAAC CCACCGTCAA	7440
GTACAATTAC AACCAGGTGA TACCGTATC TTCTCTTCTA GTCCCATCCC TGGAAACACT	7500
ACTAGTGTCA ACAAGCTGAT TAACATCATT TCTGAAGCTG GTGTCGAAGT TATCCACGGT	7560
AAAGTGAACA ATATCCATAC ATCTGGACAC GGTGGTCAGC AAGAGCAAAA ACTCATGCTC	7620
TGCTTGATTA AGCCAAAATA CTTTATGCCT GTCCACGGTG AATACCGCAT GCAAAAAGTC	7680
CACGCTGGAC TAGCAGTGA TACTGGTGTG GAGAAGGACA ATATCTTTAT CATGAGCAAT	7740
GGCGATGTGC TTGCCCTTAC TGCTGACTCA GCTCGTATCG CAGGTCATTT CAACGCCCAA	7800
GATATCTATG TCGATGGAAA TCGTATCGGT GAAATTGGCG CAGCTGTCTT CAAAGATCGT	7860
CGCGATCTAT CTGAAGACGG TGTCGTTCTG GCAGTTGCAA CTGTTGACTT CAAATCGCAG	7920

1218

ATGATTCTAT	CTGGTCCAGA	CATCCTCAGC	CGAGGCTTTG	TCTACATGAG	AGAGTCTGGC	7980
GACTTGATTC	GCCAAAGCCA	GCGTATCCTC	TTCAATGCCA	TTCGTATCGC	ACTGAAAAAT	8040
AAGGATGCTA	GCGTGCAATC	TGTCAATGGT	GCCATTGTCA	ACGCTATTCG	CCCCTTCCTC	8100
TATGAAAATA	CCGAACGTGA	ACCGATCATC	ATCCCGATGA	TCCTCACACC	AGATGAAGAA	8160
TAAAGCAAGA	AAACAGCCCC	GTCCCTCGGAG	CTGTTTTTCT	CTATGCTTTC	TTTTGAGATT	8220
AAAACTCATA	CTCAATGAAA	ATCAAAGAGC	AAACTAGGAA	GCTAGCCGTA	GGTTGCTCAA	8280
AGCACTGCTT	TGAGGTTGTA	GATAGAACTG	ACGAAGTCAG	TAGCCATACC	TACGGCAAGG	8340
CGACGTTGAC	GCGGTTTGAA	GAGATTTTCG	AAGAGTATCA	ATAAAAAATCG	AAATCAGACT	8400
AGAAGGCTAA	GCGAAAGCAT	AACTTGAGTT	AGCTCCATA	GTTCCGGAAA	CTATGGGAGG	8460
CTGGAGATGA	ATCAAAGCCA	AGCTTTGAAC	TCATTCGTAA	GAAGCCGACG	ACGTATCATT	8520
TTGATTTTGG	AAGAGTTTGA	GAAATACTAC	GATTTTTTACC	TTCCAGATAC	ACCATCAAAA	8580
TAGAAATATC	TGCTGGGTTT	ACTCCCGAAA	TACGGCTGGC	TTGGCCGATG	GTTTCTGGAT	8640
TGATGAGTTT	GAACCTCTGA	CGGGCTTCGG	TTGCGATAGA	ATCAATGTCA	TCCCAGTCGA	8700
TATTGGCCGG	AATGCGTTTT	TCTTCCATGC	GTTTCATCTT	GGCAACCTGG	TCCATGGCTT	8760
TGGAAATATA	GCCTTCATAC	TTGATTTCTG	TTTCAATCAA	TTCGATAATC	TTGTCAATCA	8820
AGTCTTCTGC	AGCTGGTCCG	ATGAAGGCCA	CCACATCTTG	GTAAGAAACT	TCTGGACGGC	8880
GAAGGAATTC	CTTGGCTGTC	ACTGCATCGG	TCAAGGGTTT	GAAGCCCATC	TCCTCAACCT	8940
TGGCATTTGGT	TTCCCTTGACT	GGCTTGAGTT	TGATACTGTC	TAGGCGCTTC	ATCTCATTAT	9000
CAAATTGATT	TTTCTTGATT	TCAAAACGAG	CCCAGCGTTC	ATCGTCCACA	AGGCCAATCT	9060
CGCGTCCCAT	CTCAGTCAAG	CGCATATCAG	CATTGTTCATG	ACGAAGAATG	AGACGGTATT	9120
CAGCACGACT	GGTCAAGAGA	CGGTAGGGTT	CAATGGTTCC	CTTGGTCACC	AAGTCGTCTGA	9180
TCATCACCCC	GATATAACCA	TCACTGCGCT	TCAAAATCAA	TTCAGGCTTG	CCTTGGATTT	9240
TCAGAGCCGC	ATTGATACCC	GCGATAATCC	CTTGGCCTGC	TGCCTCTTCG	TAACCTGATG	9300
TTCCATTTGT	CTGACCAGCA	GTGAAGAGAC	CTGAGATTTT	CTTGGTTTCC	AAAGTCGCAC	9360
GCAACTGATG	AGGCAAGACC	ATATCATACT	CAATAGCATA	ACCTGTCCGC	ATCATCTCTG	9420
CATTTTCCAA	ACCTTTGATG	GAATGCACCA	AGTCACGCTG	GACATCCTCA	GGCAGACTGG	9480
TTGAAAGTCC	TTGCACATAG	ACTTCCTCAG	TATTGCGCCC	TTCTGGCTCA	AGGAAGAGTT	9540
GGTGACGTTT	CTTGTCCGCA	AAGCGCACAA	TCTTGTCTTC	AATCGACGGA	CAGTAACGAG	9600
GCCCCACTCC	CTTGACCACA	CCTGTAAACA	TAGGCGCACG	GTGGAGGTTG	TTTTGGATAA	9660
TCTCATGACT	GGTACCATTG	GTATAGGTCA	ACCAGCATGG	TACTTGGTCC	TTGACATAAT	9720

1219

CCTCATCACG TGAAGTGTAT GAGAAATGAT TAGGCACTTC GTCTCCTGGC TGAATTTCTG 9780
 TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC 9840
 CGATTTTCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT 9900
 TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTC CCCACGGAGA GCAGTCCCTG 9960
 TCGTCACAAT AACAGCCTTA GCAGCATATT CTTGATGGGT GGCTGTACGC ACACCGACAA 10020
 CCTTGCCATC TTCCACCAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT 10080
 GGTTTTCAAC CGTCTTGC GC ATCTCCTTAG AGTAAAGTTC CTTGTACAGC TCGCACGAA 10140
 GGGCACGGAC AGCTGGCCCC TTCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTTGT 10200
 CAATGGTMTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG 10260
 CAGAACCACC GATAGAGGGA TTACAAGGCA TGAAGCCAG CATTTCAATA TTGATGGTCG 10320
 CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGTG 10380
 CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT 10440
 ATTCCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTTAAAA 10500
 AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC 10560
 TTTTCTCATC TTCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA 10620
 ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAGCTA 10680
 GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCTTCAC TTCACGGACT ACCGCGTCTT 10740
 CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTA AFACTTGCCC TTGTCTTTGG 10800
 TAACTAGAAG CTTGTGATTT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT 10860
 TGCTACTTTT TGTCGGAAAG TCTTGTGAG TCATTCTTGT CCTTTCCTT AAACGACACA 10920
 AAAACAGTCA AAATAACAAA GAAGTGCAGG ACAAAAAGC CTGCAACATC CAGG 10974

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CCCGTTATGA TTATGGATAG CGCTTTCAAA TTTTAAACT CCTATCCCAT CCTTTTATCT 60
 ATATAATAAG TGAAAATATA ATAAGTGTCA AGTAACTGAA GTGAATTTTA TAAAAAAT 120

1220

ACAAGCCAAA TTTGTAAAGT TTACTACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG 180
 TTTATTGTGC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAACATATCAA 240
 CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAAT 300
 CAAGATAAAA ACATGTGTAA GCAAATCTGC TACTACTTTAC TGGAGGACGC CAAGAATAAG 360
 AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTTGTAC AGACGATTCT 420
 AAACATATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT 480
 CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG 540
 GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGACTTTTAC 600
 GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAAGTCA ATATATCTCA CTTTTTCAAC 660
 GACAAGAAA AGGCTGATAA TCTACCAACC TCTTATCTG AACCCATCAC TCCATCACTT 720
 TTTAGCTTCA TTCGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATCCCCTT 780
 ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TCGGCTATTT CAACCAATTT 840
 TTTAGAAATC AGAGGGCGGC TCAAGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC 900
 ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTFAA CATCAATGAC 960
 ATAAGATTCT ACTGCCCAAA CCTTAAG 987

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTTCGAG TGTAGCCCAT AGCTTTGAGC 60
 GCATAGTGGA TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTTCAGT CAAATAAGCA 120
 TCTGGATTGT CAGTAAGATA GTTTTTAAGT CTATCTCTAT CAACTTTTCT TGGTTTGTGTT 180
 CCTTTTACTT GGTGGTTTAG CTCTCCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG 240
 GTATTACGTG AGATTTGGAA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACAA 300
 TAAGAGAGAA CTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT 360
 GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACTT 420
 CAAAGCACTA TAAAGTAAAT TGAACAAGA ACAATACAAA CAATCTCTGT AAACGGATTG 480
 CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACCAACCGTT 540

1221

CCTCTTTTTT	ATTACTAAAA	TTCAAAGAAT	TCCAATGCTT	TTTTCAAGAG	CAAATCCGTA	600
TATTCCTGGAT	CTTCTTGGGC	TACTTCTATT	TCCCGCTGAA	CTTTTTCCAA	ATCATCTGTA	660
ATCACTCCAT	CTACTCCTAA	GTGAAGAGAT	TGCTGATAG	CTTCTGAATC	ATTGACAGTC	720
CAGACATAAA	GTTTCTGATC	CGTTGTCCAT	AGTTTGCTTA	CAAAATATTC	ATCCAAGGTT	780
GAGTACTCCA	TAGTATATCC	TGTCGCTCTT	GTTTTAGGAA	AGACAGAATT	GTAGGGCATG	840
ATGAAATAAA	CTGGTAGTTC	GGCATCATAC	TGTCTTACTT	TTTCGACAAC	ATGGTAGTCT	900
AAAGACTGGA	TTTGATGTCC	ATAAATCTTG	AGCTTTCAG	CATAACGGGC	TAAAAAGCGG	960
TTCATCATGT	CTGGACTATC	TTTTTTACTG	GTTTTAATTT	CAATTAGTAA	TTTTTGACCA	1020
AGTTCGTTGG	CTCGACTGAG	ATAATCTTCA	AAGCTTGAAA	TTTTAGTCTG	GTAGCCATTT	1080
TCAAAAATAT	CAATCCCTTT	AAGCTCTCC	AAGTTTAAGT	CTTGAGGACT	TTTATTGATA	1140
CCTGCTAGAT	TTTTCAAGTT	AGCATCATGC	ATCATGACAA	ACTGCCCATC	TTTTGTTTCC	1200
TGCACGTCCG	TCTCCACCAA	GTCTGGTTTG	AGTTGTGCTG	TAGTTTCCAA	GGACTCTACT	1260
GTATTTTGAA	TCCCATTTGC	ATTGGAAACC	CCTCGGTGAG	AAATAAGTTG	AGGTAGATGA	1320
ACCATGGGAG	CCTCCAGATA	AATATAACCT	TCTAAGGCAA	AGAAAAGACT	GGCACAAGTC	1380
ATGACACCCC	ATCGCACGAT	GTGATCTTTT	TCTCTCCTAG	GAAGCATATC	CAGCTCCTTT	1440
CCTGTCAAAA	ATGAAACAAA	TTTAACCAAA	AAATAAGTCA	GAGCCATATA	ATAGAGATTT	1500
TTAATCACGA	CAAAATTCAA	AATACCAAGA	ATCAGAGACT	CTCTCTGAGT	GATATCATCT	1560
ACCAAAGTTT	GAGCCAATAA	TAAAGGAATC	AAAGGAAGAT	AATAATAATA	ATGTGCTTTG	1620
AGCAAGATGT	AAAATAAATT	CCAAGCATAA	AAAGTAACTC	TCTTCTTGGT	TTTCTCCAAG	1680
CTAAACATCA	CTGCTTCTCG	AACAGTCAGC	TGATCATATA	CAATCTTCGG	AAGGGCAAAC	1740
ATCAATCTGA	CAGAGACATA	GAGAAAGATA	AGAGATAGAA	GTAGGATGCT	CAGCCACCAC	1800
ATCCAATATC	TATCTTCTAA	ATAAGCTTGG	ATAAATCTG	GAATGACGAT	TTTATTAAGA	1860
TAATAAATCT	TCAGCATTTT	CCGTATAAAA	GGAAACAGCA	TAGCTATATA	GAAAAAGATA	1920
AACAAGGCTT	TAGCGCAAGT	TAGCTTTTTC	ATAAATCCAA	AACTTTCATG	GAAAACCTTG	1980
CGGATATACT	CAATTAGCCT	TCGCTTTTCA	TTATAGAGGA	GATGACGAGC	ACCAATAAAG	2040
AGGAGTCCTA	TTTGAAAATA	AGCAACCAGA	AGGTTAATTA	CAATCAAGGC	TAAAAAAGCT	2100
AGACTAATCA	ATGGAGAATG	AGTAAGGATG	GCTAAGACAT	TGTTATAGGA	AATAAAAAGA	2160
TAACCTGTCT	GATCTAATAA	GAAGCTAGCC	AACCATGAAT	TGAATGGTAC	CCACAAATAC	2220
TCCACTATCA	TAAAAATCAA	GAAAAATAGA	AAGAGGATTT	TATCAAGATC	GAGGTAAATC	2280

1222

TGTTAAGAC CCAATTTTTT AGGTTTTTCA GGTTCATAG GCACTCCTAG TCAAATAATT	2340
GAGACAAGTC CAAGCCACCA AAAGGATTGT TTGATAAGCT ACTTCTGTGC TCTACAATT	2400
CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCATC CGAGCATCCT	2460
CTAAACTATT ATGAGACTGA CCTTGAATC CAAGAAATGA GGCAACAGTT TGCAATTTGA	2520
GATTGGCAAT ACCATGTAAA TCTGAACTCC GACGTTCAA AGCTTCATCA TACAAATCCA	2580
CCTGTACTG TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACTTTTAG	2640
CAGCATTGTA G	2651

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGTTATAATA AACTTGTGAA AAAATTAACA AAGGATATCG TTCCTTGAAA GCTATGGAGG	60
AAAAATATGGC TGATAAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC	120
ACGTAGATGA GTTGGTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATTGGATC	180
AAGAACAAGT TGACTIONATC GTTGCCAAAG CATCAGTAGC AGCTTTGGAT GCCCACGGAG	240
AATTGGCTTT ACATGCCTTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA	300
AGAACTTGTT TGCCTGTGAA CACGTAGTAA ACAACATGCG CCACACTAAG ACAGTTGGCG	360
TTATCGAAGA AGACGATGTA ACAGGATTGA CTCTTATTCG TGAACCAGTT GGTGTTGTTT	420
GTGGTATTAC TCCAACAACA AACCCAACAT CAACAGCAAT CTTCAAATCA TTGATTTTCAT	480
TGAAGACACG TAACCCAATC GTCTTTGCCT TCCATCCATC AGCACAAGAA TCATCTGCTC	540
ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGCTCCTGAA AACTGTGTGC	600
AATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCCT TATGAACCAC GAAGGTGTTG	660
CGACAATCCT TGCAACAGGT GGTAATGCCA TGGTTAAGGC GGCTTATTC A TGTGGTAAAC	720
CAGCTCTTGG GGTAGGTGCC GGAAACGTTC CAGCTTATGT TGAAAAATCA GCAAACATTC	780
GTCAAGCAGC ACACGATATC GTCATGTCTA AATCATTGTA TAACGGTATG GTCTGTGCAT	840
CTGAACAAGC AGTTATCATT GATAAAGAAA TTTACGATGA ATTTGTAGCA GAGTTCAAAT	900
CTTACCACAC TTACTTTGTA AACAAAAAAG AAAAAGCTCT TCTTGAAGAG TTCTGCTTCG	960
CGGTCAAAGC AAACAGCAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGGTA	1020

1223

AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAAACATTC	1080
TTGCTGCAGA ATGTAAAGAA GTTGCGGAAA ATGAGCCATT GACTCGTGAA AAATTGTCAC	1140
CAGTTATTGC AGTTTTGAAA TCTGAAAGCC GTGAAGATGG TATTAATAAG GCTCGTCAAA	1200
TGGTTGAATT TAACGGTCTT GGACACTCAG CAGCTATCCA CACAGCTGAC GAAGAATTGA	1260
CTAAAGAATT TGGTAAAGCT GTTAAAGCTA TTCGTGTTAT CTGTAACCTCA CCTTCTACTT	1320
TTGGTGGTAT CGGGGACGTT TACAATGCCT TCTTGCCATC ATTGACACTT GGATGTGGTT	1380
CTTACGGACG CAACTCAGTT GGGGATAACG TTAGTGCCAT TAACCTCTTG AATATCAAAA	1440
AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAAACT TCCTTCAAAA ACATACTTTG	1500
AACGTGATTC AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA	1560
CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGGACCTTC	1620
GTCGCAATAA GGTGTTTAC CAAATCTTTG CGGATGTAGA ACCGGATCCA GATATCACAA	1680
CTGTAAACCG TGCTACTGAG ATTATGCGTG CCTTCAAACC AGATACCATC ATCGCACTCG	1740
GTGGTGGGTC TCCAATGGAT GCTGCCAAAG TAATGTGGCT CTTCTACGAG CAACCAGAAG	1800
TGGACTCCG TGACCTTGTC CAAAAATCA TGGATATCCG TAAACGTGCC TTCAAGTTCC	1860
CATGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG	1920
AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAAACAA CCGTAAATAC CCAATCGCTG	1980
ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTTGGTATTG ACAGTTCCAG	2040
GATTTGTTGC TGCTGATACT GGTATGGACG TATTGACTCA CGCGACAGAA GCATACGTAT	2100
CACAAATGGC TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG	2160
AAAATCTCGA AAGCTCAGTT AAGAATGCAG ACTTCCACTC ACGTGAGAAA ATGCATAACG	2220
CTTCAACAAT CGCTGGTATG GCCTTTGCCA ATGCCTTCCT AGGTATTTCT CACTCAATGG	2280
CCCATAAGAT TGGTGCACAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC	2340
CATACGTTAT CCGTTACAAC GTTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA	2400
ACTACTACCG TGACAGATGAA AAATACCAAG ATATCGCACG CATGCTTGA CTTCCAGCTT	2460
CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAACTC GGTGAACGTA	2520
TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAAGAATGG AAAGAACATT	2580
CTCGTAAATT AGCCTTCCTG GCTTATGAAG ACCAATGTTT ACCAGCTAAC CCACGTCTTC	2640
CAATGGTAGA CCATATGCAA GAAATCATCG AAGATGCATA CTATGGCTAC AAAGAAAGAC	2700
CAGGACGCCG TAAATAATTG TTTATCAGTC TAGAAGCAAG ACAAAAACCTC AATTTGAGGG	2760

1224

AAAGATCCAG TAATTTTTCT ATGATAAAAG GCATCCTATC AAGGTTTTTG AACACCTGAT 2820
 AGGATGCCTT TTTATGATAT TGAGGCCTTT TTGCCCTTTT TGAAAACTA GAATAGAAAC 2880
 AAAATATATA ATAGATTGAA ACTAGAATAG TACATATCTG CTTCTAAAAC ATTGTTAGAA 2940
 TTCGATTTGA CTGTCCTGAT CGATTTGTCC TGTTCCTTAT TCATTTTGAT ATATAAAAAA 3000
 TATAGTATAG TAGACTGAAT CTAAAATAGT ACGAAACAAT TGCTAAAACA TTTATAGAAA 3060
 TTAATTTTAC TTTTCTGATA GAGTTGTTCA CATCTTATTT CAATTCACCTA TAGTTTAATT 3120
 TAAGAGTAGT ATTTACTAAG GCCCAATTAA AATCAAAGAG CAAACTAGAA AACGAGTGCC 3180
 ATTCAGCTCA AACACTGAT TTGAGATTGC AGATAAGACT AGCCCCCTCA TTAACAGATT 3240
 TACGATAAAA CGATGACAAG GTGTGTTGCT TTTTGATTTC TAAAGAGTAT AATGATAGAT 3300
 CTCTATAAAA TAAGTGCGAA GGAAATGAGC TTTTATAGTC CTTTCGTTTT AAAATACTAT 3360
 CTCAGATATT CTTATATCGA CAAGAAGTTT TTGAGTCATT CCCTCATCAT ACATATTAAG 3420
 TAAATAGTGG CTCATTCAAT TTTTCACTAG AATAATAAGC TAGTATAGTA AACTGAAATA 3480
 AGATATAAAC AAATAAATG GAGCTTAACA TCCATTCCA GCAATTTTTT AGAAACTACA 3540
 GTGGACTATT CTAGATTCAA CATATTATAA AAAGTAGAGT AAAAGAAAAG GATTGGATCT 3600
 TGTGTAATGC AGGATCCAAT CCTTCAATC ATTTTGTCCA ACTTTGGAG GTTCCACAA 3660
 TGTAGTCGTC ATTAATAAAG ACAGATGGGA ATGACAGTGT TCCTATTTAT TTTGATAGAG 3720
 ATCGATGAAT TCTTTAGATA GCAACTGAAT AATCTCTGTT GAAGCCATTT GGTCTTCTGC 3780
 ATGCATAAAT AGCAAGGAGA ATCCTATTTT TTCCAGTA GCTTCTTTTT GTATGAGATT 3840
 AGAGTGAATC TTGTGCGCTT CTAATAAGGA GTCTTCCGCT TCTTCAACTT TAATTTTCGC 3900
 TTCTTTTAAA TTTCTGCCT TAGCTAGTTG GATGGCTTCA ATAAAGGATG ATTTGGCTGC 3960
 TCCACTATTG GCAATGAGCT GAAAACAGAT ATATTCCATT TCTTCTGTCA TCTTATTTCT 4020
 CCTATCCATG CAAGTGCCTG TTCCAGAACT TTTGCTCCAT TCATCATTCG GTAATCCCGC 4080
 ATATCAATGG TATCTACAGG GATATTTCCCT GCAATTTCTT TCACAGCAAG TAACTCATAA 4140
 CGAATTTGTG GCCCAATTAG AATGACATCT GCTTCATGGA TATTCTTTTT AGCTTCTGTC 4200
 ATTGATTTTG CTTGGATAGA GATTTCAATC CCACGTTCCAG TCGCACTTTG TTGCATTTTT 4260
 TTAACAAGCA TACTTGTCGA CATTCCCGCA TTACATACTA ATAAAATTTG TTTCATAATC 4320
 TTAACCTTCC ATTTCTTGTT CAACAACCTT GTCATTAACT TTGATAAATG GAAFGTATAG 4380
 AAGAACTCCA AGTGCAAAGA TGATGAATG AACTAGAACT GCTCTCACGT CCCCTGCTGT 4440
 TGCTAACCAT GCATTTAAGA ATACTGGTGT AGTCCAAGGA ACTTGTATAA ATGCAGGACT 4500
 CATGAATCTT GTAACCTGTT CTAAGTAGCT GATTAATAA CCAAGGACTG GAACTGTGAT 4560

1225

AAATGGAATA GCTAATGAAA TGTTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCATT	4620
GATATGGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTGTAGAGA CAGCATGCGG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC	4740
GAATGTTTGT ATTTGTGATA GGTGATGAT GTGTGGAATG GCTTGTCCAT TATTTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTCT AGGATGGCAC TGTAATAAAC	4860
TGCTTGGTGA ATACCAAATA GCCATAACAT ATTTCTTAA GAGTAAATAA TAATGACCCC	4920
GATTAAGCTT GTACCAATAT GACGAATTGG TTCTTGAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC	5100
AAGTTCATT TGTAAGCTT TAACGTTTGA TAATCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCCAGCGAA CATTGCGCCT GTACCTGTGT TGTGGAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAACTACAG AAAGTGTATT TGGCATCATC	5280
ACAATTAAG AAATAATGA TAGCATTGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATACTGAAATACT TAAAGTACCG	5400
TTTGCAATTG TTATPCCCCA ATATTGGAAT CTTGTTAATG TATCCCCTTG GAAAATCCAC	5460
TTAAATACCG TGTGTGTTCAA AAGAACGATT AAACCTGCCA AAATATATAA TGGCATTACT	5520
GTTACGAATG CATCTCTTAG GGTTTTTTAA TGAATTTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGG GTTATTAAAC CCCCTTTTT AAAAAAA	5638

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTGTCTT GAACTATTTT	60
GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GGTGTGTAG ACCACCACCG TGTGGCTAAC TTTGAAACTG CAAGCCCACT TTACATGCGT	240
TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTTACCGTA TGTCAAAGA ACATGGTGT	300

1226

GCTGTGCCTA AAGAGATTGC AGGTTTGATG CTTTCAGGTT TGATTTTCAGA TACCCTTCTT	360
TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCATTTG CTCCTGAATT GGCTGAATTG	420
GCTGGTGTGA ACTTGGAAGA ATATGGTTTG GCAATGTTGA AAGCTGGTAC CAACTTGGCT	480
AGCAAATCTG CTGAAGAATT GATTGATATC GATGCTAAGA CTTTTGAACT CAACGGAAAT	540
AATGTCCGTG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTTTGGGA ACGCCAAGCA	600
GAAATGGAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG	660
ATGATTACAG ATATCGTCAA CTCAACTCA GAAATCTTGG CTCTGGTGC CAATATGGAC	720
AAGGTCGAAG CGGCTTTCOA CTTCAAACTT GAAAACAATC ATGCCTTCCT TGCTGGTGCC	780
GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAGATTTT	840
GGGTGTGAGC TCAAAAATCGG AAAGTCTAGT TTGCCTTATA TCGCAAGGAG TTTCGGCTCC	900
TTTTTTCTAG GAGTGAAGTA TGTTAGAAAA TGGCGATTTG ATTTTTGTGA GAGATGGGTC	960
AGACATGGGA CAGGCCATCC AGACTTCCAC AGGTAACATAT AGCCATGTTG CCATTTATTT	1020
GGATGGGATG ATTTATCATG CTAGTGGACA GGCTGGTGTG GTCTGTCAAG AACCGGCAGA	1080
CTTCTTTGAG TCCAATCATT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC	1140
GGTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCTTAC AATGCTTCTT TCTATCCAGA	1200
TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAAACTAT	1260
TCCTATGAAA TTTGGAGwTG GGGAGCAGGA GATTAGTGAT TTTTGGAGGG AGTATTACAT	1320
AGAACTAGGT CTGCCTGTTT CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGGCAGC	1380
ATCGCCTCTG TTACAATGTA AAGAAAGGAA TCTTCATGAT TCAGATTTTT AATCCATCTC	1440
GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT	1500
GATTCTACGG GAAATTAAGG CTCAATTTCC AGATGTTGCA GTTGATAAAC TCATGGAAGA	1560
GTATATAAAG GCAGGCTTGA TTCTACGTGA AAATAAGCGC TATTACCTCA ATTTTCCTAC	1620
GCTTGAATCA CTTGATAGTC TTGAACTGGA TCAAGAGATT TTTGTCAGAG AAGCTAGTCC	1680
GGTCTATCAA GCCTTGTGAG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC	1740
AGCTATTTTA GTTGAAGAAGA CGGACTTTGC GCGCATTTAA ATGACCCTGT CCAATTTATTT	1800
TTACAAGGTC AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT	1860
AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTTTTGT TGAAATTTCT	1920
CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGATATCTTT GTGGACAGTT AGGTTGTCTT	1980
AGGCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATCGATT TTGATAAGGA	2040
GAGGTTAACT TTCTACTTAG CGTGATTTCT TGTTTCTGAG TACATTTGTT GACTTTCTCT	2100

1227

AGTATTCGGT	ATAAACTATA	TGTAACCGGT	AACACATATC	GGAATAAACT	AAAGGAGACA	2160
ATCATATGTC	ACTTGAAAAC	AAATTGGAAC	AAGCAACAGG	CGCTGTCAA	GAAGGTTTGT	2220
GTAAAGTTAC	TGGAGACAGC	AAGACAGAAC	TTGAAGGAGC	TGTTGAAAA	ACAGTTGCTA	2280
AGGCAAAAAG	CGTTGTAGAA	GACGCAAAAG	GTGCTGTAGA	AGGTGCCGTT	GAAGGTTTGA	2340
AAAACGTTTT	TACTAAAGAA	TAGGAAAAAA	TCAAGGGTTT	CATTTTCCCT	TGATTTTTTC	2400
TATTCCTATA	AATAATTTTC	TGCGACGGCT	GTATCTCCTG	GGTAGGATTC	TTTCTTGCCC	2460
TGGATGATTT	GGTAACAATC	GGCTCCCTTA	CCCACAATA	TAAGTGCATC	TAATTCGTGA	2520
TTTGTGATAG	CCATTGCCGC	CTTGATGGCT	TCTTGGCGAT	CCGCAATCTT	TTCAACAGGA	2580
TGATTGATGT	AGCTACTAAT	TTCATCTGCA	ATGGCCATTG	GGTCTTCATA	GTTAGGGTCA	2640
TCAGCAGTCA	GAAAGACTTG	AATCTCAGGG	TGTTGATTGA	GGAGGAGGCC	AAAGTCCCTA	2700
CGACGACTTT	CTCCCTTGT	TCCTGTTGAT	CCCAGAACCA	GAGCAATCTT	TCCGGTTTGA	2760
TGAGTTTCAA	CCACATTGAT	GAGTTTTTTC	AGACTATCCC	CATTGTGGGC	ATAGTCGATG	2820
AAGACCTTGG	CTCCATTTTT	CTGAGTGAGG	ACTTCCATAC	GACCAGGAAC	GCGGGTTGCA	2880
GCGATGCCTT	TTTTGATGTC	CTCAAGACTT	GCTCCGAGAC	GGAGACAAGC	AAGTCCAGCA	2940
GCAACTGCAT	TTTCTTGTT	GAAGTTGCCA	ATGAGTTGAA	TATCATAATC	TCCAGCGAGT	3000
TTACCCGTAG	CTGAAAAGCT	AAAGGCTTTG	GAATCTCGA	TTTGGTTATC	AAATTGGCTA	3060
CCATAGAAAT	CATGGTCTTG	ATCTTCAACC	TGTTCTTTCA	AGACTGAGAA	GTGGTCCATG	3120
TCACTGTAA	TGATGACTGC	TCGGCTCTTT	TCCATCAAGA	GACGCTGTG	GTAGAAATAG	3180
TCTTCAAAGC	TAGGGTGTTT	AATCGGGCCG	ATATGGTCTG	GGCTGATATT	TAGGAAAAC	3240
CCCACATCAA	AGGTTAGACC	ATAGACACGT	TTGACCAGAT	AGGCTTGACT	GGAGACTTCC	3300
ATGATGAGGT	GGGTACGGTC	ATTTTGCA	GCCTGATTCA	TCATGTCAA	GAGGTCAATA	3360
CTCTCAGGG	TTGTCAACGC	TGACTTAAAG	AAAGTCTCGC	CATCAAGAGT	TGTGTTTCATG	3420
GTCGACAACA	TAGCAGGTCT	ATGCCCTTGA	GATAAGATGT	TATAGGCGAA	ATAGGCTGCT	3480
GTTGTCTTAC	CCTTAGTACC	AGTAAAGGCA	AGGAGTTTGA	GTTTTTCTG	TGGATTACCA	3540
TAGAACTCCA	TGGCAATCAA	ACTCATGGCT	TTCTTTATAT	CGTTCACAAT	GATGACAGGG	3600
ATACCGACTT	CGTAGTCCTT	TTCAGCTACA	TACCAAGCTA	ATCCTTGTGT	TATAGCAGAA	3660
AGAAGGTATT	CTTTTTTAAA	GGCAGCGCCT	TTTGCAAAA	AAAGAGTGTC	TTCTGTFACT	3720
TTTCGGCTGT	CGTAGCTGAT	GCTATCAAAA	ATAACTTTGC	TGTAGTTGTA	GTGGTAATGA	3780
CCTTGGTCAA	TAATTTCCGC	AAAAAGGCCA	TCTTTCTTTA	AAATATCTAA	TACGGTTTCA	3840

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ATCTTAATCA TACTTTCTAT TGTAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCCAGA TGTTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACTTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT	4140
TCTTGTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGATATGCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGTT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCT	4440
ATGCCATGAG CCAAATGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT	4500
TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAAACCTTG	4560
CTGCCTTTGT CGGTATGGTA GCCAGTTTGT CAGTCTTGAT TTATTTCCCTT GCCCAAGAAG	4620
GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGGTTG	4680
ATACCATTAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA	4740
TTTTG	4745

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAAACCATC ACACCAGTTA TACCATTTTG CTTCATACCC ATCTTGAGCT	120
AGGATACGAT CTTCTAAATC AAAAACAGAG TAAATCTTTC TTTCTCGCA AGCTTGCGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA	240
CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG	420
ACTTTCATTT CTTTCTCCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTTAAATCGC	480

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CATTGGAAGC GGAgCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCC CAAGCCCACA	540
CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAActCCCA GATAGACTCT TGATACCAGC	600
ACACTGACTA GGTAGAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA	660
ATCCGCTGAC TAAGAATAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATGC	720
CCACTTGGGA AGGAAAATCC CTTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC	780
TGGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCAGCATG	840
AAGAACTTT CTATCTTCCA TCGCTTACGA TAAAAGACAA AAGCTGTAAT GACAACCCAA	900
GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAAGAAT AGTCAAATAA	960
TCTGGTAAAGT CTCCTCGAAT GGCAGTCTGA ATCGATTGGT CAAAATTGAC CAACATTTCA	1020
GGGTAATAAT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAA ACTGCCCTTC	1080
ATTAAAAATG TTTGTTTATC TCTCATAATG TTTTAAAGTT GGTTC AAGA GAACATACAA	1140
CAACCAGAAT GAAACGGAAA AGATAACACC TTCAATCAAG TTAAGGTA ATACCATGGT	1200
CATTAGGTAG TTGGAAAGTC CCAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA	1260
CAAAGGAACA GCATAACAT AGTTGAGAAC CAACATGGCC AAGGTAAAC CAATAGTTCC	1320
AGCTAGAGAG CCTAGTAGGA AACGAAGGT TGTCCGTTC TTTTCCAAA TCAAAGCAA	1380
TACGATGACA AAAACTCCCA AAGCTACGAT ATTCATCGGC AAACCAATGT AAGTATTCAC	1440
TCCTTGCTG TTAAGAAGCA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmCsC	1500
AGGCAAATCC ATGACCACCA GACCCACAAG GACTGGCAAG ATACTAAAT CGATCTTGAG	1560
GAAAGATGCC GCTGGTAAAA GCGGAAAGTC AAAGTACATC AGCACAATG AGATGGCTGA	1620
TAGAATTGCA ATGGTCGAAA GTCGACGTGT GTTGTGTCATA ACAGGTTCCCT CCAATTTTCT	1680
ATAAAATCAG AAGAAGTTGG AAAGGATTC TCTATCTATT CTCACTTTT ATATCCCAA	1740
AGTTCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTACAATCCG GCTATAAATC	1800
TATCAAACA GACAAGCTA TTCTTTCGTC TTCTCCATC CAGACTATAC TGTCGGTTGT	1860
GGAACTCAC CACATCACGT TGCGCTCAC GACTTCTTTA	1900

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT	60
GAATAATGAT ATTTTTTACC ATGATAGTAA TTTGAAAAAG CCTAACCACC TCCTGAACCT	120
TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTCATTTTA	240
TTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA ACAAATAAA TCCTCCTCTC	300
TCTTTTATTG AAACCGCTTT CTATGTGAT AAGAATAACT TTTTATtAT TGTTGTCAA	360
GGAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG	420
TAGTTTTATT TCAAAATAAT ATGCAACCAG TACTAACCAA ATATAAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTTAACT	540
AAAAAGCAAT TCAAACTATT GTAAAATTC TAGCAAAAAG AGAGCCGAAA CTCTCTTTT	600
TATCTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT	660
AGGATCAACA TGGCTATTGC TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTCAGAAAA	720
GATAGAACCA ATAAAAATCAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTCTGG TGTCGCAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG	840
ACTAAATAGA CCATCTTCT CTCTTCTAG CTCTTATTCA GCTGATTTTT TCTTCTTGTT	900
AGCTTCTCA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGGATAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG	1020
AGGCGTCTTG ATAACAGCTG TTTGGTCCTT AGTAGCTGAA CGAACGTTGG TCATTTGTTT	1080
TGCCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTC	1140
TTCATAAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTTCTTCGA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC	1260
AATTTCCCTT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAAA CCACGCGCTG GAACAAGGAA	1380
GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTT	1500
AAATGGTTCA CATTTAATAC CGTCGATTTT TTTTACGATA ACTTCTGGAC GAGATACTTG	1560
AAGTTCATAG CCCTCACGAC GCATTGTTT GATAAGGATT GACAAGTGCA ATTCTCCACG	1620
TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT	1680
TTGCAATTCT GCCTGCAAGC GTTCTCCAC CTTACGAGAA GTTACCCATT TACCTTCTTT	1740

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ACCAGCAAAT	GGTGAGTTGT	TGACCAAGAA	AGTCATTTGA	AGAGTTGGCT	CATCGATGTG	1800
TAGGATTGGA	AGAGCTTCTA	CTGCATCTGT	CGGAGTGATG	GTTTCACCGA	CAAAGATGTC	1860
TTCCATACCT	GAAACGGCAA	TCAAGTCACC	CGCTTTGGCT	TCTTGGATTT	CACGACGTTG	1920
CAAACCAAAG	AAACCGAAGA	GTTTTGTAAC	ACGGAAGTTT	TTAGTTGTAC	CGTCAAGTTT	1980
AGAAAGGGTA	ACTTGGTCCC	CAACCTTAAC	TGTACCACGG	AAGACACGAC	CGATACCGAT	2040
ACGTCCAACG	AAGTCATTGT	AGTCCAAAAG	TGACACTTGG	AACTGCAAAG	GCTCATCTGA	2100
GTTATCTACT	GGAGCTGGGA	TATGGTCGAT	AATCGTGTCA	AAGATTGGTG	CCATAGTCGC	2160
TTCTTGGTCA	GCTGGATCAT	CTGACAATGA	AGAAGTCCG	TTGATCGCTG	AAGCATAAAC	2220
CACTGGGAAA	TCAAGCTGGT	CGTCATCTGC	ACCAAGCTCG	ATGAAAAGTT	CCAAGACTTC	2280
ATCCACTACT	TCTGCTGGAC	GAGCTGATGG	CTTATCGATT	TTGTTAACAA	CCAGGATTGG	2340
GACAAGGTCT	TGTTCCAAGG	CTTTTTTCAA	TACGAAACGA	GTTTGTGGCA	TGGTTCCTTC	2400
ATAGGCATCT	ACGACCAAGA	CAACACCGTC	AACCATTTTC	ATGATACGCT	CAACTTCTCC	2460
ACCAAAGTCC	CGGTGTCCTG	GTGTGTCCAT	AATGTTGATA	CGAGTTCCTG	TGTAAGCAAC	2520
GGCAGTATTT	TTAGCAAGGA	TGGTAATTCC	ACGCTCTTTT	TCGATATCGT	TTGAGTCCAT	2580
AGCACGCTCT	GCCAATTGAG	TCCGTGCATC	AAGCGTTTCT	GATTGTTTCA	ATAATTGCTC	2640
AACCAGGGTT	GTTTTACCGT	GGTCAACGTG	GGCGATAATC	GCAATGTTAC	GGATATCTTC	2700
TCTTAATTTT	GTCATGATTT	CCTCTATAAT	ATTCAAAATT	TATTTTCTAA	CTGAACGATT	2760
ATACCATAAT	TTCAAATAAA	TAACATAACT	CAAGCAAGTG	TAAATGTTTT	CACTCTGCTT	2820
TTCTTTTTCAC	GTCAAGCCTT	TTCAAAGCGA	GCGACTTATG	ATAAGATAGG	CACAGTATGC	2880
GTTTAGATAA	TTTATTAGCT	CAAGAAAAAA	TCAGCCGAAA	GGCCATGAAG	CAAGCACTCC	2940
TCAGAGGGGA	AATTCTAGTC	GATGGTTGCC	CAGCCCGCTC	CCTAGCTCAA	AATATCGATA	3000
CAGGACTACA	AGAACTCCTT	TTTCAGGATC	GAATCATTCA	AGGCTATGAA	CACACCTATC	3060
TTATGCTTCA	TAAACCTGCT	GGTGCCGTTA	CAGCCAACAA	AGACAAGGAA	CTTCCGACCG	3120
TCATGGACCT	GCTTCCATCT	AACATCCAGT	CTGACAAGCT	CTATGCCGTT	GGCCGACTGG	3180
ACCGAGATAC	AACGGGACTC	CTCCTCTTGA	CCGATAACGG	TCCCTTGGGC	TTTCAGCTCC	3240
TCCATCCCCA	ATATCATGTC	GATAAGACTT	ACCAAGTTGA	GGTTAATGGA	CTTCTAACAC	3300
CTGACCATAT	CCAAACCTTT	CAAAAAGGAA	TTGTCTTTTT	AGATGACACT	GTCTGTAAC	3360
CCGCAAAACT	AGAGATTCTA	TCTGCAAGTC	sCTCCCTCAG	TCAAGCCTCT	ATCACCATTT	3420
CAGAAGGAAA	ATTTTCATCAA	ATCAAGAAAA	TGTTCCCTCTC	GGTTGGTGT	AAGGTGACTA	3480

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GCCTCAAAAG	AATCCAATTT	GGGACTTCA	CATTGAACCC	AGATTTAGCA	GAAGGTAAC	3540
ACCGCCCTTT	GAACCAAAAA	GAGTTACAAA	TCATTA AAAA	CTATTTAGAG	ATGAGTCGAT	3600
AAAACAAAA	AAGCTTTAAA	ACTAAAGCTT	TTTTCTTTTA	TTTACCGAAA	AATTAAGGCG	3660
ATTGTACAA	TCCAGTTAAC	TACAGAAATC	ACAATTCCTA	AGATATTAAG	AATCTTTTCT	3720
ATTTTATAGT	CTAATGTGA	CTCTTTTGG	TATGAAATAG	CCAAGACCAA	TCCTATGATA	3780
CCCAAAATCA	GGCCTACAAT	TGGAAATAAC	AAACCAAGAA	TAATCGACAA	GATACCCACA	3840
AAAAGTGAT	TTTTCTTCTT	TTCTTTTATG	TTCTAAGAAC	TCCTTAAAT	TTATACAAAT	3900
TAATTATACT	ATAAAACAAT	AGCTTCATCC	TATCATTCGA	CTAATTTGGA	AATAAGGTTA	3960
GCTAGTCTTC	ACTTCCCTT	TCCAAGAATC	CAAGCCATAA	GAAAGGATAT	AAATCTCAGA	4020
AAAACCTTGT	TTTTTCAAGT	AAAGAGCTGC	ATTTGTAAC	CGTTGCGCAC	GTTGGTTTTC	4080
GTAGAGAAGG	ACAGGTTTAT	CTTTACGAAG	GGCTGCAAGA	CTAGTTTCA	ACTGACTTGA	4140
AGGAATATTG	CGTGCACCAA	GGATATGTTT	TCTGTGGAAT	TCTGCTGGGT	CGCGCAAATC	4200
AATCAATTGA	CCCCTACGAA	TCAAGCTTC	AAACTCCTCA	TTGTCCACAA	TTTTAGCCGC	4260
ACGGCGAATA	CGAAGATAGT	TAAAGCCCAT	CCACGCCAAC	ATTGCTAGTA	TAAGTGCCCA	4320
CAAAATCCAA	GTAACCATTA	GTTCTTTTCT	CCATTTTCT	CAATATAATC	CAATCTACC	4380
TTGTGCTCTC	TGCGAAGAAC	TGCTTCTGCC	TCTAGATAGT	CTAATTTATC	CATCAACCCT	4440
GCATCGTAAA	TCCGAGATAG	TTCCAACCTC	ATCAGTTCAA	TATCATATAA	GCGTTTCCC	4500
ATGTAACAA	TAATACCAA	TCGTTTGAGG	AATTGCTGCA	CATCATAGAA	TGTTTTCATA	4560
AGACTCATTC	TAGCAAAAT	TTGTGTTTTT	TTCAAGAAGA	GACTCACACA	ATGCTCCTTA	4620
TTTTCCATC	TTCTTAGCG	ATTCTAAGGC	AAGTATGGTA	CAATAAAAAC	ATGGGGATTC	4680
AACAATTACA	TT					4692

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC	TGATAATCTT	CGACTCCTGT	ATATGATGTG	TCTTTTCATG	TAAGACACGC	60
GCCGCCAGAA	TCATGGCAAG	AGCTGCAAGA	CTGGCAAGTA	AGAAGCCGAT	AAGATAGGCA	120
AAAAGATAAG	TGAATTTGAC	AAAGAAAGTC	AAAAGAACTA	GGAAACCAA	GCCTCCTCCA	180

1233

AAAAC TACCA AAGCTCTTCG TAAATCCCAG ATTTTATCCA ACTGCTTGAC GAGGGAAGTC	240
GTCTGACGAA CGCCTACAAT AGTTGCTAAC ATACTTCCTA AAAAGAATGG ATAGACATGA	300
GTTAAACTGG AGAAATAAAC AGAGGAATAA GAGGTCAC TA GAAAAC TACC AATAAACATG	360
GAGAAGAAAC TGATCAAGAA GGCAACAGCA GATAAGAGAA AGACCATCCC CTTCAACTGA	420
CCATTTGATT TAGCTTGTTT GGATAAGAAC CAAACTGCCA ATCCCCAAAG AATATAGTAG	480
TGAACCTCAA CTGCCAAACT CCAATTATGA ACAAACAAAT GAGGAATGAA CTGAGATTCA	540
TAAC TCCCAC CTGTTAGGAG TTCATAGAAG TTGGTCATAA AGCCTAAGAC GCCCGCAATC	600
TGGCCACCAA TTCCAGCAAC ATAGTCTTGG CGAACCAAGA AAGTAAAAGG CATGGTCACC	660
AAGACCATCA AAACCACAGG TGGCACAATC TCGATAAAAAG CGTCTT	706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTGATGG GCAATATCAG TCATAGAAAT TTTTCAATT AACTTTTGAG CAATTTTGTG	60
GTTGATGATA CGAGGGATTT GGTGATTTTT CTTTACCAGG GGAGTCTCAG CAACCATCAT	120
TTTTGAACAG TGATAGCACT TGAACGGCG TTTTCTAAGG AGAATTCTAG AAGGCATACC	180
AGTTGTTTCG AGGTAAGGGA TCTTAGACGG TTTTGAAAG TCATATTTCT TCATTAGACT	240
TCCACAATCA GGGCAAGATG GAGCCTCATA ATCCAGCTTA GCGATAATTT CTTTGTGGGT	300
ATCCATATTG ATGATATCTA GAATCTTGAT GTTTGGGTCT TTAATATCGA GCAGTTTGTG	360
GATAAAATGT AATTGTCCA TATGATTCTT TCTAATGAGT TGTTTTGTCG CTTTTCATTA	420
TAGGTCATAT GGGACTTTTT TTCTACACAA AAATAAGCTC CATAATATCC ATAGGGGATT	480
TACCCACTAC AAATATFATA GAGCCC GAAA ATATGGGAAA ACTGATCCTT GTTCTGCTT	540
TTGTCTATAG AAGAATAATA AAGATTATCT TCTTCAAAT CTCCGATATT CTCTAAAGTT	600
TTGTGCAAGT TGCACAGAAC TTGTTTATTT TTTTGGTCAT CTGCCATAG AAATATAAAG	660
CGTTTTCATA TATAATATAA TTATCAAAAAG ACAAAGGAG TTCACCTCAT GGTAGAATTG	720
AATCTAAAA ATATTTACAA AAAATATCCA AACAGCGAAC ACTATTCAGT TGAAGATTTT	780
AACTTGAACA TCAAAGATAA AGAATTTATC GTTTTCGTAG GACCTTCAGG ATGTGGTAAA	840

1234

TCAACTACAC	TCCGTATGAT	TGCTGGTCTT	GAAGACATTA	CAGAAGGTAC	TGCATCTATC	900
GATGGCGTAG	TTGTCAACCA	CGTAGCTCCA	AAAGACCGTG	ATATCGCCAT	GGTATTCCAA	960
AACTACGCTC	TTTACCCACA	CATGACTGTT	TATGACAACA	TGGCTTTCGG	TTTGAAATTG	1020
CGTAAATACA	GCAAAGAAGA	CATTAACAAA	CGTGTCCAAG	AAGCAGCTGA	AATACTTGGA	1080
TTGAAAGAAT	TCTTGGAACG	TAAACCAGCT	GACCTTTCAG	GTGGTCAACG	TCAACGTGTT	1140
GCCATGGGGC	GTGCGATTGT	CCGTGATGCG	AAAGTAT'TCT	TGATGGACGA	ACCTTTGTCA	1200
AACTTGGATG	CCAAACTTCG	TGTATCAATG	CGTGCTGAAA	TCGCTAAAAT	TCACCGTCGT	1260
ATCGGAGCTA	CAACTATCTA	TGTAACTCAC	GACCAAACAG	AAGCGATGAC	ACTTGCAGAC	1320
CGTATCGTTA	TTATGTACAG	TACTAAGAAC	CCTGCTGGTA	CAGGTACTAT	CGGACGTGTA	1380
GAACAAATCG	GTACTCCTCA	AGAAGTTTAC	AAAAATCCAG	TTAACAAATT	CGTTCAGGA	1440
TTCATCGGAA	GCCCAGCTAT	GAACTTCATC	ACCGTGAAAT	TGGTTGGTAG	CGAAATTGTT	1500
TCTGACGGTT	TCCGTTTGAA	AGTGCCAGAA	GGAGCATTGA	AAGTTCTTCG	TGAAAAAGGC	1560
TACGAAGGAA	AAGAATTGAT	CTTTGGTATC	CGTCCAGAAG	ACGTGAATGC	AGAACCTGCT	1620
TTCTTGAAA	CATTCCCAGA	CTGTGTTGTA	AAAGCGACTA	TCTCTGTATC	AGAACTGCTT	1680
GGTTCAGAAAT	CTCACCTTTA	CTGTCAAGTT	GGTAAAGACG	AGTTTGTTCG	AAAAGTTGAT	1740
GCTCGTGACT	ACTTGCAAAC	AGGTGCAACA	GTTGAGCTTG	GATTTGACTT	GAACAAAGCA	1800
CACTTCTTCG	ATGTAGAAAC	TGAAAAACA	ATCTACTAAA	ATAAATAAAA	TTCAAAGCAC	1860
TACAAGAAAA	GATATCTCTT	TATCAAT'TGT	AGTGGAGAGA	TATCAGTTAA	TCTAGGGAGA	1920
GAAACAAAAT	GCTTCTCTCC	TTTTTGCTAG	AGAAGTCATA	TTATGCATCT	ATATTGTGAT	1980
GCTCTTTAAT	ACTCTTCGAA	AATCTCTTCA	AACCACGTCA	ACGTGCGCCTT	GCCGTACGTA	2040
TGATTACTGA	TTTCGTCAGT	TTTATCTGCA	ACCTCAAAGA	TGTACTTTGA	GCAGCTTACG	2100
GCTAGTTTCC	TAGTTTGCTC	TTTGATT'TCC	AT'TGAGTATT	ATTTGTGGGT	ACCATCTACA	2160
AGTGAAGCTA	TATGCGTAAA	CTACGTGAGC	AATGAATTC	GAAGTAGAGA	GGTAATAATA	2220
AATTTATGCT	ATAGTTATGG	TGACTTGTAT	GCTTTTGATT	CTAGTTTATC	AAATAATAGA	2280
TTAGAATTGT	CAGATAATAT	CATTTTGTGT	TATAATGAAG	AAAAACAGA	GGTGTTCAAA	2340
TGTCAGAAGC	AGGTCATAAG	TTTTTAGCAA	AAT'TGGGAA	AAAACGCTTA	CGTCCAGGTG	2400
GAAAGCGTGC	CACAGATTGG	TTAATTGCAG	AAGGAGGATT	TTCAAAAGAA	AAGAGAATAC	2460
TAGAGGTTGC	GTGTAATAGG	GGAACACAG	CAATTGAGTT	GGCACAGCGT	TTTGGTTGCA	2520
AGATAACTGC	TGTTGATATG	GATGCTCAAG	CTTTAGAAGT	GGCTAAAAAA	TCTGCTGGAA	2580
CGGCAGGTGT	TGCTCATTTA	ATCAGTTT'TG	AAAGAGCAA	TGCAATGAAA	CTTCCTTATC	2640

1235

AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG 2700
 CTAAGAAAAA ATGTGTAATG GAATATCTAA GGGTATTAAA ACCTGGAGGT CTTCTCTTGA 2760
 CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA 2820
 TTCATGTAAA TGTAGGTCCT TTAAGTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG 2880
 GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA 2940
 TTTATGACGA AGGTTTGCTA GGAAC TTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA 3000
 ATAGAAAGCA GTTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAACAG AAATTGGGCT 3060
 TTATTGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTTT 3120
 CCTTTTTTCT TTCTTAAAAA ATATGCTATA ATAGAGAGTA AAAAAGTTTG AAAGAAAGAA 3180
 AAAGATGAAT TTTAAAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG 3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT CAAATGGGTT AGTTTGCCAC ACTTGGTTTA TATGGTCGTG GAAAGCATGG 60
 CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGCTATTTT TGTTTAGGTT 120
 TGTAAGTTAA TTCATTGTCA CATATTACTC TTAACTGAT TGAGTGAGTA CCGCTTATAT 180
 TTGATGCCAA ACGCCTTAAA AGTGTTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC 240
 CGCTCATFTG AACTATCTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT 300
 TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA 360
 ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA 420
 GTAGCTTCAA ACTCTGTAAG TGTTGCACCT TTACCATAAT TCCACCCCTC TTTAATTTGT 480
 TTGATCATTT CGGTTAGGCT TACAAAAAGC ACACTCTFAG GTTCTCCTTT TGTCTTATAC 540
 CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAAGTG TTTTCCCAAT CCCTGTACCT 600
 CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA 660
 AATTCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTAA AATCATCAA AGTTTTAGTT 720
 TTAAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT 780

1236

AGTTTAGCAT	TCAAATTATC	AGCAATCGCA	TCTTCTTCAT	CTTGCTTTTT	CTGTTCTTCT	840
TGGCATTGTT	CACAATAGGG	TGGGATACAG	CGAACTTCTT	TTATTGCCTC	TCCGTTCTCA	900
TTCCACCCCA	CTACTACATG	TCTTTCTCCT	TTGATTTGTG	TTAGCTGTAT	TTCATGCTTA	960
GGACACAATT	CGTCTAGTTT	AAATGTCTCA	ATATTTCCCTA	AACTAGATTG	TAATGATTTT	1020
ATTTTCTGAC	CTCCTAAAAT	GGTTTTTCTT	GTGTTGGTAT	CCAATCTTCA	TAGCTGGTAG	1080
GCTCTAGTTG	ATTGGTTTGC	TGTTTTTTAG	CCTCACGCGC	TGCCCTGCTA	TTTCTAACAA	1140
GTTCCACCGT	CAATAAATG	TCCTGTTTCC	AACGGTTAAG	GATTACCTTG	ATGTATGCAA	1200
AGTTTGCTTT	ACCCTGACTG	ACAGCCTCTT	TTAACGCCTC	ATGGATAAGC	TCTGGGCTAA	1260
AATCTTCTAG	CATATACTGC	AATCTTTGAA	TCTGTAACGG	TGACAATGCT	TTACCTGTCT	1320
CAGCTCGCTT	CATATTC AAC	AAGTCGTCTA	TTTCCACACT	GGTTACTTTT	TTATTTACAA	1380
AATCAGAAAT	CAGTTGAAAA	ATGTTTGGAC	TTTGTAGCTG	GATTCAGCC	ATTACCTCAT	1440
CAAATCTGTC	TTGTGTCATG	TTGTCTAAAT	CTAGTGTCAT	TGCATTGCCT	CCTCAAACCT	1500
CTCTATAAGA	CAACTTTTAT	TTGCTTTCTG	AGTTCATTT	TTAGAGTTAA	AAAGAATATC	1560
TTTTAAGGTT	ACAGTAGCCT	CTAAATACTC	CTTTTCAGCA	TGCTCTATAT	ACGCCTGTTG	1620
CTCTGCTTCG	TTCTCAAAAA	AGTGCTTAGC	TTGGCGTTTA	AAGAATGCTT	TTCGCATAGC	1680
GTCCATTTC A	AAAATACCAG	GGGCGAAAAA	CATTCCCGTA	GTGCTTTTAG	AGACCGCTTC	1740
GATTTTATGG	CTTTCATTCA	ATTCAGGAAG	TTCAATCCAA	AGTAAACGGG	ACAACTCATC	1800
TTTGATGGAT	TTTGTCTGAC	TTTCCAATAA	AGAAAGGAT	CTTAGGCCAT	TTTCTTCGCT	1860
AATTTCTCGC	ATTTCTGCGC	TAATPCTGTC	TATACGTCTA	GTTAAATTCT	CATATGTTGT	1920
TTCTGTGTCATG	TTTTTACCTC	TGTTTCTTTG	TTGGTGTGAT	TTTTTAGCTT	ATTTTTTTAC	1980
TTCTAAACAT	CATTGTCTTA	ATTTCCCTGAT	AACTCATTTT	CAATCAATC	ATAGCTATTG	2040
CCATATCCCTC	AAATGCCTGG	TACTGCTCCA	ACTCCTCACT	AGTCAAGCTA	TCGATACCGT	2100
TATAGCCCCC	ACGCTCTTCT	CTTAACTGCT	TAGCGTTCAT	GTCTGTTACT	GCCTTTAGTA	2160
GCAAGTTGTT	CATGGTGCTA	TGCGCGTGCT	TTGGTGCATT	AGGCCATGTT	TCTATACTGT	2220
CATGCAAGGT	TTTTCTTTTC	GGTTTTTCTA	GCGCCCTCTG	CAGACGAATT	TCAGAAAGTT	2280
CCTCACGCAT	TTCAAAGAA	GCTTTGACTA	GGTTTAGTTT	GAATTGCCGT	ACTGTTTCGG	2340
TATTCTTTTAA	ATAAGTGATC	AGAAAAGTAG	CCTGTTGCTC	GTTCAGAATA	TAGGATTTTT	2400
TAGGTTGTCC	TCTAGTATCT	AATTTATGGA	TTTTAAATCC	AAGTATTCCC	AACTCTTCAA	2460
AGTCAGCCTT	ATTTTCTCTT	ATTAAGCGCG	TGATAGTGTG	GTGTTGTA	TCAGCACATT	2520
CAGCGATGAT	CTCGCTTGTG	GTGTACGGCT	CTTTCTTACC	GTCCATGTAA	ACTAGTTCCA	2580

1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTTAATGCC TCCTCTAGCC	2640
TCTTTTFTAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCTCT	2700
ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCGTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATTCAAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA	2820
AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCCT TTCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGACTAATTT	60
ATGTATTTTT ACGAGTCAGT ATCTTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTGTAC	120
TACTTGTAA AACTGGGATA ATTTTCGACT GTTAAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAATG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAAC TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCCTGA GGTTTTATCA CCTGCAGGGA CTTTAGAGAA GCTAAAGGTA GCTGTTTCACT	360
ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATGG TCTTCGTAGC CGTGCGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT	540
TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACTATGA AACCCCTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCCG	720
GTGAGGTTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGGAGCTATG TGTATTTTCACT ACTCTGGACG TTGTACTCTT TCAAACCACA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC	900
TTTACGATAT GCCATTTGGG AAAGAACGTA AGAGTTTGCA GGGTGAGATT CCAGAAGAAT	960
TTTCAATGTC AGCCGTTGAY ATGTCTATGA TTGACCACAT TCcAGATATG ATTGAAAATG	1020

1238

GTGTGGACAG	TCTAAAAATC	GAAGGACGTA	TGrAGTCTAT	TCACTAyGTA	TCAACAGTAA	1080
CCAAC TGCTA	CAAGGCGGCT	GTGGATGCCT	ATCTTGAAAAG	TCCTGAAAAG	TTTGAAGCTA	1140
TCAAACAAGA	CTTGGTGGAC	GAGATGTGGA	AGGTTGCCCA	ACGTGAACTG	GCTACAGGAT	1200
TTTACTATGG	TACACCATCT	GAAAATGAGC	AGTTGTTTGG	TGCTCGTCGT	AAAATCCCTG	1260
AGTACAAGTT	TGTCGCTGAA	GTGGTTTCTT	ATGATGATGC	GGCACAACA	GCAACTATTC	1320
GTCAACGAAA	CGTCATTAAC	GAAGGGGACC	AAGTTGAGTT	TTATGGTCCA	GGTTTCCGTC	1380
ATTTTGAAA	CTATATTGAA	GATTTGCATG	ATGCTAAAAG	CAATAAAAATC	GACCGCGCTC	1440
CAAATCCAAT	GGAAC TATTG	ACTATTAAAG	TCCCACAACC	TGTTCAATCA	GGAGACATGG	1500
TTCGAGCTCT	TAAAGAGGGG	CTTATCAATC	TTTATAAGGA	AGATGGAACC	AGCGTCACAG	1560
TTCGTGCTTA	ATGTAGTTGT	TTAGTTTAA	AAAAC TATGC	AAAGCTCCAT	ATACAACACT	1620
TAAACGAGAT	TAAAGAATGG	CGAAA TCCCT	TGATGCGCAA	GAGATTAGCT	GTCTTTTFTA	1680
TTTTTTAAGT	GATAAAGTCG	GAGTTTAGGC	ATCAAAGCCT	ATCAAATTA	ACAAAGAAGC	1740
GATGTCTTAG	ATATTTTGAA	AAAAATTAAT	AAGCAGAAA	CTCTCTATTA	TTTTGTGTGA	1800
GAGAGTTTTT	TGTTAATAAA	ATTTCAAAA	ATGACATTTA	TATATTGCAT	TAAGTTAGAT	1860
ATATGATATA	ATATTGTTAA	AAAGAGGCGC	AACTTTTAA	AATTAATGAG	AATCAAAGAG	1920
AAAACCAATA	ATATTAATGG	AGGAATAAAA	AATGTAAGTA	AGCATTATGG	TCATTCAATC	1980
ATTCTCAAAG	ATATAAATTT	TGCAC TTAAC	AAGGGTGA	TTGTTGGTCT	AGCAGGGAGA	2040
AATGGAGTTG	GTAAGAGTAC	GTTGATGAAA	ATTCTTG TTC	AGAATAATCA	ACCGACTTCA	2100
GGTAATATTA	TAAGCAGTGA	TAATGTTGGG	TATTTAATCG	AAGAACCAA	ATTATTTFTA	2160
TCTAAAACAG	GTTTAGAGAA	TTTAAAATAT	TTGTCAAAT	TATATGGTGT	TGACTACAAT	2220
CAAGAAAGAT	TTAGATGTTT	GATCCAAGAG	TTAGATTTGA	CTCAGTCTAT	TAATAAAAA	2280
GTAAAGACCT	ATTC TTTGGG	TACAAAACAA	AAATTAGCTT	TGCTTCTAAC	TCTCGTACG	2340
GAACCTGATA	TATTGATTTT	AGATGAACCG	ACTAATGGTT	TAGATATTGA	ATCATCACAA	2400
ATAGTTTTAG	CGGTCTAAA	AAAATTAGCT	TTACATGAAA	ATGTGGGAAT	TTAATATCG	2460
AGTCATAAAT	TAGAAGACAT	TGAAGAAAT	TGTGAGAGAG	TTCTTTTCTT	GGAGAACGGG	2520
CTTTTGACAT	TTCAAAAAGT	AGGAAAAGAT	AGTCATAAT	TCTTGTTTGA	GATAGCTTTT	2580
TCATCAGCTA	CAGATAGAGA	CATTTTCATT	ACCAACAAG	AATTTGGGA	TATTGTTTAG	2640
GAAGAGGGAT	TGAGAATTAC	TATGTCTGGG	AATAT TCAA	ATAGTGAGCT	TTTTAAATTT	2700
TTTAACGAAA	ACTCTATTAA	AGTAGTTGAT	TTTGAAACTA	AAAAAGAGAC	GCTTAAAGAT	2760
ATTTACCTAA	ATCGTTCAA	ATAAAGGAAG	GTTATAATCA	TGAAATTA	TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCTT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA	2940
GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATw TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTGC GG AACTCAGAA AAGAAAGCAG	120
ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC CTTGGAATTT ACAGAGTTCA	240
CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC	300
AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAGT GCCAACAAGT	420
ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC TGTACCGAAT GACGCTACAA	480
ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAAC TGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACTTG AAAATCACTG	600
AATTGGACGC TAGCCAAACA GCTCGTTCAT TGTCATCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG	720
ATGAAAAC TC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATGG GAAACATCAC	780
CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT	900
GGGAGAGAAA ATTCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC	960
GTTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240

TTGAAAAGGA	TCATGTAGCC	CAGCATTATT	TTGAGGTTTT	GCGTACCTTG	ATTTCTAAGA	1080
AATCAGTCTT	TGCCCAGCAG	GTGGACTCA	AGGAAGTCGC	AAATTATCTG	GGTGAGATTT	1140
TCAAGCGTGT	TGGAGCTGAA	GTGGAGATTG	ATGAGAGCTA	TACAGCGCCC	TTTGTCTATGG	1200
CACATTTCAA	GAGTTCGCGT	CCAGATGCCA	AGACCTTGAT	TTTCTATAAC	CACATATGACA	1260
CTGTGCCAGC	GGATGGGGAT	CAGGTCTGGA	CAGAGGATCC	KTTTACGCTT	TCGGTCCGCA	1320
ATGGCTTCAT	GTATGGGCGT	GGGTTGATG	ACGACAAGGG	TCATATCACA	GCTCGCTTGA	1380
GTGCTTTGAG	AAAATATATG	CAGCACCATG	ATGATTTACC	TGTC AATATC	AGCTTTATCA	1440
TGGAGGGAGC	GGAGGAATCG	GCTTCAACAG	ACCTAGATAA	GTATTTGGAA	AAGCATGCAG	1500
ACAAACTCCG	TGGGGCGGAT	TTGTTGGTCT	GGGAACAAGG	GACCAAAAAT	GCCTTGGAAC	1560
AGCTGAAAAT	TTCTGGTGGC	AATAAGGGGA	TTGTGACCTT	TGATGCCAAG	GTAAAAAGCG	1620
CTGATGTGGA	TATCCACTCG	AGTTATGGTG	GTGTTGTGGA	ATCAGCTCCT	TGGTATCTCC	1680
TCCAAGCCTT	ACAGTCTCTT	CGTGCTGCCG	ATGGCCGTAT	CTTGGTTGAA	GGCTTGTACC	1740
AAGAAGTACA	AGAGCCCAAT	GAACGAGAAA	TGGCCTTGCT	AGAAACTTAT	GGTCAACGAA	1800
ACCCAGAGGA	AGTTAGTCGG	ATTTATGGAT	TGGAGTTGCC	TCTCTTACAG	GAGGAGCGGA	1860
TGGCCTTTCT	AAAACGTTTC	TTTTTCGATC	CAGCGCTTAA	TATCGAAGGA	ATCCAGTCTG	1920
GTTATCAAGG	TCAGGGTGTT	AAGACTATTT	TACCTGCAGA	AGCCAGTGCC	AAGCTAGAGG	1980
TTCGTCTGGT	TCCGGGCCTA	GAACCGCATG	ATGTTCTGGA	AAAAATTCGG	AAACAGCTAG	2040
ACAAAAATGG	CTTTGATAAG	GTAGAATTAT	ACTATACCTT	GGGAGAGATG	AGCTATCGAA	2100
GCGATATGAG	CGCACCAGCC	ATCTCAATG	TGATCGAGTT	GGCCAAGAAA	TTCTATCCAC	2160
AGGGCGTTTC	AGTCTTGCCG	ACGACAGCGG	GGACAGGACC	TATGCATACG	GTCCTTGATG	2220
CCCTAGAGGT	ACCAATGGTT	GCATTCCGGTC	TAGGAAATGC	CAATAGCCGA	GACCACGGTG	2280
GAGATGAAAA	TGTGCGAATC	GCTGATTATT	ACACCCATAT	CGAATTAGTA	GAGGAGCTGA	2340
TTAGAAGCTA	TGAGTAGAGA	TATTATCAAG	TTAGATCAGA	TCGATGTGAC	TTTTACCCAA	2400
AAGAAGAGAA	CCATCACAGC	GGTTAAGGAT	GTGACCATTC	ACATCCAAGA	AGGGGATATC	2460
TACGGAATCG	TTGGATATTC	TGGAGCAGGA	AAATCAACCC	TTGTACGGGT	GATTAATCTC	2520
TTGCAAAAAC	CATCTGCAGG	GAAAATTACC	ATTGACGACG	ATGTGATTTT	TGACGGCAAG	2580
GTGACCTTGA	CGGCAGAGCA	GTGCGTTCGT	AAACGTCAAG	ATATCGGAAT	GATTTTCCAG	2640
CATTTTAACC	TGATGAGCCA	AAAGACAGCA	GAGGAGAATG	TAGCCTTTGC	CCTTAAACAC	2700
TCTGAACTCA	GCAAGGAAGA	AAAGAAGGCT	AAAGTAGCTA	AGTTGTTGGA	CTTGGTTGGT	2760
TTGGCAGATC	GTGCTGAAAA	CTACCCTTCA	CAACTATCTG	GAGGGCAAAA	ACAGCGTCTG	2820

1241

GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT 2880
 GCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA 2940
 TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC 3000
 CGTGTTCAG TTATGCAGGA TGGGCATTG ATGAAGAGG GTAGTGTGCT TGAAATCTTC 3060
 TCAAACCCTA AACAACCTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA 3120
 GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGCTTGAAAA CAGTCTCTTG 3180
 GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG 3240
 CATTACCAAG TAATGGCTAA TATTCTCTAT GGAATATCG AAATTCTCGA TGGTACTCCT 3300
 GTTGGAGAAT TGGTGGTGGT TTGTTCAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA 3360
 GCCATTCTGC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC 3420
 ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG 3480
 GGAACGGCT ATCTACTTAA CTCTTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT 3540
 CTTGGGGCTA GTGGCAGGTC TCTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGAGAA 3600
 TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCTTTTAT 3660
 CATCCTCTTG GCAATCTTGT CACCACTTC TCACTTGATT GTTAAAACAA GTATCGGGCC 3720
 AAATGCAGCC CTGTGCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG 3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTCGTC GGGACAGGAG CTGTTGTTTT 60
 TGGAAATGGT CTGATGGCC TTGGTCACCT TGGAAATCGCC TTGCCCTTG GTTGGCAAT 120
 CGTGGTGCA GCCTACTCAA TCGGAATGT TTCAGGTGCT CACTTGAACC CGGCTGTTTC 180
 GATTGCTATG TTTGTAAACA AACGTTTGT ATCTTCAGAA CTGTAAACT ACATCCTTGG 240
 TCAGGTTGTT GGAGCTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAACCTCAGG 300
 TATGTCAACT GCTAGTCTTG GTGAAAATGC CTTGGCAAAC GGTGCTACTG TCTTTGGTGG 360
 TTTCTTGTTC GAAGTCATCG CAACTTTCTT GTTGTATTG GTTATCATGA CTGTGACTTC 420

1242

AGAAAGCAAG	GGCAATGGCG	CGATTGCTGG	TTTGGTAATC	GGTTTGTCAT	TGATGGCGAT	480
GATTCTTGTC	GGATTGAAGA	TTACTGGACT	TTCAGTAAAC	CCAGCTCGTA	GCTTGGCACC	540
AGCTGTCTTG	GTAGGCGGCG	CAcCCTTCAA	CAAGTTTGGA	TTTTCATCCT	TGCACCAATC	600
GCTGGTGGAG	TTCTTGCAGC	CCTTGTGCA	AAAAATTTCC	TTGGAACAGA	AGAATAATTG	660
AAACTCAAAA	AGCCTTGCTC	CTCATCTTGA	GGAACAGGGC	TTTTTCGTAT	GATACTCTTC	720
GAAAATCTCT	TCAAACCACG	TCAGCTTCAT	CTTGCCGTAG	TATGGTTACT	GACTTCGTCA	780
GTTCTATCCA	CAACCTCAAA	ACAGTGTTTT	GATCTGACTT	CGTCAGTTCT	ATCTGCAACC	840
TCAAAACAGT	GTTTTAAGCT	GACTTCGTCA	GTTCTATCTG	CAACCTCAAA	ACAGTGTTTT	900
AAGCTGACTT	CGTCAGTTCT	ATCTGCAACC	TCAAAACAGT	GTTTTAAGCT	GACTTCGTCA	960
GTTCTATCTG	CAACCTCAAA	ACAGTGTTTT	AAGCTGACTT	CGTCAGTTCT	ATCCACAACC	1020
TCAAAACAGT	GTTTTGATCT	GACTTCGTCA	GTTCTATCCA	CAACCTCAAA	ACAGTGTTTT	1080
GATCTGACTT	CGTCAGTTCT	ATCCACAACC	TCAAAACAGT	GCTTTGAGCA	AcTGCGGCT	1140
AACTTCCTAG	TTTGCTCTTT	GATTTTCATT	GAGTATGACT	TTAGCGGTTG	TCAATTTTCT	1200
CTGGATAAAG	GTCGTGTTGG	AAGAGGCGTT	GTCTGCCAA	GCCTCATAC	TTAGTTCCCT	1260
GCTTACCGTA	GTTGTAGTAG	GGGTCGATG	AAATGCCACC	GCGCGGAGTG	AATTTTCCCC	1320
AGACTTCTAA	ATAGCGAGGG	TCTAGCAAGT	TGACCAAGTC	TTTCCCGATG	GTGTTGATAC	1380
AGTTTTCGTG	GAAATCTCCG	TGTTTCGGT	AGCTAAATAG	ATATAGTTTG	AGGGATTTTG	1440
ACTCGACACA	GAGCTTGTC	GGAATGTAGG	AAATATGAAT	CGTCGCAAAG	TCTGGCTGAG	1500
CAGTGATTTG	TCCCAGCAGA	GACATATCGA	GGATATGGTG	ACGAATGCCC	TGTTCCCTTAG	1560
CGATTTCTCT	AGTAATTTGA	ATTTGAGGT	GATGACGTTG	GCCGTAGGCA	AAGGTGACAG	1620
CTTCGACTGT	TTCATAGTGT	TGCATGACCC	AGAAAAGGCA	GGTTGTTGAA	TCTTGACCAC	1680
CACTAAAGAC	GACCAAGGCT	AATTGACGTT	TCATAGTACT	CCTTCCAAA	TGGGAAATGT	1740
TCAGAGCAG	CAAAAAGCTC	CCATTAGGGA	GCTAAAAAAT	ACCAAATCGA	GGTTTTTTTA	1800
GCGATGGCAT	ATCCCAAACA	TCGTAATATT	CTACTTATAT	AGTAAAATGA	AATAAGAACA	1860
GGACAAATCG	ATCAGGACAG	TCAAATCGAT	TTCTAACAAT	GTTTTAGAAG	TAGAGGTGTA	1920
CTATTCTAGT	TTCAATCTAC	TATAGTCTAG	CATATTTTTT	GAAAAATGGC	AAAGGGCAAG	1980
AAAAAAGAGA	CCAAAGAAAG	TACTTGGTCT	CTCGTTTGAT	TAGCTCAATT	CAGCAATGAT	2040
GGCCTTGATT	TGTTCTGCTG	TGTGAACACC	TGCAACTTGT	TTGACAACPT	GGCCGTCTTT	2100
TTTGAAGAGA	AGAGTTGGAA	TAGACATGAT	TCCAAAAGCA	CGAGCTGTGT	TTGGATTTTC	2160
ATCAACGTCC	ATTTTAACGA	TTTTCAAGAC	ATCTTCTGAA	AGTTCTTCAG	ACAATTTGTC	2220

1243

CAAGATTGGA CCTGTCATAC GACATGGACC ACACCAAGTT GCCCAGAAGT CTTACTAAGAC	2280
CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT	2340
TCTCCTTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC	2400
CATAAGTCCC ATGGTAGTCC AAATTATGAC CCTTGTAAGT TAATTTTTGG ACAGGGTAGT	2460
AkkCTGCGAC GCCGATAAGG CAAGCTTGT GCGAACGTTT AAAGTCTTCA TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGTTTT CAAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA	60
AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA	120
ACATTCGAAA ATTATAATGT TTTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA	180
GTCTTATCAA CACCCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTTTATCT	240
ATTGGTAATT TTTAAACAAA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAAACTAAA	300
TTCGCTAGAG TATTATTAGG TGTTTTGAAA GTTACTCAGC ATAATTCACG CAAAACCTGG	360
TATTACGTCC CCCTCCAAGA CTTTACGGTC AATTCGGACA TTGATTGGAC ACAATCAGTG	420
ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATGCGCTTT	480
ATTGAGAATC ATGTAAGGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC	540
AATGATCTAA AATGACTATA TAGGATTAGG TCAGGAAGCA TACGATGCCC TGACCCTTTT	600
TGTACTTATG AGATGAGAAA GTCATTTGTT AGATAAATTG ACTCGTTAGC AAACGTTCAA	660
AAAAGGAAAA CTTATGCCAG TAGAAATTA AACCCTAAA GAAATTCATC CTAAAATCTA	720
TGCCTACACC ACACCGACAG TAACCAGTAA TGAAGGCTGG ATTAAGATTG GGTATACAGA	780
ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GCTCATATAG CTACAGATGT	840
CTTATGGACT GGTGATGCAG CTTATACAGA AGAGCCTGAT AAGGGGAAAA CTTTCAAGGA	900
CCATGATTTT CACCATTTC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG	960
GTTCTATTTT AATGGAATC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTTCAGCA	1020
TGATTTGTCT GGTTATCAGC CTGAAAAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA	1080

1244

AGAAGCAGTT	GCTAAGACAT	TAGCTTATTT	CCAAGAACAT	GCTGGAGGCA	AGTTTCTCTG	1140
GAATGCCAAG	CCACGCTTTG	GTAAAACCTT	GTCTACCTAT	GACCTAGCTC	GACGGATGGA	1200
AGCTGTCAAT	GTCCTAATTG	TAACAAACCG	CCCTGCCATT	GCTAACTCAT	GGTATGATGA	1260
TTTTGAAACA	TTCATAGCAG	GTCAAACGAC	TTACAAGTTT	GTTTCTGAAT	CAGATAGCCT	1320
TAAGAGTCGT	CCAATCTTGT	CACGACAAGA	ATTTCTTGGT	ATTTTAGCTG	ACGATGTAAG	1380
ACAACTTGCT	TTTATCAGTC	TCCAAGACTT	GAAAGGATCT	GTTTATTTAG	GTGGAGAGCA	1440
CGATAAACTC	AAATGGGTAA	CTGATCTGCA	TTGGGACTTG	TTGGTTATTG	ACGAGGCTCA	1500
TGAAGGAGTT	GATACCTTCA	AGACTGACCA	AGCCTTTAAT	AAGATTCGAC	GAAATTTTAC	1560
TCTGCATTTG	TCAGGTACAT	CATTTAAAGC	ATTTGGCTAAA	GGAGATTTTA	CAGAGGAACA	1620
AATCTACAAC	TGGTCTTATG	CTGATGAGCA	GGCTGCTAAG	TATTCGTGGT	CTCTTGAGCA	1680
AGAAGAGGAA	AATCCTTATG	AAAGCTTGCC	TCAGTTGAAT	CTCTTTACCT	ATCAAATGTC	1740
TCAGATGATT	GGCGAAAAGT	TAGAAAAAGG	CGCTCAGATC	GATGGTGAAA	ATATTGACTA	1800
TGTTTTTGAC	TTAAGTGAAT	TTTTCGCTAC	AGATGATAAA	GGGAAATTTA	TTCATGAGCA	1860
TGATGTCAGA	AATTGGTTAG	ATACTCTATC	AAGCAATGAA	AAATATCCAT	TTCAACCAA	1920
AGAACTCCGT	AATGAACTCA	AGCATACTTT	TTGGCTTTTA	GAACGTGTCG	CTTCGGCCAA	1980
AGCATTAATA	GCCCTACTAG	AAGAACACC	AATCTATGAA	AACTATGAGA	TCGTTCTAGC	2040
TGCTGGTGAC	GGACGTATGT	CCGAAGAAGA	CGATAAAGTC	AAACTCAAAT	CCTTGGACTT	2100
GGTTAGAAAA	GCGATAGCAG	AGAATGACAA	AACCATTACC	CTATCCGTTG	GTCAGCTGAC	2160
GACAGGTGTC	ACTATCCCTG	AATGGACAGG	TGTATTGATG	TTATCAAATT	TGAAATCACC	2220
AGCTCTTTAT	ATGCAGGCCG	CCTTCCGTGC	TCAAAATCCT	TACTCATGGA	GCGATAACAA	2280
AGGAAATCAC	TTTCGCAAAG	AAAGAGCCTA	TGTATTTGAC	TTTGCGCCGG	AAAGAACCTT	2340
GATTCTCTTT	GATGAGTTTG	CCAACAACCT	ATTGCTTGTA	ACTGCAGCTG	GTAGAGGAAC	2400
TTCAGCTACA	GCGAAGAAA	ATATTAGAGA	ATTATTAAC	TTCTTTCCAA	TTATTGCCCA	2460
AGACCGTGCT	GGTAAGATGG	TTGAAATGA	TGCAAAGGCA	GTTCTAACCA	CTCCTCGCCA	2520
GATAAAAGCT	AGAGAAGTTC	TTAAACGAGG	TTTATGTCC	AATCTCTTAT	TTGATAATAT	2580
TAGTGGTATT	TTCCAAGCAA	GTCAAACAGT	TTTAGATATT	TTAAATGAGC	TGCCAGTTGA	2640
AAAGGAAGGG	AAGGTACAAG	ATAGTTCTGA	TTTATTAGAT	TTTTCAGATG	TTACAGTCGA	2700
TGATGAGGGA	AATGCAGTAG	TAGACCATGA	AATGTAGTT	AATCAGCAAA	TGCGACTTTT	2760
TGGTGAAAAA	GTTTATGGAC	TTGGTGAATC	TGTTGCTGAG	TTAGTCACAA	AAGATGAGGA	2820
ACGAACTCAA	AAACAGCTGG	TCAATGACTT	GAGTAAGACC	GTTTCTTCAG	TGATTGTAGA	2880

1245

GGAATTGAAA GCAGATTATT CTCTAAAAAC AAGGGAAACT GAGCAAATTA AGAAACAAAT	2940
TACAGCAACA CTTGAGAATG AAATTCGAAA AAATGATATC GAAAGAAAAA TTTCTGAAGC	3000
TCATATCAAG CAAGAGTTGC AACAGCAGCT CAAAGAAGCA AATGATAAAG CGCAAAAAGA	3060
TAAGATTCAA GAAGATTTGG AAAAACGTTT AGAAGAAAAT AACTCATTC ATAAAGAAAA	3120
ACTAGAACAA ACACTCAAAA AAGAAGTGA AAAAATGCCT GAGAAATTTA TCGAACAGGT	3180
TGAGATAAAA CGTGTGGAAC AGTTGAAACA ATCAGCTCAA GATGAAATTC GTGACCATTT	3240
ACGAGGGTTT GCAAGAACAA TTCCAAGTTT TATTATGGCT TACGGTGATC AACTCTAAC	3300
ACTTGATAAT TTTGATGCCT TTGTTCTGA ACATGTTTTT TATGAAGTAA CAGGGATTAC	3360
GATTGATCAG TTTAGATATT TGCGAGATGG TGGGCAGGAT TTTGCAGGGC ATCTCTTTGA	3420
TAAAGCAACA TTTGACGAAG CTATTCAAGA ATTTCTTCGC AAGAAAAAG AGTTGGCGGA	3480
TTATTTTAAA GATCAAAAAG AAGACATTTT TGACTATATT CCACCGCAGA AGACCAACCA	3540
AATTTTCACT CCTAACGAG TGGTAAAAAG GATGGTAGAT GATTTGAAA AGGAAAATCC	3600
AGGGATTTTT GATGATCCAT CTAAGACTTT TATTGATTTA TATATGAAGT CAGGCCTCTA	3660
TATTGCAGAA CTTGTGAAGC GGTATATAA TAGCAATGGC TTGAAAGAGG CCTTTCCAAA	3720
TCCTGAAGAA CGCTTAAAAC ATATTTTGA AAAGCAAGTT TATGGATTTG CTCCGTCTGA	3780
GATTATCTAT AACATTTCCA CTAATTTTAT ATTTGGCAAT CTTTCTAAAG ATATCAGTAG	3840
GAAGAATTTT GTTTTAGCAG ATACCATTCC AGCGGCTAAA GAAGGGAGCA TTCAAAAGTT	3900
GGTTGATTCC TATTTTAAA ATAATTAAA AGAAGCCGA GTCAAAATTC TTTGAAATCA	3960
GAAAAACGC ATAATATTGA GTGCTTTTGT ACTGCCCCC AAAAGTTAGA CAGAAAAAT	4020
CTAACTTTTG GGGGCAGTT CAGACAATCC TTGGTATTAT GCGTTTTATT GTGGGAAGAT	4080
GTATAATGGA TTGAAATAAG ATATGAACAA ATCAATTAGG AATTTAAAGC ATTTTATAAC	4140
AACGTTTTAG AGTAATGGGG GGCTATTTCA ACTTCAACCT ACTATAATAC AGAAAAAAC	4200
AACTCCCTGA TAATCAAGG AGTTGTCTAT AGTTAAATTA GTTTTITAGAA GCTTCTTGGA	4260
ATTCTGGGTT TTTCCATGCT TCGTCAATGA TAGCTTGTA TTTCTTAGCA GATGCTTGCA	4320
TTTTTTGAGT TTCTGCGTCG TTCAATGGGA TATTTACTGG ACGAACGATA CCATGTGCAC	4380
CAACAACAGC TGGTTGACCG ATAAAGACAT TCTCAACTCC GTATTGACCT TCTTGAATA	4440
CTGAAAGTGG AAGTACTGCG TTTTCATCGT CAAGGATTGC TTTAGTGATA CGAGCAAGGG	4500
CTACTGCGAT ACCGTAGTAT GTTGCACCTT TTTTGTGAT GATTGTGTAG GCTGCATCAC	4560
GAACACCTTC GAACAATTCA ATCAATTCAG CTTCTTGAAC ATTTTGAGTG TCTTTAAGGA	4620

1246

ATCTTTCAAG GTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC	4680
CGTGTTCACC CATGATGTAG GCGTGCCTG AACGAGCATC CACATCCAAT TTTTCAGCAA	4740
GTGCTTGACG GAAACGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTCTTTAG	4800
GGAAACCAGA GAATTTCCAA GTTGAGTAAG TCAAAACGTC AACTGGGTTA GCAGCAACAA	4860
GGAAGATACC TTTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTTG TTGATAGCAA	4920
GGTTTTTACC TACAAGGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCTGCAGTGA	4980
TCACAACAAG GTCAGCGTCT GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTLAGGTG	5040
AAGTGAAGGC AAGGGCGTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT	5100
GTGGAATTC GATAATCCA AGCTCTTGTG CAATTCCTTG GTTAACAAGT GCAAAGCGT	5160
AAGATGAACC TACAGCACCA TCACCGACAA GGATAACTTT TTTGTGTTGT TTAGTTGAAG	5220
TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC TCTAAAAAAT TTTAAGGAGA ATCTAGCAA TGGAATTCAC ATGGGCACCTG	60
AAGTATGCCA CTGAATTTTT GGGAACTGCC ATTTTGATCA TTCTTGGGAA TGGTGCAGTT	120
GCCAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAGTG GCTGGATCGT CATCGCTGTT	180
GGTTATGGTA TGGGGGTAT GATCCCAGCC TTGATGTTTG GTAACGTATC TGGGAATCAC	240
ATCAACCCTG CTTTCACTCT AGGGCTTGCA GTTAGCGGTC TTTTCCCTTG GGCACAAGTG	300
GTACCTTACA TTATCGCGCA AGTCTTGGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA	360
ACATACCGTC CATTCTACTT GAAAACGTAA AACCCAAATA ACATCTTGGG AACTTTCTCA	420
ACTATTTCAA GTATTGACCA TGGTACAAA GAAAGTCGCT ATGCAGCAAC TGTC AATGTT	480
TTGATTAATG AGTTTGTGTT TTTCAATTTT TTGTTCTTTG CAGCTCTTGG TTTGACTAAA	540
AACTTCTTTG GTGCTGAAAGT GCTTCAATTC ATGAAACAAA AGGCAACAGA AGCAGGACAA	600
ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAGGA	660
CTTCTGTGG CTCACTTGGC ACTTGGATTC CTCGTTATGG CTTTGGTAAC ATCACTTGGG	720
GGACCTACAG GACCTGCCTT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT	780

1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG 840
 GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT 900
 TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA 960
 TCAGACTGGk TCTCTCTTTT kGATTTTtaG GGAAATGAAA GAAcTCTAAA CAAACTCCTC 1020
 TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT 1080
 GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCTCC 1140
 AATCAAATTG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT 1200
 CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTTCT 1260
 CAAACATTGT GAGGAATTGA TTTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCAATTT 1320
 TACTATAAAA TAAGCGATTA GGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC 1380
 TATGATTGTT ATCGTTTTAT CTGCAATTTT ATACTCAATG AAAATCAAAG GGCAAACATA 1440
 GAAGCTAGCC GCAGGTTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAACTAG 1500
 AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT 1560
 TGCCCTATTC TTGTTTCATT TTAATATATA AACAGAGAC TGTTTACATT TTCAGCAAGT 1620
 GAGTGGATGG ATAATGCTGA AACTCCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA 1680
 ATTAGTTAAA TTTTTACCAA GAATAATFCA CAAAACGTT GTAAAACACT TGCAATTTAG 1740
 CTGAAATTTG ATAAAATAGT AAGGAAAGTT AGACTGTATT GCCTACTGTC TATCTATAAAA 1800
 ATATATTTTA TTGGAGGCTT TTAATCAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC 1860
 ACACGTTAAC ATGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC 1920
 TATCACAACCT GTTTTGGCAC G 1941

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTGG GGAAGTTTT 60
 ACTTGGAACCT GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTTAAAAAG ATAGGGAGTG 120
 ATAATCATGC AAGATAACTT TTTATTTGAG GAAATTGAAG AAATTCAGT ACCAGTTAAT 180

1248

GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTTGGTT TAGCAATCCT TGCTCTTGCT 240
 GGTGTTGAA GTTTGTTTCAT TTACTAACAT CAAGCTTTTT CAATTTTCATF TTAGACAGTC 300
 ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT 360
 TGATTGCGGA CTGAGGGACT AGAGTATGTT TTAAGATAAT ACCTACTCCT TATGAGGGAC 420
 TTAGGTTTGT TATGAGAATF GTTGATAAGA TTAAGATAAT ACCTACTCCT TATGAGGGAC 480
 ACTATCATT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA 540
 ATGGTTAGAG CAACTAATAG GTCAAGAATF TACCATATCG GACTTATTAG TGTAGTAGG 600
 GAAGAAATAT TTTTAAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT 660
 ATAAAAGATT TAATAAGAAT TTTGAAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG 720
 ATACATGAAA TTAGTCATGC AATAATTGCT AATAA 755

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGAATTG ATTTTCCAAA AAGAATACAA 60
 TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG 120
 CCAAGATGAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA 180
 CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC 240
 CATCTCTATT TATGTGGAG TTTGGGGATG TGAAGGAGA TAAACAAGTT AATGTTTACG 300
 TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGACT 360
 AAAGTGAGAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTTAGGTG AAGGCAATCA 420
 TCGCTTTATA TTATTTTTC AAGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA 480
 ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTT CTTTTTTAGT AGTAGGATTG 540
 ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCAGAG GAAATGGATC GATGCGCGT 600
 GGGGATGATT ATCCTGCTTA TTATAAAAAT GGGAGCCAGG AGATTGATCA GTGGCGCATG 660
 TATTCTCGTC AGTGTACTTC TTTTGTAGCC TTTCTTTTGA GTAATGTCAA TGGTTTGTAA 720
 ATCCGGCAG CTTATGGAAA TGCGAATGAA TGGGGACATC GTGCTCGTCG GGAAGGTTAT 780
 CGTGTAGATA ATACACCGAC GATTGGTTCC ATFACTTGGT CTAAGTGCAGG AACTTATGGT 840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT 900
 GGTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTTATT 960
 CATTTTAAAG ATTTGGATGG TGGCAGTGGT GGAATAGTC AATCCTCAAC TTCAACAGGC 1020
 GGAACTCATT ATTTTAAGAC CAAGTCTGCT ATTAAAAGCT AACCTCTAGC TAGCGGAACT 1080
 GTGATTGATT ACTATTATCC TGGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC 1140
 GGCTATAAGT GGTTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG 1200
 GCTGTGAATA AAAATCCTCT AGGTAAtTCT GTTCTTTCTT CAACAGGTGG AACTCATTAT 1260
 TTTAAGACCA AGTCTGCTAT CAAAAGTAA CCCCTAGTTA GTGCAACTGT GATTGATTAC 1320
 TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG 1380
 TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT 1440
 TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG 1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1027 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGAAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT 60
 GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTCTTGT TGGTGGTGAA AACACTGTTG 120
 TCGGAACTCC ACTTGTGCT GGAGCTACTG TAGTTGGAAC TGTGAAAAA CAAGGAAAAC 180
 AAAAGAAAGT GGTACTTAC AAGTACAAAC CTAAAAAGG TAGCCACCGT AAACAAGGTC 240
 ACCGTCAACC ATATACAAA GTTGTCAATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC 300
 ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA 360
 CTGGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTCTACGC 420
 TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTTGCAGG CTATGAACCA ATCCTAGAAT 480
 TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC 540
 AGAGAGAAAT GACCCAGTTA TTCTTTGAAT CATTPTTCTT AGGTATGGCA AACTTATCGG 600
 AGAACTATTC TGAGTTCGTC CAAACCAGAG TTATCACAGA AAATAACAC GGAGGAAAAC 660
 ATTATGTTAA AAATGACTCT TAACAACCTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT 720

1250

TCTACATCAA	ACGGACGTGA	TTCACAAGCA	AAACGTCTTG	GAGCTAAAGC	AGCTGACGGA	780
CAAACGTGAA	CAGGTGGATC	AATCCTTTAC	CGTCAACGTG	GTACACACAT	CTATCCAGGT	840
GTAACGTTG	GTCGTGGTGG	AGATGATACT	TTGTTGCTA	AAGTTGAAGG	CGTAGTACGC	900
TTTGACGTA	AAGGACGCGA	TAAAAACAA	GTGCTGTTT	ACCCAATCGC	TAAATAAAAA	960
GGTCCATTGA	ACCTTTTATC	CCGAACCTTG	AAATGTAGAG	GTGAGGAAGC	TAGAAACAGC	1020
TTAAAAAT						1027

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT	GGTGCAGGTA	AATCTACGTT	AATTAATCT	ATTGTAGGTT	TTCAAGAGAT	60
TTATTTAGGA	GAAATAGAGT	ATTGTGATAA	AGATTTGATA	GTTAGTTCTC	AACCTTTTGC	120
TCATTTAGGC	TTTACTCCTC	AAACCACAGT	AATTGATTTT	TATACTACTG	TGAAGGACAA	180
TGTAATATTG	GGGCTGAACC	TTGCTGGAAA	GTTTGGGAAA	AATGCTGAGA	AGTTGTGTCA	240
AATAGCCTTA	GAAATGTGTG	GGTTAGCTGA	TAAAAAAAT	AATTTGGTAG	AAACATTGTC	300
AGGTGGACAA	CTGCAACGCG	TCCAGATTGC	TAGAGCAATA	GCTCATAATC	CAGATTTTTA	360
TATTTTAGAT	GAACCTACCG	TTGGTTTAGA	TACTGAATCT	GCCGAAAAAT	TTTAAATGTA	420
TTTAAAAGAT	AAGAGTTTGG	AAGGAAAAAC	TATTATCATA	TCTTCACATG	ACATAAATCT	480
ACTCGAAAAG	TTTTGTAAAA	AAATACTTTT	TTTACAAAAT	GGCTCCATAT	CATTTTTTGG	540
TGATATGCGT	GACTTTGTAG	ATAATTCAAC	TATCAAATTA	AATTTTTCAA	TGCAGAATAG	600
AATTTCTAGA	TATCAAATTG	AATTTTTAGA	AAATTTTTAGA	TTTAAAGTTC	ACATCGAAGA	660
TAATGATAGT	TTTACAATAG	AAGTCCCTAT	AGAAGAAAAG	ATCTTAGATG	TTATCAATGA	720
GGTAGGAAA	GCATGTGAAA	TTAAAACTT	TTCAACAAGT	AAATTAACCT	TACAAGAAA	780
TTATTTGCAA	AGAATAGGAG	GAGAAAAATG	AAGGCTGATC	AATTAAGGCA	CAAATCGGAC	840
TTAGGTTTAA	GAGGTCTAGC	GATTATTGCT	AAAAATGAGA	TTATTGCTTT	TTTLAGAAGT	900
AAAGGTTTAA	TTATTTCTCA	GTTTCTACAA	CCAATCTTAT	ATGTTGTTTT	TATAATAATA	960
GGATTAAATT	CTTCGATAAA	GAACATTCAG	TTTAATGATA	TAAAAACCTC	TTATGCAGAA	1020
TATACAATCA	TTGGTGTAT	AGCTTTATG	ATAATCGGGC	AGATGACTCA	AGTTATTTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTTGCTCTTA AGTTATGCAG TGGAGTTCGT	1140
CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTTCAAGAA	1200
ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTTTT	1260
TATACAGTTT TGTATCTAT TGTGTTTTTA TTATTTGGG ACTCCCTTGC AATTTTACTT	1320
ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTTGT ACTAACACCG	1380
CTTGGTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG	1440
ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAACTATTT TGAGAACTT TTATTTTAAA	1500
AATCAACAA CTTTGAATT AGTTTCTTA TTGTTAACAT CATTACTTGT CCTTATATCT	1560
GTATCTTTTA TTATACCAA GATAAAATG ATACTGATAG AAAGATAAAA GTTGGGTCAT	1620
CCAACTTTTT TGTGTCTCC CGAAAACCAC TAGCTATGCT AGTGTTCCA TAGAGCTTTT	1680
AGCGTGGTAA CAAAAAGAAC CTCCTAAAAT GATAAGATAG AAGTGGTTTC TCCGCCACTA	1740
CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC	1800
ATGGAATTGT AAATATCATA TTGTTTTTGC ACCCAAATAT CGTCGTCAA TCATTTATGG	1860
CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAT	1920
AATCCATGAA GCGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA	1980
ACTTAGTGTT	1990

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAACATATTT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT	60
ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCATAT TTAGGTCCTG GACGTGGAAT	120
CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT	180
CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG	240
TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG	300
TACAAATAAT GGTAAAATG CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGGAGTGC	360
ACCGGAATAT TTGAAATTTG TTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA	420

1252

TTATAGCCAA	TTGATTGATG	GTAAAAAGGC	TGTCATTTTA	AGTACTCCAA	ACTCCACAAA	480
TGGTCGTAAA	CACGGACAAA	TTTGGATTGG	TCTAATTAAT	GATGATAATA	CAATGATTG	540
GCGTTATCAT	CACGACGTTG	ATTATAGTAA	CTATGGATAC	TCATATTCAA	CATGACAGA	600
GTTACCAAAT	CATGAAATTG	GATTGATGTT	TGAAAAATTT	GATTCATGGT	CTCGTAATGA	660
ACTTCATATG	AAAAATGTTG	TACCATATAT	AACATTTAAG	ATTGAAGATC	TGAAAAAGAA	720
TTAAAGCTGA	AATTTGAAAA	TATATAAAAA	GAGGATAAAA	ATTATGGTAA	ATTACGGTAT	780
TGTTGGAGCT	GGATATTTTG	GAGCTGATTT	AGCTCGCTCA	ATGAACAAAA	TTGAAGATGC	840
AAAAGTGGTT	GCGGTATTTG	ACCCAAATCA	TGGAGAAGAA	GTTGCTCAAG	AGTTGGGATC	900
AGATGTTTGT	GCAAGTTTAG	ATGAACTTGT	AGCACGTGAA	GATATTGATT	GTGTGATCGT	960
AGCTTACCT	AGTACCTTC	ACCGTGAACC	AGTTGTGAAA	GCTGCTCAAC	ATGGCAAACA	1020
CGTATTTTGT	GAAAAGCCAA	TTGCATTGTC	TTATGAAGAT	TGTAAAGCCA	TGGTTGACGC	1080
ATGTAAAGAA	AATAATGTCA	TCTTTATGGC	TGGTCACATC	ATGAACTTCT	TTAACGGTGT	1140
ACACCATGCT	AAAGAATTGA	TTACTCAAGG	TAAAATCGGT	AAAGTTCTTT	ATTGCCATGC	1200
TGCTCGTACA	GGTTGGGAAG	AACAACAACC	AACTGTATCA	TGGAAGAAAC	TTCGTTCTCA	1260
ATCTGGAGGA	CATTTGTACC	ACCATATTCA	TGAATTAGAT	TGCATTCAGT	TTATCATGGG	1320
AGGACTTCCT	GAAAAAGCGA	CAATGGTAGG	AGGCAATGTA	TATCATAAAG	GTGAAAACCT	1380
TGGTGATGAA	GATGATATGC	TCATTGTAAA	CTTAGAATAC	TCTGATGATC	GTTATGCTGT	1440
TTTGGAAATAT	GGTAATGCTT	TCCGTTGGGG	TGAACACTAC	GTCTTGATTC	AAGGAACTGA	1500
AGGAGCTATC	AAACTTGACT	TGTTCAATAC	TGGCGGTACT	CTTCGTGTTA	AAGGTGAAGG	1560
AGAATCACAC	TTCTTAGTTC	ATGAAACTCA	AGAGGAAGAT	GATGATCGTA	CAGCTATCTA	1620
TACCGGTCGT	GGTATGGATG	GAGCAATTGC	GTACGGTAAA	CCAGGAGTAC	GTTGCCCATT	1680
ATGGTTGCAA	ACATGTATTG	ATAAAGAAAT	GGAATATCTA	CATGACATCA	TTAAAGGTGG	1740
AGAAATTACA	GAAGAATTTG	AAAAACTTCT	CAATGGTGTA	GCTGCTTTAG	AATCAATCC	1800
TACCGCTGAT	GCATGTACTT	TATCAGTTAA	AGAAGATCGA	AAAGTAAGTC	TTTCAGAAAT	1860
CACAAATGCT	TAACTTTTGT	AAAACAGAAT	AGTAAATTCT	TGTCATTATA	TAATTTCTAA	1920
AGTTCTGTGA	TACAACTCAT	TGAATAAAGA	AATAGAGATG	GGACTGGGAT	AATGCCCAGT	1980
CCCATTTTTT	ATCAAAAAGT	AATGAGATCA	AAAATGTGGG	AGTGTGAAA	TGAAGATTAT	2040
AGGTATCGAT	ATTGGCGGAA	CAACAATTAA	GGCAGATTTA	TACGATGAGT	TTGGAACGAG	2100
TTTGAATCAT	TTCAAAGAGA	TAGAAACAAT	TATTGACTAT	GATTTGGGAA	CGAATCAGAT	2160
ATTAAATCAG	GTCTGTGATT	TAATTGGTGA	GTACTTTTA	AATCATTCAA	TTGATGGTGT	2220

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TGGGATTTCC	ACTGCTGGAG	TTGTTAATGC	TAATACTGGA	GAAATCATCT	ATGCAGGCTA	2280
TACAATACCA	GGGTATATCG	GAGTAAACTT	TACTGCCGAA	ATAGAAAAAC	GTTTTGGGTT	2340
GTATACTTTT	GTGAAAAATG	ATGTTAATTG	TGCTGCATTA	GGTGAATTGT	GGAAGGGACA	2400
AGCCAAAGAT	AAGAAAAATG	TAGTAATGGT	TACTATTGGA	ACAGGTATAG	GAGGCAGTAT	2460
TATTGTCAAC	GGACAAATTG	TTAACGGATT	TAATACTACT	GCTGGTGAAG	TAGGTTATAT	2520
TCCTGTAGGT	AATTCGGATT	GGCAAAGTAA	AGCCTCAACA	ACCGCATTGA	TTCATTTATA	2580
TCAAAAAAAG	AGCTTGAAAA	CTAATCAAAC	TGGACGTAAT	TTCTTCACTG	ATTTAAGATC	2640
TGGAGATAAA	GTGCTGAAG	AACTTTTGA	AATTTTGTGA	GAAAATCTAA	CAAAAGGTTT	2700
ATTAACGATT	TCTTATCTAC	TTAATCCAGA	AATTCCTATA	TTAGGAGGTG	GGATTCTGGA	2760
TAGTAAGGAT	ATTTTGTAC	CTGAAATCA	AAGTTCTTTA	GCTAAAAATG	CAATGGATAA	2820
TAGGTTTTTA	CTAAAAATC	TTGTGGCAGC	TACATTAGGA	AATGAAGCTG	GTCGTATAGG	2880
AGCTGTAAAA	AATTTCTTAG	ATAGAATTC	TAATAAATAG	TATGTAAGAT	AAGGAGGTGT	2940
CACAATGACT	AACTCTGTAT	TTTCGACAAT	GCAAGATATT	GAGAATGTTG	CAACCGATAT	3000
TATAAAATCA	TATGATAATG	AGATTTATAC	TTATAAAGCT	GTTTCCCAAG	AAGAATTGGA	3060
AAAAC TAGAA	AAAAGTTATG	ATGAAAAAAG	TCACGAAGAA	TTAGTTTCAA	TAGAAAGCAA	3120
TTTAGAAATG	AAACAACAGA	ACCTTATTGA	TGAGGTTAAT	AAAACAATCA	AGGAAAATGA	3180
TGCAAATATT	CAGTATATTT	CATCAAGTAG	GAGAGGAGAA	TTTGTAGAAA	AAATTATTGG	3240
TAGGGTGGTA	GAAAAATATG	GCCATTAGTC	AGATGAAAAG	AATCTCTCTA	CTATTTTCTA	3300
AAAGTAGTCT	TGATGATGTT	TTAAAACTA	TTCAAGAACT	AGAGTCAGTG	CAGTTCCGTG	3360
ATTTAAAGGT	TCAGGATAAC	TGGTCAGAAG	CCTAGAAAA	AGATGAAGTT	GTATTTCCAA	3420
CTATTCAAAT	TTTTCATACT	TCTAATTCCA	ATCATGGGGT	TATTGAGGGA	AATGATGCCT	3480
TGACTTATTT	GATGAATCAA	CAACAACATT	TAGAAGCAAC	TGTAGAGAAA	TTACAAGAAT	3540
ACCTACCGAA	AGAAAACACG	TTTAAATTAT	TGCAGCAACC	TCCGATAACT	ACCTCTTATG	3600
AAGAATTAGA	GAAATTTGGT	AAAGCTAATG	TTGCTGAGGG	TGTTCTTAAA	AAAGTGAATC	3660
ATCAAATTA	CAGAGTTCAT	GAATTAGAAA	GACACATFCA	AAGTAATAAT	GAGGAAATAG	3720
AGCGATTAAT	AAAGTGGGAA	AAATTAGAAA	TTGTTCCCTGC	GAATTTAGAA	CAATTTTCTT	3780
TCTGTAAAGG	AAAAGTCGGA	ACAATTCCAA	GGACTGAAGA	TAATCGCTTA	TACAATAGTC	3840
TTTTAGAAAA	CAATATTGAA	GTCAAGAAA	TATTTTCTAA	TGATAGAGAG	TACGGTGTG	3900
TTGTTTTCTA	TCAGTCTAGT	TACTCTATAG	ATTTTGATGA	ATACTTATTT	GAACCATTTG	3960

1254

ATTATCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT	4260
CGGAAACATT GACGGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA	4320
TTGAACCATT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC	4380
CTACACCTGT ATTAGACCA TTTTACTTTA CATTTTTTGG AATGATGGTT GCTGATTTAG	4440
GCTATGGTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTAA AAATCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG	4560
GTGGAATCTA TGGCTCATT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT	4620
CTGATGTCAT GACTATATTA GTAGTGCAG TTGTGTTTGG GTTTATTACA GTATTTGCAG	4680
GTTTGTAGC TTCAGGACTA CAAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTTGC GTGGTGTGT ATTCTG	4766

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA	60
CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCAGA	120
AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA	180
TCTTGTGAA GATAGAGCCT ACCAAGGCGC ACTTGTATC GTCTGTGATA CAGCTAATAC	240
TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAAGA TTGACCACCA	300
TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAg	360
aGaTGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT	420
TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCCTTCT CTACCCCTCT ACCACTGCAC	480
GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GCAAAATGGA CACTATGAGC TACAAAATTG CTAAACTGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTGA	TGAAAATGGT	GCTGCTCGCG	TTATCCTGAG	TCAGAAAATC	TTGAAACAAT	660
ACAATATAAC	CGATGCTGAA	ACTGCGGCCA	TTGTAGGTGC	ACCTGGACGC	ATTGACAGAG	720
TGAGTCTCTG	GGGAATTTT	GTCGAACAGG	CTGATGGCCA	CTACCGAGTT	CGCTTACGCA	780
GTAAAGTCCA	TCCTATCAAT	GAAATTGCCA	AGGAGCATGA	TGGTGGAGGC	CACCCTCTAG	840
CAAGTGGTGC	TAATTCCTAT	AGCCTAGAAG	AAAACGAAAT	CATCTACCAA	AAGTTAGAAG	900
ACTTGCTTAA	AAACTGATAA	AATACTTGCC	AAACTTTTCA	GAATCTGATA	GACTAGTATA	960
GTAACAATCT	ATGGCTCGCA	AAGAGACCAT	GGCAGAAAAG	AAATATTGCA	AAATGAAAAT	1020
AGATATCCAT	CCAGAATATC	GCCCAGTTGT	CTTCATGGAC	ACAACACTG	GTTACCAATT	1080
CCTTAGCGGT	TCAACAAAAC	GCTCTAACGA	AACAGTTGAG	TTCGAAGGCG	AAACTTACCC	1140
ATTGATCCGT	GTGGAAATTT	CATCAGACTC	ACACCCATTC	TACACTGGAC	GTCAAAAGTT	1200
CACTCAAGCA	GATGGACGCG	TGGATCGTTT	CAACAAAAAA	TACGGTCTCA	AATAATGATA	1260
AGAGAACAGT	TTTGGCTGTT	CTTTTTTGTT	TCTTGAAATC	AACTGCTGTT	TTCATGTTCC	1320
AGACTCATCT	GTAGGTTCGA	TTTCCATGCT	ACTAGGCAGG	AAGGAAATAG	CTGTTTCAAC	1380
ACGTCCATAA	TGAGCTATAC	TATTGTCACG	AACCACACTT	TCATTGATGG	TCCAAGTGGA	1440
ATTCATTTTC	TTAAAAGCTT	CTCGGACTTT	TTCCAAATCT	TTGGAGGCAA	TGGCCTGCTC	1500
TAAGGTTTCA	AAACGAGGAC	TTATACTCAT	CTGCTTTCAA	AAAGCATTCT	AGTCCATCTC	1560
CGATTACCGA	TGGACTTTAT	CACCTCCTTC	TCCAGTCCTT	GTATGACATC	TTGAAGTTGA	1620
TTCATGACAT	CTTCCAAAGT	TCGAAAAGCT	TTATTCCTAA	ATCCACGTTT	ACGAATCTCT	1680
TTCCACACTT	GTTCAATGGG	TTTCTCTCTG	GTGTGTATGG	AGGAATAAAG	GTAAAATCAA	1740
TATTAGTCGG	AATATTTAAG	GTACTTGATT	TATGCCATAT	AGCATTGTCC	ATAACGAGTA	1800
AAAGGATAAG	CTTGTGAAAG	CTCTTCTAAA	AAGGCGTTCA	TCCACACTCC	TTTTTATAAA	1860
CCTGAAATAA	GGCATCAATT	GTAACAAATT	CTCCTGCCTC	TGTAGCCTTC	AAATGACGGG	1920
CAAGAAAGGC	TTTCTCTTCC	TCAACTGTCA	TATATGCATG	GTTACGACCA	CCACGTGTTT	1980
CTTGAAGGAG	AGAGTCGAGT	CCGAACTCCT	CATATTTTTT	TACGTTTCGC	CAAATCGTTG	2040
TTTGATTACA	GTCTAAAAGC	TCTATAATCT	CTTTATAAGA	TTTGCCCATC	AGACGAAATA	2100
TAGTAGATTG	AAACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTGTTAG	AAATCGATTT	2160
GTCCTGTTCT	TGTTTCATTT	TACTATAGAA	CGATTTGAAG	GCGTTTATAA	TATTTAGCTG	2220
TACGAGAGTC	TTTTAAAAGT	GTTTTGATGG	TTTGATTTTC	TTCTTTAGTT	GATTTTCATAT	2280
TACTATTATA	TAATGCTTTT	TGATTTTAGT	CTGGTATAAA	TATTGCTTTC	CTCCAAAATG	2340

1256

GTCATAGTTT TACTGGCAAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTTCTTTTCT TATAGCATA CTTAAGATTT TGTCTTTGAG AAAGATATTT	2460
CCAAGAAAA CGTTCGTTTT TTGG	2484

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA	60
AAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTCGTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT	180
TCATTTGAAG AAGGAGAAAA TATCGATTTG TATCAAAATA AAGGTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTTAGA AGAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAATACTT AAAAAGTTAA CATTCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTAAATGTT CTAATATCCA AATAGAATC AAGCTATAAA AATTCAGCAA	540
ACTTTAGAAA CATTGTATAA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTGG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTAATTAAGTA TTCTAACAGA TATTGCAAA	660
AAAAAACAG GGTAAAAATC AAAATGACAG TATTAAGAGG AGATAACTTA GAAATATTA	720
AAACTATGA ATCCTCAAGT ATGATTTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTCGAAGAT ACGTGGACT	840
CGATTGAGGA TTACAAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTTC GTTCATTGTC ATAAAATTGC AAATCATCAT ATTAGATTAA	960
TTTTAGATA TATCTTTGGA GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AACATTTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG	1140
ACCAAATACT AGTGAACGA AAACGAGATG GAAACTCTAA AACTATATAT AAGTTGATA	1200
ATAATGGTAA CTATATCTA GCAAAAGAGA AAAATGGAGT TCCCCTTCA GATGTTTGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA 1320
 TTCTGTTATT AGAACAAATT ATAAAGATTG CTAAGTATAA AAATGATATA GTTTTAGACC 1380
 CGTTCTGTGG AAGTGGAAC ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG 1440
 GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGAA AATGTTATAA 1500
 AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAA ACTGAGGAAG 1560
 AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATTGTTC AAGAAATAAA GGAATTGATG 1620
 GTTTTTTACC TAAACATTTT CAAAAAAAC CGATACCTAT AAAAATTC AAATAAATG 1680
 AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AACTCCAAA AAATTGATT 1740
 TTGGAGTAGT TATAAAAAC CATTCC 1766

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 748 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAAATCA AATCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG 60
 CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA 120
 GCGCGGAGAA TTTCTAATTC TTCCTTGGTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTC 180
 TCATCTAATA CTAAGTTC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG 240
 TAGCCCACCA TACGCTTGAT CTGATGAAAC TTCCCTTCTG CAATGGTCAC ACGGATTTGG 300
 CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTG ACAGGTAAAG 360
 TCTTTGAGAG GAATACCCTC AGCAAATGTC TCCACATCTT CTTGGGTCAT GATTCCCCTG 420
 ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC 480
 TGACCATCAT TGGTCAAGAG CAAAAGACCA TCGGTGTCAA TATCCAAGCG TCCTACTGGG 540
 AAAACTTCCT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTCT GTGCTTGGGA 600
 TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTTATCA TGTAGTAGAC AAACCTTCA 660
 TACTCCAACA CTGCCCATC AAAGCGAATC TCATCTATTT TTTCATCAAT CTGCAATTA 720
 GCTGATTTT CTTTTGACC ATTTACAG 748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

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AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT      60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA      120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG      180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGCGCCT GTTCGTAAGC CAGGTA AATT      240
GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT      300
GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTTCTTATT GTAGATGACC TTTTGGCGAC      360
AGGTGGA ACT GTTAAGGCAA CTATCGAGAT GATTGAAAAA CTTGGTGGTG TTATGGCAGG      420
TTGTGCCTTC CTTGTTGAAT TGGATGAATT GAACGGCCGT GAAAAAATG GTGACTACGA      480
CTACAAAGTT CTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTTT CTCTACACTA      540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAAACTAT AATTGAAAAC TATATCTTCT      600
TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTTGTCTT CAAACATATG CAATTATTCC      660
TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTCGAAT TGATAAAAAA TTGCCAGCTG      720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAG      780
ATATCCGTCC TTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAATG GTCACAGAGA      840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACA ACT GGATATTGAT TTTCTCTATA      900
TGGAGAGCCA CCGTCTTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAACTT      960
TTCTTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC     1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA     1080
AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC     1140
GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA     1200
CCCTAAAAGA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCATT     1260
CACGGCACAC GGAGATTCTT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT     1320
CAGAAGGACC TCAGGTTGGG GTTTCTATTW TGGCCAGTCG TGATTTACGA GAAATTTATA     1380
GTTTTGGTCA TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG     1440
ATGCAGGTT
    
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1259

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 904 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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TACCCGCTTC TTCAAGAGT TGGAGCAGGG CTGTTTGCG ATCTTTTGTC ATAGTTCTTC      60
CTTTTAACGG CGTTTTCGAA GCACTTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT      120
ACTATGGATA ATTGTACCAA ATCCAAC TAG TACAAATAGA ACATAAAACA TATTTTCTAC      180
ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC      240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA      300
TTTTTGTAGG TAAAGAGCTC CTAAGCACC AAAAGATATA TGGGAAAAG CCCGAAAAC      360
GATAACCATG GGATAGCCAG CCATCAAAA TCCAAAATA GAGGCTAGGA TGACAAAAC      420
TGCCATCAAG GCGACAAGA ACATGGCTAT AAAAATAGCG ATGTGGCTCC CCAAAGTATA      480
GGAAGCAGGT GGAATGACAA TCTTGAAGG CATAACAATT GGAATCAAAA TCGCAATAGC      540
CGTAAAAGG GCTGTCATTG TCATAAATG TGTCTTTTTC CGTGATTCA CAAGAATCTC      600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAACCA GACAATAAAG CAAGAATTFA      660
CTTGGGTTTA TAGATCATTT TTTAGTAAA AGTTATAGTA GATTGAACT AGAATAGTCC      720
ACCTCTACTT CTA AACATT GTTAGAAATC GATTGGCTG TCCTGATCGA TTTGTCCTGT      780
TCTTATTCG TTTACTATA GTAAAGATTT CATAAAAAG AACTGTATA GAGCAAAATC      840
TCCACCTTCA GTTTGGAAG GCGGAGATG TTTnTTATTT TTTCAGGGT TTGTAGTCGT      900
GGGA                                                                                   904
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(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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CACTCAAAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT      60
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1260

CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACTTCGTGT ATACGGTGGA ACTTCTTCG TCTTCTCTGA CTATGTGAAG	180
GCAGCTGTCC GCTTGTGAGC CTTACAAGGA CTTCTCTGTGA CTTATGTCTT TACCCATGAT	240
TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTT AGCAGGTCTT	300
CGTGCTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGTTGCTA AAGTGCTTA TGTGTATAT	480
GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GCGAAAAAA TCCGCGTAGT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATCT TCCAAATGCA	660
GTCCGCCGTC GTGTTGCAGT CGAAATGGGT GCAAGTCAA ACTGGTACAA ATATGTTGGT	720
CTCGATGGTG CCGTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAGT TGTTCGAAAC TTGAAATAAT	840
CCTAAAAATC AGGGCGTAAG CTCTGGTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAGG ACAAAG	946

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCc TAGTTCCTAG GGAGCTATTT TTGTTTTTTC AAGAAGTTAT CTTCTTGAT	60
TTTATACTCA ATGAAAATCA AAGAGCAAGC TAGGAAACTA GCCGTAssTG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTTGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTAAC TGGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATGTGGCAG CGAGTCTAGG CCGTCTCTTG AAAAAATCGTG	420
GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA	480
GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTTGGACT	540

1261

TGGGTCACTA	TGAACGTTTC	ATCGATATCA	ATCTCAACAA	ATATTCCAAC	GTGACAACCTG	600
GGAAAATTTA	CAGTGAAGTT	CTTCGTAAAG	AACGCCGTGG	AGAATACCTT	GGGGCAACTG	660
TTCAAGTCAT	TCCTCATATC	ACAGATGCTT	TGAAAGAAAA	AATCAAGCGT	GCCGCTCTAA	720
CGACCGACTC	TGATGTCATT	ATCACAGAGG	TTGGTGGAAC	AGTAGGAGAT	ATCGAGTCCT	780
TGCCATTCCT	AGAGGCTCTT	CGTCAGATGA	AGGCAGATGT	GGGTGCGGAT	AATGTCATGT	840
ATATCCATAC	AACCTTGCTT	CCTTACCTCA	AGGCTGCTGG	TGAAATGAAA	ACCAAACCAA	900
CCCAACACTC	TGTCAAAGAA	TTGCCGTGGCT	TGGGAATCCA	ACCAAATATG	TTGGTTATTC	960
GTACAGAAGA	GCCAGCTGGT	CAAGGAATTA	AAAATAAACT	GGCCCAGTTC	TGTGATGTGG	1020
CACCAGAAGC	CGTTATCGAA	TCGTTGGATG	TTGAACACCT	TTACCAAATT	CCACTGAACT	1080
TGCAGGCACA	AGGGATGGAC	CAAATGTTTT	GTGATCATTT	GAAATTAGAC	GCACCAGCAG	1140
CGGATATGAC	AGAATGGTCA	GCCATGGTGG	ACAAGGTCAT	GAACCTCAAG	AAACAAGTTA	1200
AGATTTCCCT	TGTTGGTAAG	TATGTGGAGT	TGCAAGATGC	CTATATCTCA	GTGGTCGAAG	1260
CCTTGAAACA	CTCTGGCTAT	GTCAATGATG	CAGAAGTTAA	AATCAATTGG	GTCAATGCCA	1320
ATGATGTGAC	AGCAGAGAAT	GTAGCAGAAC	TCTTGTCTGA	TGCGGACGGG	ATCATCGTAC	1380
CAGGTGGTTT	TGGTCAACGT	GGTACAGAAG	GGAAAATCCA	AGCCATCCGC	TATGCGCGTG	1440
AAAATGATGT	TCCAATGTTG	GGAGTCTGCT	TGGGAATGCA	GTTGACATGT	ATCGAGTTTG	1500
CTCGTCACGT	TTTAGGTCTT	GAAGGTGCCA	ATTCTGCAGA	GCTTGCACCA	GAAACAAAAT	1560
ACCCTATCAT	TGATATCATG	CGTGATCAGA	TTGATATTGA	GGATATGGGT	GGAACCCTTC	1620
GTTTGGGACT	TTATCCGTCT	AAGTTGAAAC	GTGGCTCTAA	GGCTGCTGCT	GCTTATCACA	1680
ATCAAGAAGT	GGTGCAACGC	CGTCACCGTC	ACCGTTATGA	GTTTAATAAT	GCCTTCCGTG	1740
AGCAGTTTGA	GGCAGCAGGT	TTTGTCTTTT	CAGGAGTTTC	TCCAGACAAT	CGTTTGGTAG	1800
AAATCGTGGA	AATTCCTGAA	AATAAATCTT	TTGTAGCTTG	TCAGTATCAC	CCTGAACTGT	1860
CAAGCCGTCC	AAACCGACCA	GAAGAACTCT	ACACTGCCTT	TGTTACTGCA	GCAGTTGAGA	1920
ACAGCAATTA	GCAAAATCAG	AACCTTTGAG	AAAAATCTCA	GAGGTTTTTT	GCATACGATG	1980
ATATTGCAGT	ATATCTGAGG	TAGGGTCCCT	CTGTATGTAC	CTGCTACCGT	TGAAATCAAT	2040
AGCGACTCCC	TCTTGCCCTG	TGCTAGTGAA	TGGATTTATC	AGTATATTGA	AATGAAATAA	2100
AATTTGAACA	AATTAATTCG	GAAAGCCAAA	TCAATTTCTA	GCAAAGTTTT	AGGAACTGGA	2160
TTGTATAGTG	AATTGAAATA	AGATGTGAAC	ATCTCTATCA	GGAAAGTCAA	ATTAATTTAT	2220
AGAAATATTT	TAGCAGTCAA	GATGTACTGT	TATAGATTCA	ATACATTATA	CTTTTTTAAT	2280

1262

TTAATCCACT ATAGTAAAAT GAAATAATAA CAGGACAAAT CGATCAGGAC AGTCAAATCG 2340
 ATTTCTAACA ATGTTTGTAGA AATAGAGGTG TACTATTCTA GTTTC AATAT ACTATCCCAA 2400
 ATCATT CATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT 2460
 TTCTTCCTCC TCATGAGGTC AGTTTTACTT TCTGCTGTTC CAGTATCGTT TTTCCCTCGCT 2520
 AGATTTCCCTC AAAAGGGCAG ACTCCTCCCT TGGTGCCTCA CACGATTTTT TCATCTCGAC 2580
 TGTTCCTTAA TGCATCATTA ACGACGCTTT TCTTCTAGGT GGTT CATAAG GAACAGGAAG 2640
 ATTCAGGTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAATTCCG AATAGGCATA 2700
 GAGACTAGAC AATTTGAGGA GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG 2760
 AAGA 2764

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATTGTT CAG TACTACA ACT TACGTTGTAG CGCCCTGCAC ATTGGTTCGT 60
 CTGTTCAGT TTTCAAAGGT CTTGTCTACT TGCTTCTCTC AAGCGACAAC TATATTAGTA 120
 TATCACA ACT GCTTTCGCTT GTCAACACTT TTTTGAAGAT TTTTAAGTTT TTTTAAACTT 180
 TTTTTCATCA AGTGGTCTG ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT 240
 TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTATTATTC 300
 AACTCTTACT ATTATACAGT CTTTTCAAAC TTTGTCAACT ACTTTTTTAA ACTTTTTTTA 360
 TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT 420
 AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAAATCAG AGCCAAGGTC GAAACATTAC 480
 AAGAAATATA AACCATTTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT 540
 CCAGACCTGT ACGTGGTGGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTG TACC 600
 AACGAGGAAT AATCTCTTCT GCCGTTCCAG CTTCATAATG AGTATTGTCA AATCCCATTC 660
 TTTTAGCATT TCGCTTGGA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG 720
 TTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA 780
 AATGGTCTTC TTTATCAACA TCCAGCGCTT T TACTGCTTC GCTATAGAGG ACTTCTGTTT 840
 GCTCAGGATT TAGTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC 900

1263

CTTCTTGAAT ACTCTCTTGC CCCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG	960
TTTTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACCTC TGGGAAATCT TTAACCAACT	1020
CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTTCGTAAC AATAATAATC TGAACCTGTC	1080
CGGTCCTTCT CGCGCGTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG	1140
TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT	1200
CCTTATCTTG TACCAGGCAG TCTTTCAACT CTACTAAATA GTGAGAGTTT TGTGCATATA	1260
AGCCCGCCTT GACCTGATTT TTAAATTTTC GAGTCTGAAA TTGTAACCTA GCTCTGTAAT	1320
ATTTTGGTTC CTGCATTCCA ATAGTTGGAC GAATTCATA ATTTTCATAT CCTGCAGGAG	1380
CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTGAA CTCCAGCTGC TTATCATAAT	1440
GCAGGTGCAT GATTTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC	1500
GAAATTTAGA CTTCCTGTG ACCTTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG	1560
AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT	1620
TTTGGTAAAA GCCGATTCCC TCACCGTTAA TTCCCATGCG CTTGATTTTT AATGGTATTT	1680
TT	1682

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TTAACTTTGG TCAATTCCTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC	60
CCTTTATTGC TAAATCACC AATCCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT	120
TTCAAATTTT CAAAATATCT TGATTGCAAA ATACCATCTG CTAACAATTT ATTTTCTTGC	180
ACAATCGTTG CATTCATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC	240
AGTGTATTCA CATGGTATTT AGCGTGTATG TGACTAGGAC CACCTGCTAG AGGATAGAAG	300
TGAACATTTT GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC	360
CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT	420
TGAGAAATTC TTTCAGATAA AATTGTTGGA GTATCATCAA ATTCATTTGG AATAATTTCT	480
AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATTGGTATCA	540

1264

AAATTCTCTA	TTTCAATTTT	ACAATTCCT	ACATTCCTTG	CTTCTGTAA	CATTCTACTA	600
ATAGAGGTTC	TATAAATTC	TAATTTTGCT	GCTATTTGTG	ACTGATTTAA	GTTTTCAATA	660
TAATACAGAT	AAGCAATTTT	AGAAAGCAGT	TTATTCCTAT	CTTGATTCAT	ACACTTAACC	720
TCTTACGAAA	CTACCTTAAC	CATTATCCCA	GCATTTTCTA	ATGTAGCTAT	ATTTTGTTTA	780
GAAAGTTTTT	CGTCTGTTAT	TACTTCATAG	ACTTGACTTA	AAGCAAATCT	TCTTACTGTA	840
CCTCTTTTAT	CAAATTTACT	TGAGTCAGTT	AGGACAATGA	CTTTATCCGA	CACTGCTGAA	900
ATATATTGAA	CTACCTCACT	GCGCATTTAA	TCTTTTCCGG	TAAAGCCCAT	CTCTTTATCG	960
TAACCATCTG	TCCCAACAAA	AGCTTGACAC	ACATGAAAAG	TCTGTATCAT	TTCTTTTAAT	1020
AAAGGTCCTA	CAGTCACCTG	TGAATCTTTC	TGAAACTCAC	CACCAAGAAC	AATAACACGA	1080
CATGAATCAT	AAGCTCTCAC	AAAATTTGCT	ATAAAAAACG	AATTTGTTAC	AATCGTAACA	1140
TTTCTTTTTT	GCTTGCAAAT	TTCTCAGCA	AGTAAAGCAC	AGGTCGATCC	AGATTCTATC	1200
ATTATTGTTT	CATTATCTGA	CACCAATTTT	ACTGCTTCCT	GAACAATTTT	TCTCTTAGTT	1260
TCATAATTAA	TTGACAAAACG	TACATTTAAG	TCATCTCCAC	TATTTAATAC	AGCATATCCA	1320
TGCTCTCTGT	GTAATAAACC	TTTGACTCT	AATTTATCTA	AATCTTTTCT	AATCGTTACT	1380
TTCGATACAT	TTAATTTTTC	CGATAATGTA	TTAACGTCGA	TCTTTTCATA	TTCTGATACT	1440
AATTTAATAA	TTTGTTCCAA	TCTTTTCATT	TTACACCTCC	GTTTTATTCT	ACCAAAATAA	1500
AAAGCAAAA	ACAACAAATT	AACCTTTCGT	TCGTAATTGT	TTTTCTTTCG	TTTTTGTGAT	1560
AGGATAGACT	TATGAAGAGG	AGGAACTCTT	ATGAAAATAT	CTAAAGGAAT	TATTTTTAAT	1620
ATTCAACACT	TTTCAATTCA	TGACGGTCCG	GGTATTTCGTA	CAACTGTTTT	TTTAAAAGGA	1680
TGTCCTCTGC	GCTGTCCATG	GTGTTCTAAT	CCTGAATCTC	AAAGAATGAA	ACCTGAAAAA	1740
ATGAAAGATG	CTCAACGAGA	GAAATTCACC	TTAGTCGGTG	AAGAAAAGAC	TGTAGAAGAA	1800
ATTATTACAG	AGGTATTAAA	AGACAAAGAA	TTTACGAAG	AATCCGGTGG	AGGTTTAACT	1860
TTATCAGGAG	GTGAAATATT	TGCTCAGTTT	GAATTTGCTA	AAGCCATCTT	AAAATCAGCT	1920
AAAGAACATC	ACATACACAC	TGCCATTGAA	ACTACTGCCT	TTGTTGATCA	TGAAAAATTT	1980
ATTGATTTAA	TTCAATATGT	GGATTTTATC	TACACAGACC	TAAAACATTA	TAATTCTATA	2040
AAACATAAAA	AAGTGACTGG	GGTTTTTAAT	CAAATGATTA	TTAAAAACAT	TCATTATGCT	2100
TTTTCACAAA	ATAAAACTAT	CGTTTTAAGA	ATCCCAGTTA	TTCCTAATTT	TAACAATAGT	2160
TTAGAGGATG	CAGAAAAAAT	CGCTACTCTA	TTTAACTCAT	TAAATATCGA	CCAAGTTCAA	2220
CTACTCCCTT	TTCATCAATT	TGGTGAAAAC	AAATATCGTT	TATTAAATCG	GAAATATGAA	2280
ATGGATGGAA	TCAACGCACT	TCATCCwGAA	GATCTTATTG	ATTATCAAAA	GGTATTTCTG	2340

1265

AACCACCATA TTAATGTGTA TTTCTAGTTT ATTTCCCTGA AATGCTCTAG CTATTTGCAG	2400
ATAACAAGCA TCTATAATAC ATACTTAACT TTTCAAAAGG TTTAGCTAAA AAATTTTAGC	2460
CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAA	2520
AACG	2524

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTTGGG GGCTTGTGGT CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA	60
CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGACTTG AATGATGTTT	120
GGATGATTCA GTCAAGTAGT GGTATTCACT CCTTTGAACC TTCGGCAAAT GATATCGCAG	180
CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA	240
GTCTGGATCC AAATCTAAAA AAATCCAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA	300
CCTTGGAACG TGTCCCTGGA CTAGAGGATG TGAAGCAGG GGATGGAGTT GATGAAAAAA	360
CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA	420
TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCGC	480
AAGCCTTTAT CAAAAAGCT CAGGAATTGA CTAAGAAAT CCAACCAAAA TTTGAAAAAG	540
CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTTG	600
GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC	660
TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTAA AACGATTTTT ACAGAAAGTA	720
ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAATCAAC AGGTGTGGGT CTTAAAACCTC	780
TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA	840
ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTA TAAAAAATAT	900
CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTGTGTT CCTATGAGCT TGGACGTTAC	960
CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT	1020
GGTCAAAAGG CAGAAAACCT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC	1080
GAACAAATTG TTATCAAGAT TACGGATCAA GTTATGTGA CCTCTCATGG AGACCATTAT	1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCACGGC	1500
GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTT AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTTATCAGAA	1740
CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCACAAG TCGAACCGCC	1800
AGAGGTGTAG CTGTCCCTCA TGGAACCAT TACCACTTTA TCCCTTATGA ACAAATGTCT	1860
GAATTGGAAA AACGAATGC TCGTATTATT CCCCTTCGTT ATCGTTCAAA CCATTGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTCTCGTT ATATCCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAAGTGGCCA AGCAGGAAAG TTTATCTCAT	2160
AAGCTAGGAA CTAAGAAAAC TGACCTCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTAAGTGGTA ATAAAGGTCG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGGAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG	2340
TTAGTGGAAG ATATTCTTG	2359

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTAAAA	60
TTTGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTAAAA CATCGTCAAA	120
AGCGATTGAG AGCGTCGTTT TGTAGTCGTT TCTGCGCCTG GTAAACGCAA TGCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCGGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAAA AATTTCTAAA AGCATTACAG CCTTGGCCAC TCTTCCTATT	360
GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA	420
TTGATTGCTG CCTACTTTAA CCAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGPCA TTCCTGGTTF CTTTGGTGTC	600
ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTC CTGAGTTGAC CTACCGTGAA	780
ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCCTGCC	840
TACCGTGAA AAATTCCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
CGTATCGTTC TAAAACACAG TAATGATGAA TTTCCAGTTC TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 855 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTGCTGA CTGGTGGGAA	60
AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGAGTTGAT TCAGAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC	300
AACTTAAAGC AAGTATPCTC CAAAGAGCGA TGGAAAGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAGA GAATTAAGC TGAAAAAGAA AAACCTATCA	420
GTGAAGGAAA AATCAAACGA GATAAAAAGG AAACCTGAGAT ATTTGCTGGT GATGATGGGA	480

1268

AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAGAAAT TGATGTTCCCT TATGATATTC	540
CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAATAAGC	600
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAAG AACATAATCA	660
ACTACAAAA TCTACAATAT CTTTCACCTG AACAGCGCC TTCCCGTGCT AGAAAATTAG	720
TTTCGCAGAA TAGTGCTTA TTTTCAACAG TTAGACCATA TCTAAAAAAT ATTGCTGTAG	780
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA	840
CTTAACGAAA CATAT	855

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT	60
ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAAGTCTCT TGAATTTATT	120
GCAACGCAAT ATGATGCTTT TGAAAATGGT GAGATAATTT TTGATTTGCC GAAAATTTTA	180
CAGGAAATTA CTTTAGAGGA TGTCCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC	240
ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG	300
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC	360
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG	420
CAATGGAAGC AGACGATTTG GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA	480
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTCTG	540
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTGCTAGAC	600
GTTCAGTAA GAAAAAGAAG AAAAAACAT CATTTTTACC TTTATTTTAT TTTATCCTGG	660

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

1269

CCGGTTGCAC	AGGATCGTGC	ATAGTCAACT	CTTCAAGTAT	AGCATATCTC	CTATTTTCTT	60
ACAAGTAATA	ACACCTAAAA	TGAAGCTTTT	TCTTTTACTT	TTTTCTGCCA	AGAGGCAAAA	120
AGCATGCTGA	GGTAAAAAAC	GTCATCATA	ATAGGAACAC	CAAGAATGGT	CTTTTCATGA	180
TAGAAAATCG	TCAAATAGGC	TGAAAAGACA	ACGCCAAGGA	CAAACTACT	AAGCAGGCTA	240
ACAAATATGA	ATCCTTCACG	CAAAAAAGGA	GTGTGCTTGG	TTCGGAAATA	ATCTCCAAAA	300
GCCAGCATGG	TCCGTTTGAT	ATCCCTGTC	ATAAAAGCGT	TATTATAGGC	AATACCCGAC	360
ACTTCTCCAA	AAGCAGTTGT	CACCAGTCCC	ATACAGAAGG	CCAAGGGCGG	CACTAGATAG	420
ATATTATCCA	CAGTTTGCGG	CACAAAAGCA	ATAATGATTG	ATAAGATTGC	CAAGGGAATC	480
AAGGACAGAA	TAGGTTTTTT	CACAATCTC	AATTTTTCTT	TATAAATCGT	TAATAAAAAAG	540
ACTCCCATCA	TAAACGCTAG	CAAGGTGAGA	ACCTTGTCCT	TAACATCCGA	AACATTATTT	600
TTAATTAATT	CTACTGAAAG	AAAGACAACA	TTTCCAGTTT	GTCCAGCTAC	AAGGGTATTC	660
CCGCGAACAA	TAAAAGTGTA	AGCATCCACA	TATCCAGCAC	AAAACGTCAA	AAAAAGTGCT	720
AACCTTTTAG	ACTGACGTGA	TATTTTTCTT	ATAGGTAATA	ACCTCATTTT	ACCTCCCATT	780
GTATTTTCTC	TTAGAAATAT	TGTACCATTT	TCTTCTAAA	AAATCGTAGG	CTACCATTTA	840
GATTTTACTA	TTAGCATAAA	AATAATAATA	GACAACTATT	TATCCAAAAA	TAGATAGATG	900
TAACATGTTT	GCAAACAAAG	CATACGAACC	TTTAGTAAAA	TCATTTCCAT	GAAACTAGAA	960
TAGAGCCCTC	TTAGCAAAAA	TCATTATTTT	AATTTATTTT	TAATCACTCC	TTGACATAAA	1020
TAACCTCAC	CAATAAAAAG	CTATGTCTTA	AAAAAATGGT	ATAATAAAAT	CAATACTTGG	1080
GCTTGATGGC	TATGCTACTA	ATAACAATTA	GGAGAGAAAA	TCAGGCACTT	GTAAACAACA	1140
AGGATTATCC	CCTTGAGATG	AAAGGAACTT	TAGAAATCTT	ATGATGAACA	TGCAAAACAT	1200
GATGCGTCAA	GCACAAAAAC	TTCAAAAACA	AATGGAACAA	AGCCAAGCTG	AACTTGCTGC	1260
TATGCAATTT	GTTGGCAAAT	CTGCTCAAGA	TCTTGTCCAA	GCGACCTTAA	CTGGCGATAA	1320
GAAAGTTGTC	AGCATTGATT	TCAATCCAGC	TGTCGTTGAC	CCAGAGGACC	TTGAGACTCT	1380
TTCTGATATG	ACCGTTCAAG	CCATCAACTC	TGCTCTTGAA	CAAATCGATG	AAACTACCAA	1440
GAAAAAACTG	GGTGCTTTCG	CTGGGAAATT	ACCTTTCTAA	AAACAAGGAG	CTAGAACAAT	1500
GCTTGTCGAT	AACAAAGGCT	AAGAAAGGTG	CAAAAATGAC	TCTATAATAT	TTGTAGTGGG	1560
TAAATCCCCT	ATGGATATTA	TGGAGCCTAT	TTTTGTGTAG	AAAAAAGTCC	CATATGACCT	1620
ATAATGAAA	GCGACAAAAC	AACTCATTAG	AAAGAATCAT	ATGGAACAAT	TACATTTTAT	1680
CACAAAATTA	CTAGACATTA	AAGACCCTAA	TATCCAGATT	TTAGACATCG	TCAATAAGGA	1740

1270

TACACACAAG GwAATCATCG CCAAACrTGGr CTATGAAGCT CCATCTTGTC CTGAGTGCGG 1800
 AAGTC 1805

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTTAA 60
 CGTCGCCGCG TTGGGGTTCG GATACAACrTA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG 120
 GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG 180
 CCTATAGTGG GTCAGATATT ACCCCGGTAT ATTCATGGG GTCTGGCTCT AGGATTGTC A 240
 TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC 300
 CACAATTGG AAATCATGTA AGAATTCATA CTTCAGGTTT TTGGAATCCA GATTCTTATT 360
 AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTGATGTG GGGTGTAGCA TGAAAAAAGA 420
 ATGCTACACC CTATTTTTAT TATAAGGAGG AGTAAGGATG GAATTTTTCA TTTGTAATCT 480
 TGTACGAGTC GTTCAATCAC CTCGATTTTA TATGCTTTA TTTTGGACCC TTCTTTGCAT 540
 GAGTTTAGGA AATTCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGTT TATCGATTTT 600
 TTTTGCCGCT TCTTCTATTC GAGGATTTTC ACCGATTAGC CTAGTAGCTG CACTTATCTG 660
 TACACTGCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA 720
 ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTT 780
 TTCTTTTCTA GTCTTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC 840
 TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAGAAGAT TATTTGATTC 900
 CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT 960
 CTCTATTTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT 1020
 CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTGGGCT ATTTTAGGGC TATCTTACTT 1080
 AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCITT CCTTAGTTAG 1140
 TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGGTT GTTTATGGTA CTTTTTTTCT 1200
 ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTTCTTA 1260
 GCAGTATTGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA 1320

1271

TTGCGCtGTC GCCAATATTC AATCCATCCA AATGTATTAG AATGGATCTT AGTTTTACTT 1380
 CAAGATATGA CGACTGGAGT ATATTGCTTT CCGTTCACAT ATATATTGTT CTTTTTTTAT 1440
 TTGATGAATA ACTATTTTAA TAGGTTGGAG TGTCGCATTC GTCTGAAATC AATTAAGCAC 1500
 TTTACCAGTT TTAGTTTCAA ATTAGCAGCT CTTAGTACGG GGATTTGGAC GCGCACTTA 1560
 TTTTTATTGA TTTTTCTAAT TGCATTTAGT AATGGTTTTA GCTTCTCTTT GGAGATAAAG 1620
 GAGGTTGATT TTTTAAGAGA ATTTTATGGT ATAAGTATTG CAAACAATGC TAGTTTCTTT 1680
 ATAGGATTTT TTTTCTCTTA TATAGCATAC TATTTCTTTT TATCCTTACT TACTATTAGC 1740
 AGTTTTTCTT GGTTTAAAAA ATCAAACATG AGCTTAGTAT TTCTGTTTAC TTTTTTATTT 1800
 GTAGAATCCT TATTCTGGAT TTATCAGTTG GACAATGGGA TAATTGGATT ATTGCCAATT 1860
 TTTCAGTATA TGGTAAATTC CAATCCGTAT GCATTGATTT ATTGGCTTAC ATTACTATCT 1920
 ATCATAATTC CATTGACTGT ATTTTCTGTT CATAGAAACT GGAGGAGAGT GTAAAAGTTG 1980
 GAAATGGGAA AGTTAAGTAG TCACATGTGG AGGTTGAATC AGATAATCTA TACCAAGTAC 2040
 TTTTGGGGTT ATGTTCTTTT TTGGATATTG ATTTGTTTAG GATTATGGTA TTGGTTAGAA 2100
 GGAAATGATA GACTTGTAT AGAAATTTTA AAAGGGCCTA ATCTGAGTCA AAACCTCTTT 2160
 TAGTCTTAT CTATATGGTT GCTTCATTGG TTTATTATTC ATACATTTT TCTAGCAGTT 2220
 GTATATCGTA GAAGAGCATC CGATTTCTTT ATGGAAGTGA TTCGATTTTC TTCTATTAAG 2280
 CTCTGGATTA GGTATCAGAT TTGGACCTGT TTTCTTTATG GACTCATTTT AATCATGGTA 2340
 AAAGTCTAG TGATTC AATT TATGTTACAG TTACCAAACCT GGGATATAGG AGTTTTGTTT 2400
 ATAGTTGATT CTTTGAATGC TTGTGTGTTA GTCTTGTTTT GCTTTATGTT ATACGCACTA 2460
 GGAGCGAATG TACAAATGAA CTTTGCTTGC GTTAGTTTCT TTTTACTCAT GATTGG 2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT TTGTAAATTT TCTAGCACTT GTATGGTAAA ATAGATACAG GTGTTTCATTA 60
 AACTAGACTA AAAACCTATT TAAGCAGGCA AAATGAAGAA ATACCAACAA TTATTTAAGC 120
 AAATCCAAGA AACCATTCAA AACGAGACTT ACGCTGTCGG AGATTCCTT CCTAGCGAGC 180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTCCCAG AGTTTCGGAT GGTTTGGAAG GTGGTCCGCC AGCGTGTGGT	480
GGATGATCTG GTATCCGTTC TGATACGGA CTATCTGGAT ATGGAECTCA TCCCAAATCT	540
CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAACCTCT	600
TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCCT	660
CATGGACATT GGCAAAGACC CTTATGTCTG TTCGATTTAA TCAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA	780
TTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA	840
TAATATTTGT AGTGGGTAAC CCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA	900
AAGTCCCATTA TGACCTATAA TGAAAAGCGA CAAAACAACT CATTAGAAAG ATTCATATGG	960
AACAATTACA TTTTATCACA AACTGCTCG ATATTAAGA CCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA AACAACTGGT ATGCCTACTA GAATTCTCCT TAGAAAGCGT CGTTTCAAGT	1200
GCTATCATTG TTCTAAAATG ATGGTCGCTG AAAGTTCTAT CGTCAAGAAG AATCATCAA	1260
TTCCCTCGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG	1320
ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG	1364

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTCCCATT	60
GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA	120
CATCGGAGAA GTGCAAACAA GTGTTTGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT	180
TTTGTAGAGA ATCGAACCGC AAGGTTCGGT TTTCTTTCTC TTTTGTCTA TAATTTGGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCTC AAGACACTAG 300
 AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTT AACATGATTG 360
 GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTFATCTA 420
 TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTTGGT GGAGCGAGAC CGTAAGcTCA 480
 GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTTT AACTCCTCAA 540
 GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTTGACCTCG TTTTCTTAGA 600
 CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT 660
 TTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCGTGAAAC TTCCAGAAGA 720
 AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTTATGGA ATTAGTAAGG TGACAGTCTA 780
 TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG 840
 ATATCATTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTAT TTTTPTAATC 900
 CCCACAAACA AGGATTTCTC CCTCTTGA AA ATCGTAAACG GGGGTAGAA AAGCTGTGA 960
 AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATGGTGGTC GATGTCGCAA 1020
 AAAGACTGGG GGCTACTTGC CTAGTGCAG GTTTGGAGAAA TCGCTCGGAT TTGCAATATG 1080
 AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTTAC 1140
 ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTTG 1200
 GTCAGGATAT TGCCTGCTAT GTTCCCG 1227

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTITAGGA GTGGTAACGT 60
 ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA 120
 ACAGAAATG GCTTTTCAAC ATAAGCTTGT AAGCTTTCCT TCATCTCTTT TGCCCAATCA 180
 TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAAG CGATGTTATC 240
 AACTCATCTA ACCATTTTTT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT 300
 TCATGGTCTT TCATTTGCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT 360

1274

ACACGGCTAA	TTCGTCCACC	TTTGACAAGA	TTTTCCAAAG	TTGAAACACC	AATATAAAGC	420
TCTGTATGGT	TTTAAACCTC	TTCTACATGA	GATAAAATTG	CCTCCATATC	TTTACCTTCT	480
TGAGCTAACT	TCGCAGCCTC	AACAACCTGG	AATTTCAGGG	CTTGGTCAGT	GAAGGAACTA	540
TCAACAACAG	TCACATCTGC	AGTAGATAGG	CTAGCACCTT	GGCGTGCTGC	TTCTACCGTA	600
CCCGAAAGAG	CATGGGACAT	ATGAATAGCA	AGAATCTGGC	CACCATCTTT	GCATAGGTCT	660
TCAAAAATCT	CAGCAAAGAC	ACCTACAGGT	GGCTGACTTG	TTTTCGGAAG	ATTCTTACTT	720
TCTTGCATCA	ACTGAAGAAA	TTTACCTTCT	TCTTTCAAAT	CCGCATCAGA	ATAACAACA	780
TTATCAATCA	TTACAGATAA	TGGAACAATT	GTAATATCTA	ATTGCTTTAC	TAGTTCAGGT	840
TCAATAGTAA	CAGATGAATC	GGTTACAATC	TTAATTTTTG	TCATAGTATC	AATCTTCTA	900
TTTTAGGATT	CAGATTGGTT	TCCTTACTTC	TAATTATATC	AAAAAAAAGA	TTAAAAATCC	960
TAATGGAGTC	AATCAAATTT	TCCGTAAAAT	TTGATATAAT	CAACTTATAA	GAAAAGAGGT	1020
GTCCTATGAT	TAAAAAATTT	TACCCCATTT	TTACCATTTT	ACTAGGTGCT	GCTATTTATG	1080
CTTTTGGACT	GACTTATTTT	GTAGTTCCCC	ATCATCTCTT	TGAAGGAGGG	GCGACAGGCA	1140
TTACCCTCAT	CACCTTTTAT	CTTTTAAAA	TCCTGTTTTC	CCTCATGAAC	CTGCTGATTA	1200
ATATCCCCT	TTTCATCCTA	GCTTGAAGA	TTTTTGGAGC	CAAATCCCTC	TATCTAGTTF	1260
TACTAGGAAC	CTTAGCTTTG	TCCGGCTGGT	TAGCTTTTTT	TGAGCATATF	CCCCTTCATA	1320
TTGATCTTCA	AGGTGATTTA	CTAATCACAG	CCCTTATAGC	GGGAATCCTA	TTGGGAATTG	1380
GCCTTGGAAT	TATTTTTAAT	GCTGGAGGTA	CAACTGGCGG	AACTGATATF	CTAGCTCGTA	1440
TTCTCAACAA	ATACACTCAT	ATATCCATAG	GAAAACCTGCT	CTTTATCTTA	GATTTTTGTA	1500
TTCTCATGTT	GATTCTCCTA	ATCTTCAAGG	ATTTGAGATF	GGTTTCCTAC	ACGCTTTTGT	1560
TTGATTTTAT	TGTTTCTCGT	GTTATTGATT	TGATTGGTGA	AGGAGGATAT	GCCGGCAAAG	1620
GCTTTATGAT	TATCACAAAA	CGTCCTGACC	AACTTGCTAA	GGCGATTAAT	GATGACCTCG	1680
GAAGAGGTGT	TACTTTTATT	TCTGGTCAAG	GCTACTATAG	TAAAGAAAAT	TTGAAAATCA	1740
TCTACTGTAT	TGTCGGAAGA	AATGAAATTG	TGAAAACGAA	GGAAATGATF	CATCGAATCG	1800
ATCCTCAAGC	CTTTATAACT	ATTACAGAAG	CCCATGAAAT	CCTAGGAGAA	GGCTTCACCT	1860
TTGAAAAAGA	ATAAAAAGAG	GTAATGTCGT	GACCTCAAAA	GTTAGACTAA	ATCATCTATC	1920
TTTTGGGTTA	CAGACAACCT	CTTTTTTATT	TTATTTACTC	AAGCTCTTAA	GACCAATTCC	1980
GAGTTACTTC	TTCATCAGCC	TTTAACTGAT	CCACTAATTG	GTCAACTGAG	TCAAATTTGG	2040
TCATATCTCG	AATGCGATCA	AGCCAATAAA	CCATGACGGT	TTCCCATAA	ATATCTTGAT	2100
TAAAATCAAA	AATATTGACT	TCAAACGTG	CTTCTTCTCC	ATCAAAGGTC	ACATTTTTTCC	2160

1275

CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG	2280
TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGGAAAGCGGT GCCCCCAAAA	2340
GTTTTCTGTC TTCTTTCACA TTTCCATCTA AAATAGCTTG ACGGATACGA GTTGAACATA	2400
TCTTTCCTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AGACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAATT CTCTACACC TTCGCGCTTT AATTTTCTTT	2640
CACGTTACGC AGGGTTCAAA ATATGCAAAA ACAAATCTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGGAGA TTCATTAAGG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CCTTATGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTGGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTGT	2940
TTTTTTCACA TGAAGGTAC CTGTTTTCAA AAAGCACTTT ATCTATCGT TGCTTAACTA	3000
TGAACTTTGC AATATTCTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAACTC CTGAGAACTT TAAATTACTA ATTTGGTCCG AAAAGGTAGA ATTTAGAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTGGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACTTTCCC TAATGACAAA GAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTTCTCTCC ATCTGTAGC TTGGATTCTC AGACCGTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA	3480
GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAAACA GTGTTCTATT CCAGATTCAT ACTCAATGaw	3600
AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGGT GCCAAAGTAC AGCAAGGTTG GCTTTTTGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAAATGGAA ACTATGCTGA TAAAGAATGG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTGGG ATAAGGAATC	180
TTGGTTTAT CTCAAATTG ATGGGAAAAT GGCTGAAAA GAATGGGTCT ACGATTCTCA	240
TAGTCAAGCT TGCTACTACT TCAAATCCGG TGTTTACATG ACAGCCAATG AATGGATTTG	300
GGATAAGGAA TCTTGGTTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAAT CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGA AGCGATGGTA AATGGCTTGG	600
AGGAAAACT ACAAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCTGTTA CAGCCAATGT	660
TTATGATCA GATGGTAAA AGCTTTCCTA TATATCGCAA AGTAGTGTG TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4010 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTTGGTTGA TGATACGAGG GATTTGGTGA TTCTTCTTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC	120
ATACCAGTCG TTTCAAGATA AGGAATTTTA GAAGGTTTTT GAAAGTCATA TTTCTTCAAT	180
TGGTTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAGTCCA GTTTGGCGAT GATTCCTTG	240
TGTGTATCCT TATTGATGAT GTCTAAAATC TGATATTAG GGTCTTTAAT GTCTAGTAAT	300
TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTTCTAA TGAGTTGTTT TGTCGCTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA	540

1277

TTAGTAAAGT AAAACTATTG GAGGATATTT TAATGCCACA ACCTATTGTT CCTGTAGAGA 600
 TTCCACAATC TCGTCGTTTT GATTCTAAAA AGAGAAATGA TATTCTGCTT AAAATTCGTA 660
 TTGGCAAGCT TGAAGTAAGT TTTTTTCAAT CTCTCAATCT CGAAATGGTA GAACAGCTTT 720
 TGGATAAAGT GTTGCTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA 780
 TGTGGGAAAA CGGATATGAG GCAAGGCATT GATTCATTGG CTTATCTGGT TAAAACCCAC 840
 TTTGAATTAG ATCCTTTCTC CGGTCAAGTT TTTCTCTTTT GTGGTGGACG TAAAGACCGC 900
 TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAACG CTTTGAGAAC 960
 GGAAAAGTGA CTTGGCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA 1020
 GATTGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATAA ATTTATCAGA AAGTCGTGAT 1080
 TTCTATTGAA ATGAGGACTT TCTTTTTAGT TATAATAAAG TTAGGAAATA AGGAGAGGAA 1140
 GCCCATGGAA GAAGATTGAA AATCATTCAA CAACAGAGTG CTACAATTGA TAGTCTCACC 1200
 AATGAACTTG CCCTTCTTCG TGAACAAGTG GCTTATCTAA CGCAAAAGCT CTATGGAAAA 1260
 TCCTCTGAGA AAAGTGTGTTG CCCACTGGA CAACTCAGTC TTTTGAAGA GGAACAAAAT 1320
 ATGGAAGAAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCACCTATA AACGTAAGAA 1380
 AGCTAAAGGG AAACGTCAAG CTCTTCTTGC CCAATTTGAT TCAGAAGAAG TTCATCATCA 1440
 AGTAGAAGAG AGCATTTGCC CTGATTGTCA GGGAGATCTA AAAGAGATTG GAGCAACCCCT 1500
 TCAACGACAA GAATTAGTCT TTATTCCTGC GCAATTAATA CGAATAGATC ATATCCAACA 1560
 CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAATCG TGAAAGCTCC 1620
 TATTCCTAAA GCCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACACCAT 1680
 CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCGCCAA GAAGAAGATT GGGCTAAGAT 1740
 GGGTTTACCA ATCACACGTA AGGAAATTGC TAATGGCAT ATCAAGGCGA GTCAATACTA 1800
 TTTGGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCTTCATGC 1860
 GGATGAAACC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCCTTACT ATTGGACTTT 1920
 TTTGTCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG 1980
 TGTTTTAGTA GTACAAGAAT TCCTAGGAGA TTATTCCTGC TATGTTTATT GTGACATGTT 2040
 GCGGCAGTAA CTTAGGACTT TAGTCCTCTA GTTCTGCCTA TGCGATAGCA GTCCAAGGTT 2100
 TAGGAGTAAG GCGACGCTAA GCTTGGTAAA CTGCGAACAG CTAGAAGCTT ATCGTCAACT 2160
 GGAAGAAGCT GCACTTGTG GATGTTGGGC GCATGTGAGA AGGAAGTTTT TTGAAGTGCC 2220
 CCCCAAGCAA GCAGATAAAT CATCCTTAGG AGCTAAAGGT TTAGCTTATT GTGATCAGTT 2280

1278

ATTTTCCTTG GAAAGAGACT GGGAGGCTTT GCCAGCTGAT GAACGACTAC AGAAACGTCA 2340
 AGAACATCTC CAGCCCCTAA TGGAAGACTT CTTTGCTTGG TGCCGCCGTC AGTCAGTTTT 2400
 AGCAGGTTCA AAACTAGGAA GGGCAATTGA ATACAGCCTC AAGTATGAAG AAACCTTTAA 2460
 GACTATTTTG AAAGACGGAC ATCTGGTCCT TTCCAATAAT CTAGCTGAAC GCGCCATTAA 2520
 ATCATTGGTT ATGGGACGGA GTAAAAGAGT CCAGTGGACT CTTTTAGCCT GAGCTCAGTT 2580
 TAAAAAAGCG AGGGTGGTTA TTTTCTCAA GTTTTGAAG AGCTAAAGCA AGAGCTATTG 2640
 TTATGAGCTT GTTGGAACA GCTAAACGTC ATCAATTATA GTGCGTTGAA TCTATAACAG 2700
 TACGCATCGA CTGCTAAAAC ATTTCTATAA ATCAATTTTC CTTTCCTAAT CGATTTGTTC 2760
 ATATCTTATT TCAATCCATT ATAAATAGCG AGAAATATCT ATCCTATCTT CTAGAATGTC 2820
 TTCCAAACGA GGAAACTCTC GTAAACAAAG AGGTTTTAGA GCCTATTTA CCGTGGACTA 2880
 AAGTTGTACA AGAAAAGTGC AAATAAGAAA TCTCCAGATT AGGAACTATC CGTGAGTTCT 2940
 CTAGTCTGGA GATTTTTCAA TAGACTTCGT TATTGGACGG TTACAATTTA TTATATGAAA 3000
 ATCCCATATT APTCTCCAAT TCTATATTTT ACCTTTCTAA ATGTATAGAT TAACTACCTA 3060
 ATTATAGCAT ATAACGCAGA TTCCTTTCAA TCGTATGATT TACTGCATTA AATTAAGTAA 3120
 AAAAAATAAG GCAGTCCGAA GACTGCCGAT ATTTATCTCT CATCTCTTTA ATTATGGTAA 3180
 GTAAATAAAT AATTTCCCTA AAGATATGGA AATTATTAAT ACTATAAATA CATATTATAA 3240
 AGTTTATAAA TACTGTAAAA ATCCTGAAGT TAATTTTCTA ATAAATATCA ATATGTGTTA 3300
 GTATCTTTTA AATTTTAGA CAATTTACTA GTTCTATAGA CATGTTTAAAC AGACTCTATT 3360
 TTACAATTC AAAAAATTCAT CTGCCACTTC ATTTAAAAAT TCTATATCAT GGGAAACAAT 3420
 AAAAAATTATT TTATCCATGG TTTTATACTT ATTAATCAGT TCAGATATTT TTATCATATT 3480
 GGAATAATCC ATACCACTTG AAGGTTGTC AAAAAAGACA AATGGAGAAT TCTTGACAT 3540
 AACAGATGCT ATTGCAAGCC TTTGCTTTTG CCCTCCTGAT AAACTCATCG GATGCCTTTC 3600
 AATAAATTCG TCCAGGCATA AATCTTTTAA CCCAAATCAT TCATACCTCT CTCAACTAGA 3660
 TGTAACCTAC AAAACCCCTG ACCTCATGAG CCACTTTCTT CCTCCTCATG AGGTCAGTTT 3720
 TACTTTCTGC TGTTCCAGTA TCGTTTTTCC TCGCTAGATT TCCTCAAAG GGCAGACTCC 3780
 TCCCTTGGTT CGTCACACGA TTTTTTCATC TCGACTGTTC TTTAATGCAT CATTAACGAC 3840
 GCTTTTCTTC TAGGTGGTTC ATAAGGAACA GGAAGATTCA GGTGACTTT TCTAATCCTA 3900
 GAATAAAGTG CTGAAAACAA TTCGGAATAG GCATAGAGAC TAGACAATTT GAGGAGCTGC 3960
 TTGCGTCTG TTCGAACACA TTTTCCCACC ACGTGAAGAA AAAGATGGCG 4010

(2) INFORMATION FOR SEQ ID NO: 254:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTTTCAA TTTAAAACAG AAAAACCAG	60
GAAAATGACA TAAAAATATC ATTCCTAGGC CTATTTATGC TATTTCTCTC TGAAAAATAT	120
GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT TCCCTCGCCT AATTCATGA	180
TTCGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCCT	240
CTCGATTCAT CTCTAAGAGA AACTTCAAGA CCAAATCTCT ATTTTCAGGA TCCAGAGAAC	300
CTGTGCGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTAA GATGGCTCTA GCAACTGCAA	360
TTCGTGTTG TTCGCCCCA GACAACTCGG AGACCCTTTG ATGCAAAGTA GCTGATAAAC	420
CTACTCTCTC TAAATCTCT TCCACCTTTT TGAGCTGTGC TTTCTTAGGC AATTTACAT	480
ATTTCAGCGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAATTTTG	540
AAACAGATAA GAGATATGTT CACGGATTAT TGTTTTCGAC TTAGCAGAAT TAACCGCTAG	600
ATTTGTCTGA CAAAAATCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCAATAA	660
ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG	720
ATCAATCCTG AGAGATAAGT TATCCAAAAT CACTTTTCCC CCAATGGTTT TGGTAATATT	780
TTTCAACTCA ATCATAAGAT GCCCCCTTTC AATAACTCTA CTAGACTTCT TTTCTCCATC	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAAACCTGC AAACAGTAGA	900
AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT TCCACCCCAT AAATTTCTTG	1020
GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTACTA GTAAGAAGTA GGAAATCATC	1080
ATGCTAAGGA GACCAAACAA AGCAAAGAGT AGGTTAAAAT TCCGAACAGC ATCTCGATAA	1140
GAATCCACTT TCTCTGTGTT AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT	1200
GACAATTTCT CAACTAACTC TGTAATCTCT TTTTGATGTT GAACCGTATT TTCAATTTTA	1260
ATCGGATTAT TTAAGCCAGT TGTTGACAGG GAGGCTTCT CATCCACAT CATATCAGAA	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCTT TTCGCTTATC ACTATATGGG	1380
AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT CCATCTCCTC TATCGTTTCGT	1440

1280

TTTTGCTGCT CTTCATACTT CATCGAATGA AAGGCAATTA ACTTCCCCAA GAGCTGATTT 1500
 TTATCTTCTT CACCTTTCGT ACTTGCTGGC ATCAAAATAA CTTTTTTAAT ACCGGTATTT 1560
 GGTAGCTTGA ATCCCTTGCT CTTTAGAAAA TTGCGATTGG CATAGTAAAC ATCCACCGTA 1620
 TCTGTAACT GATATTGCTG AATCTGTTCT GATTGGACAA AATTTTTTAC AGGAAGACTG 1680
 CTA CTACTCTGCA CATAGCCCGC CTGCGTTTTT TCTACCAAAT CCTGATAAAA TCGATAGAAA 1740
 TAATCTGTAG ATTTCCCTGA CCCTGCTAGC TCTTCTTGCC ACAGATTATC ATTGAGTTTG 1800
 AAGGTTTCTA AGGTCAGGTA ATTACCTTGA CTTACCCACT GTTGCTGATA AGCAAGTTCT 1860
 TTGTTTTCTT GTTCTAACT TCTGCCACC CCAATCAGTA AGGCCGTCAG TAAAATAGTT 1920
 GTCCCTATTT TCATCACATA ATTGAAGATA AGACCAAATT TGAAAGATGA AAAACCTTTC 1980
 AGCAGAGAGC TGATTGTCAT TTTTGGATT AAGAGGTAAG TCAACCAACT GATAAAGAGA 2040
 TAAAGCTGCA ACAGCAAAAA ATGAGACAAC CACAGCATAG GAAACAAATC TTTTGGCTTA 2100
 TAATCAAGCA AGAAAAACAC GCCTAGATTG ATCACAAGAG CCCACCTAG GAGGAGGTAA 2160
 AGGTTGCCTT TTACAACATC AGCTAAAACA GCCCTATCTT GAAAACCAAG TAATTTTTGT 2220
 ACCCCAATC TTTTCATCTC CATCATCGGT TGATACACTG TCACTAACAC AAGAAGCAAA 2280
 ATAGCCAAGA CAAAAACAAT GGCAGATAAA AGCAAATCTC GATTTATGAC TTCCACTGCA 2340
 CTTTTGTAGG TCGGCTCTAG CAAGGTAGCC TGGTCTATCT TGAAAAAATC GCTCCATTTT 2400
 TGTACAATCC TATCCTTGTC CATCTCTGTG GTAGAAGTTA TCGTATAGCG ACCATTTAAA 2460
 CTACGAGATG TATCCTTGAT ATAGGTTTGA AAAGTCATAA GCTGAATAGG TTTGGCTTTT 2520
 AGAAAGGTCG GAATCGTACC AAGTTTATTG GAAATTTCTT TATTACTATA GACTCCTTCA 2580
 CCATCTGTGG TAAAATCAAG AGAAGAAATC CCAAATCTT GGTAGGGGAA GGTATCTTTA 2640
 TCAAAAACAC CAGACTTGAC CACCTCATCA CCACTGTCTG TTTTGATGAT GGAGACTTTA 2700
 TACTCCTTTG ATACATCCTC AAAAAATCGA AGAACAGACG CTGCAGGTTT GTTAATATCT 2760
 TTCAAATACA AATCCAAAGA ATCTACAGG 2789

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCCAATTT TATTAAAGAT AATGTGTTAA TTACAGCGGC TCACAACCTAC TACAGACATG 60

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ACTATGGGAA	AGAAGCGGAT	GATATTTATG	TTCTTCCGGC	TGTTAGTCCA	AGTCAAGAAC	120
CATTTGGAAA	GATCAAAGTA	AAGGAAGTTC	GTTATTTGAA	GGAATTTAGA	AATTTAAATT	180
CTAAGGATGC	AAGGGAATAT	GACTTGGCTT	TATAAATCT	AGAAGAGCCC	ATTGGTGCAA	240
AATTAGGGAC	TTTGGGTCTT	CCTACTAGTC	AAAAAAATTT	GACAGGAATA	ACTGTGACTA	300
TCACAGGCTA	TCCATCATAT	AATTTTAAAA	TTCATCAAAT	GTATACAGAT	AAGAAACAAG	360
TTTTAAGTGA	TGATGGCATG	TTCTTGGATT	ACCAAGTTGA	TACTTTAGAG	GGGTCTAGTG	420
GATCTACAGT	TTATGATGCT	AGTCACCGTG	TAGTAGGAGT	GCATACTTTA	GGAGATGGAG	480
CTAATCAAAT	TAACAGTGCA	GTTAAATTAA	ATGAACGAAA	TTTGCCATTT	ATTTAWTCGG	540
TTCTTAAAGG	TTACTCTCTT	GAAGGATGGA	AGAAAATAAA	TGGTAGTTGG	TACCATTATA	600
GACAACATGA	TAAACAAACG	GGTTGGCAGG	AGATAAATGA	TACCTGGTAT	TATTTAGACA	660
GTCCCGTAA	GATGCTTACA	GATTTGGCAA	AAGTCCATGG	AAAATGGTAT	TATCTCAATT	720
CAAAATGGAGC	AATGGTTACA	GGTAGCCAAA	CTATCGATGG	TAAAGTTTAT	AACTTCGCTT	780
CATCTGGTGA	GTGGATTTAA	TGTTGGAGGA	TATATAAAAT	GAAGCTTTTG	AAAAAAATGA	840
TGCAAATCGC	ACTAGCCACA	TTTTTCTTCG	GTTTGTTAGC	GACAAATACA	GTATTTGCAG	900
ATGATTCTGA	AGGATGGCAG	TTTGTCCAAG	AAAATGGTAG	AACCTACTAC	AAAAGGGGG	960
ATCTAAAAGA	AACCTACTGG	AGAGTGATAG	ATGGGAAGTA	CTATTATTTT	GATCCTTTAT	1020
CCGGAGAGAT	GGTTGTCCGC	TGGCAATATA	TACCTGCTCC	ACACAAGGGG	GTTACGATTG	1080
GTCCTTCTCC	AAGAATAGAG	ATTGCTCTTA	GACCAGATTG	GTTTTATTTT	GGTCAAGATG	1140
GTGTATTACA	AGAATTTGTT	GGCAAGCAAG	TTTTAGAAGC	AAAAACTGCT	ACGAATACCA	1200
ACAAACATCA	TGGGGAAGAA	TATGATAGCC	AAGCAGAGAA	ACGAGTCTAT	TATTTTGAAG	1260
ATCAGCGTAG	TTATCATACT	TTAAAAACTG	GTTGGATTTA	TGAAGAGGGT	CATTGGTATT	1320
ATTTACAGAA	GGATGGTGGC	TTTGATTCGC	GCATCAACAG	ATTGACGGTT	GGAGAGCTAG	1380
CACGTGGTTG	GGTTAAGGAT	TACCCCTCTTA	CGTATGATGA	AGAGAAGCTA	AAAGCAGCTC	1440
CATGGTACTA	TCTAAATCCA	GCAACTGGCA	TTATGCAAAC	AGGTTGGCAA	TATCTAGGTA	1500
ATAGATGGTA	CTACCTCCAT	TCGTCAGGAG	CTATGGCAAC	TGGCTGGTAT	AAGGAAGGCT	1560
CAACTTGGTA	CTATCTAGAT	GCTGAAAATG	GTGATATGAG	AACTGGCTGG	CAAAACCTTG	1620
GGAACAAATG	GTAATATCTC	CGTTCATCAG	GAGCTATGGC	AACTGGTTGG	TATCAGGAAA	1680
GTTGACTTG	GTAATATCTA	AATGCAAGTA	ATGGAGATAT	GAAAACAGGC	TGGTTCCAAG	1740
TCAATGGTAA	CTGGTACTAT	GCCTATGATT	CAGGTGCTTT	AGCTGTTAAT	ACCACAGTAG	1800

1282

GTGGTACTA CTTAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAACCT	1860
GTGATGGATA CTTAACTTTG TATAATAGGT GGATAAAAAGT CTTCAACAATC AAAAAACGCA	1920
TAGTATCAAG GTTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCCGAAGgA	1980
TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT	2100
CTCATAACCG TAAAACATTT CCGATTTTCCAG AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGAA TCGTGTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTTTGTACT TGTTCTAAGT TGGGTGAAGT	2340
TGAAAGATTA TAGGCGATAA TTTTCGCTATT AAAGCCATCT AAAACTGGTG ATAAGTAAAG	2400
CTTTTGAGTA CTTGTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT	2460
TTTAGAGCCT TCAAATTGGC CTTGAATGAG ATTCG	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTTCGC AGTTCTTTTA	60
GCAAGTCATC CACAAAATA GTTTCAGGTA CAAAAGTGG ATCTTGTAAT ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAATTAC ATTGTCTTCA TCCCATCAT AAACCGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGACTATCAT CCTGAATATC CACCATAAAG GCATCCGTTT	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTCAG CATATAGGCA ATTTTCATCAG	420
GGTTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG	480
TCGAAGCAGC TAAAAGCCAA ACAAAGGAC TGACTAGTTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT	660
GTGCTGTTT GCCATTCCCA AGCCAAGAGG CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAGTGGT 780
 TAGGATTTTC TAGTACCTTC AGCAGGCGGA TGTAGCGTCT GTCTCCTTCT TCCGCCTTTT 840
 GTTCAACTCG GGCACGATTA AGAGAAACGG 870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCCAGAG AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTTGGCC CTTTCTCCAA 60
 AATCCAACCTC AGCCTATGTA GCTATGGATA AGGCACTTGC TGACCTCAA ACATCAGGGC 120
 ACTTGCCTAT TCCGCGACAC CTGCGTGATG GGCCTACAG TGAAGCAAG GAACTGGGGA 180
 ATGCCCAAGA CTATCTCTAT CCACACAAC ATCCTGGAAA TTGGGTCAAG CAAGACTATC 240
 TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC 300
 GGGCTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGGC AAAAATCTGA AATCCTTTTC 360
 AAAAAATTGC ACTTTCCTCT TGATTTTTTT TGAAAAAGTG GTATCATATA AATATAGAAA 420
 CGCTGTGGTG TACGACTTCA CACTTAAGTG TTGACCGACT ATTTTTTGTA TTATFAGGGA 480
 AACAAAAGTC TTCTAACAGC ATGTAGGCCG TCTCACACGG AAACAGCTTC AGTTAGAGCG 540
 AGTTGCCAC CTGCTTAATT GCGCGGTTT AATACAAACC GTGAAGTTTC GGCACCAATA 600
 CAGCTTTTTT CTTTGCCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG 660
 TCACAGGTTT GATCCCTGTA GGGGCATAT AAATACAACA GGAAAAGCCT TATAATATAG 720
 GGCTTTTTTT GCTTTCCTTT TAAAAATTGT CGTGCAATTT GCCGTGTTTT TACAACAAAC 780
 TTTTCACAGC CATAAATCC TACTAATTT TTTCTCCAA GGTATGCCCA TAAACGTCAA 840
 TCAACATGGA GATATCTTTA TGTCTAAAA TTTGGCTCTT TGTCAACTGT AGTGGGTTGA 900
 AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCTTTTCT TTTTGTATAT TCAGAGCGAT 960
 AAAAATCCGT TTTTGAAGT TTCAAAGTT CCGAAAACCA AAGGCATTGC GCTTGATAAG 1020
 TTTGATGAGA TTATTGGTCG CTTCCAATTT GCGTTAGAA TAGTGTAGTT GAAGGGCGTT 1080
 GACGATTTTC TCTTTGTCCT TTAGAAAGGT TTTAAAGACA GTCTGAAAA GAGGAGGAAC 1140
 CTGCTTTAGA TTGTCCTCAA TGAGTCCGAA AAATTTCTCC GGTGCCTTAT TCTGAAAGTG 1200

1284

AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCTTG 1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAGAT AGTTTGTCTG	60
AAGCTGAGAG AGCGGCACC AGGCTTATGC TAAAGAGAAA GGTTTGACCC CTCCTTCGAC	120
AGACCATCAG GATTCAGGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT	180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA	240
AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTTGA	300
GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC	360
GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCG CATTCAGATA ATGGTTTTGG	420
TAACGCTAGC GACCATGTTC AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA	480
AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA	540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC	600
AGAGGAATCA GAAGAACCTC AGGTCGAGAC TGAAAAGGTT GAAGAAAAAC TGAGAGAGGC	660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT	720
CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGGCAGA	780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC	840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG	900
TTCTCATTTT TTTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAAACTAGA ATAGTATACC	960
TCTACTTCTA AAACATGTGT AGAAATCGAT TTGACTGTCC TGTTCCTTATT TCATTTTACT	1020
ATATCTTAAC AGATAGTGTA AATAAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA	1080
CACTAGTTAA GGAGTAATGA TGAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT	1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA	1200
GGATTACTCT TTAAGTCTAT TTTAGAAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG	1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAACGATT AGTAAAGTAG	1320
CTAAAGATGT TCCGATTAAT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT	1380

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TTGAACAAGT AGATAGGGTT GTTCCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTTTG	1440
ACCTAGG TTC TGCTAAAATG AACTTAAAA TGGTGACTGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTCAGGCTG	1560
GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA	1620
TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 970 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAATCGTT GCTGAGATTA	60
TTATTATTTT GCCATTCTA ACTAATCTAT AAGTCTTTA TATTGCTGAA AACGCAATTC	120
AAAAAGGGCT ATTAATTGTG GATTTCTTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT	180
CTCTTTTGA TTGCTTCCTT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATTGCCA	240
CGATACTTTT TCAAAAACAT CATACGGTCG TAACATCCTC TCCAACCTCGG CTCGAAGAT	300
TGGGATGTAG GAGAAAAGTT TTCGCTCCAT GAGTCTGAT AAGATATTTA AGAGTCCTTG	360
CTTCATATAC AATCGATTGT GACTAACTC TTAAATCTT TTGGATTTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGGC ATGGTATTGC AAAAGAGATA	480
GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC	540
CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC	600
ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCCTCCA ATAGCTGCTC	660
TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCACAACC TTTCGACCGA TTCGCATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAACTCA TCAAAGGTCA CATTTATACC	780
TTGGATAGCT AGAATCAACT TATCCGCAGA CAGCATAGAC TGCCCTAGTT CAAACTTGGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTCGCCAA	900
ACGTAATFCC TTGTAAAATT CCCCAGTTC CATTCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAGG	970

1286

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GTTGACCACG GGTAAAACTA CCCTAACTGC AGCTATCACA ACTGTTTTGG CACGTCGCTT	60
GCCTTCATCA GTTAACCAAC CTAAAGACTA TGCGTCTATC GATGCTGCTC CAGAAGAACG	120
CGAACGCGGT ATCACTATCA ACACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCACCTA	180
CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC	240
TCAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAAACTCG	300
TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA	360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT	420
ATTGTCAAGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA	480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA	540
TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA	600
CGTATTCTCA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT	660
TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAA AAGCAGTTGT	720
TACTGGTGTT GAAATGTTCC GTAAACAACCT TGACGAAGGT CTTGCTGGAG ATAACGTAGG	780
TGTCCTTCTT CGTGGTGTTT AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC	840
AGGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA	900
AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC	960
TGACGTTACA GGTTCAATCG AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA	1020
CGTGACAATC GACGTTGAGT TGATTCAACC AATCGCCGTA GAACAAGGTA CTACATTCTC	1080
TATCCGTGAG GGTGGACGTA CTGTTGGTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT	1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGCA	1200
AGGTTCTTTT TTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA	1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAACACATT GTTAGAAATC GATTTGACTG	1320
TCCTGATCGA TTTGCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC	1380
TCAAACATT GTTTTAGGT TGTAGATAGA ACTGACGAAG TCAGTAACAT CTATACGACA	1440

1287

AGGCGAAGCT GACGCGGTTT GAAGAGATTT TCGAAGAGTA TAATACTAGA CTAAAATCAA	1500
AAAGCATTAT ACAATAGTAA TATGAAATCA ATTAAAGAAG AAATCCAAAC CATCAAAACA	1560
CTTTTAAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTCTGT	1620
CTGATGGGCA AATCTTATAA AGAGATTATA GAACTTTTAT AGTGGTTTGA AATAAGATGT	1680
GAACAACCTCT ATCAGGAAAG TCAAATAAT TTATAGAAAT ATTTTAGCAG CCAAGGTGTA	1740
CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAAACAA CGATTTGGCG AAATGTAAAA	1800
AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAAGAAAC ACGTGGTGGT CGTAACCATG	1860
CTTATATGAC GGTGAGCAA GAGAAAGTCT TTCTTGCCCG CCATTTGAAG GCTACAGAGG	1920
CAGGAGAATT TGTTACAATT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG TTAGGTCGTT	1980
CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCCCA TGTTGGCGA AATATTACGC	2040
CACGTCCAGA ACATCCTAAG AAAGCAGATG CTCAAACCAT TGTCGCGTCT AAAAAATAAG	2100
TCTCAATFCA AGAAGACAAG TGAAGTGCAC CCCAAAAGTT AGACAGAAAA AATCTAACTT	2160
TTGGGGTGT TTTATTATGA AATTAACCTA TGATGATAAA GTTCAGATCT ATGAACTTAG	2220
AAAACAAGGA TATAGCTTAG AGAAGCTTTC AAATAAATTT GGGATAAACA ATTCTAATCT	2280
TAGGTACATG ATTAAATGTA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAAA	2340
TCGTTACTAT TCTCCTGATT TAAAACAAGA AATGATTCAT AAAGTCTGAC ATGAAGGCTG	2400
GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACGATAC TTCTTAATCG	2460
GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC	2520
TGAGAGCGGA GAATGCCATC CTAAAAAAGT TAAGAGAACT CCGATTGAAG GAGGAAAAAG	2580
AGAAAGAAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTCTGT TAGATATTCT	2640
TCTAAAAGCC ATTAAACTAG CTCGTTTGAC CTACTACTAT CACTTGAAAC AGCTAGATAA	2700
ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATTCAATCC ATTTTATATCG AACACAAGGG	2760
AAATTATGCT TATCGTCGGA TTTATTTAGA ACTAAGAAAT CGTGGTTATC TGGTAAATCA	2820
TAAAAGAGTT CAAGGCTTGA TAAAAGTACT CAATTTACAA GCTAAAATGC GACAGAAACG	2880
AAAATATTCT TCTCATAAAG GAGACGTTGG CAAGAAGGCA GAGAATCTCA TTCAAGGACA	2940
ATTTGAAGGC TCTAAAACAA TGAAAAGTG CTACACAGAT GTGACAGAAT TTGCCG	2996

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 837 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAAA TCAGAACAAG	60
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGAT TTC	120
TCTCATTTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCTT	180
TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTC TTT TGTCGGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGAT TTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCATGACT GACCAAAATC	360
ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACT TTT TACTTCACC GACCAAT TCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GCGGAGGATA ATGGTTTTCA	540
CGGTCCGAAA GCCCAACCTT AGCCAACTCT TCCTTGCAA TCTTAGTCGC TTCTTGGTCA	600
GATAATTTCT TGACAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA	660
AACAAAT TAA ACTGTTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCTTCT	720
TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA	837

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTA ACT AGCGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCGACC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT	360
GGTTTTGGTG GTAAAATTAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT ACAAACCAAC TGAAGAAAAC AAAAAATTGA TTGCGAAAAT TGAACATGTT 480
 GAAAGTCACA ATGCTCAACA AACAGACGCA AACTTCTTTA CAGAATTCCT TGAGAAATGG 540
 GATCGTGGAG AATACCACGA CTAAGAGGTG ACCTATGATT TTAACAGTCA CAATGAACCC 600
 ATCCATCGAT ATTTCTATC CCTTGGATGA GTTGAAGATT GATACTGTCA ATCGTGTGGT 660
 GGATGTAACC AAAACGGCTG GTGGTAAGGG ACTCAATGTT ACCCGAGTAC TTTCAGAATT 720
 TGGCGATTCT GTTCTTGCTA CTGGTTTAGT GGGTGGCAA CTGGTGAGT TTTTGGTTGA 780
 ACATATCGAT AATCAAGTAA AGAAAGATTT CTTCTCAATT AAGGGAGAAA CTCGTAACGT 840
 TATCGCTATT CTCCACGGAG ACAACCAA 868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG TCTTCATAAG ACTCGAAAGT CACAGTTCTT TC GTTCTTGC TGGCATCTAT 60
 ATAGGTAATT TCAATCATGT TTAAACTCC TTGTGTTAAT GCTAACTTTA TTTTACTCCT 120
 TATAAAAGAG AATGTCAAGA AAAATGATTG CGCACGCAAC TTTTTTTAAA ATCATCTTAA 180
 ATCAAGAAAT CCAAACCTGC TTCCAAGCTT TCTTCGACAG TCTTTTGTAG CGAGGCCAGT 240
 GTCTTTTGCC CATCATTTGT CAGGCAGATA AACTAGAGC GTCTATCTTG ATGGCAACAC 300
 ATGCGACTGA GTAGACCGCA ATTTTAGCT TCCAAGCGAG CCACCATCCT AGAAACTGCG 360
 CTCGGGCTCA GATGAAGCTT ATCTGGCAGG TCAATCTGGC GTAGAGATTT TTCTTCAGCC 420
 AAGTCCAGAT AGTAGAGCAG GTAGAACTCT TTCAAGGTCA GACTTTGCTC GCTCTGTTGG 480
 GCAATGGTCT CTTCCAAGAG ACTTTCAATT TCTTTCTGAC GCCGATTGAA GTCAAACCAT 540
 TTTTCCAAAT AGGTCAATAGT GTCTCCTTTC TTTTAGAGT CATAAATAGA AGAAAGTCCA 600
 TTAACGGGCA GTCTCTGCGT CACAAGATGA TTGCGCATGC AATAATTATA CTACTTTTCA 660
 AGAATGCTGG CAAGCTCTGT TTTTAGTGG TTTTATTTTT GTGTGAATAA TGGGGGAATC 720
 CTATTGTTTC AATTTCTAAC TCCTTATCAC ATTCGAATTC AGATTTTATT TCATTTCTCT 780
 ATCTATAGTT GCTTAGTTTA AAATAAGCAT GGTCTAATAA AGCTATGCAT ATAGTACTGA 840
 TTTTAAACAA GGAGCATTAG ATTCCATTAA AGGAGGGCAC AGACATGTCG AGGCGGCCAA 900

1290

AGTTTTTGAT GTCGGCGTCA GAACTCTCTT CACGTGGGAA AAGAAAGACG TAAACAAGGG 960
 AACTTAGAGC GGAAAAAGCG AGTCGTCAAA AAGCGTAAGA TCCCTTTAGA AGAATTGAAA 1020
 GCCTTTGTAG AGGCTCATCC AGACGCTTTT TTACGGGAAA TTGCGGCCCG TTTTGATTGT 1080
 GCTTTGCCCT CCGTATGGGC AGTTTTAAAG CAGATTAAGG TCATTTTAAA AAAGACGACC 1140
 AGTTTTAGGG AACAAAAGCC TGAGAAAGTT TCTGAGTTTC TTGATATTTT GGATAACCTA 1200
 AAAGATTTAC CAGTCCTATA TATTGACGAA ACGGGAATCG ACCGCTACCT CTATCGTCTT 1260
 TATGCAGGGG CTCCTAGAGG GGAGAAAGTC TATGGCAAGA TTAGCGGACG GCGTTTTGAG 1320
 CGGACTAATG AGGTGGAGCA AAAACTCAAT GGTAGTTTTC TAATCAGATA TATTGATTCA 1380
 CAAATTAGAG AATGAAAGAA TAATTATGCA TAAAAATAGG AATATAAACC AAAAATTAGC 1440
 TGATTTATAC TCATTTGCGT GTCTTTATAA AAAACTTATC TTATAATATA TATATATATA 1500
 TATACAAAAT AGTAAAATGC TTTTTTTTTT TAGCAAAAAT ACCTCAAGTT TCTTGCTATT 1560
 TTGGGTCCC TATTCTATAA TTATAGTATG GTAATTTATT TATATCCATA CATGAAAATA 1620
 ATACTCGAAA GGAAATTTCA AAATATTTTT TAGACGTCAG AAGGGTGAAT ATAGAGAAAC 1680
 AGACCGAGTA ACTCGGTCA AATTAATCAA ATCAGGGAAG CATTGGCTAC GGGCCTCGAC 1740
 TTCTCTTTTT GGCTTGTTA AGGTCTGCG AGGTGGTGT GATACTACTC AGGTCATGAC 1800
 CGAAACGGTA GAAGATAAAG TAAGTCATTC AATTACTGGG CTTGATATCC TCAAGGGGAT 1860
 AGTTGCTCGG GGAGCTGTCA TAAGTGGAAC CGTTGCAACT CAAACGAAGG TATTTACAAA 1920
 TGAGTCAGCA GTACTTGAAA AACTGTAGA GAAACGGAT GCTTTGGCAA CAAATGATAC 1980
 AGTAGTTCTA GGTACGATAT CTACAAGTAA TTCAGCGAGT TCAACTAGTT TGTCAGCTTC 2040
 AGAGTCGGCA AGTACATCTG CATCTGAGTC AGCCTCAACC AGCGCTTCGA CCTCAGCAAG 2100
 TACAAGTGCA TCAGAATCAG CAAGTACATC GGCTTCGACA AGTATTTCTG CATCATCTAC 2160
 TGTGGTAGGT TCACAAACAG CTGCCGCTAC AGAAGCAACT GCTAAGAAGG TCGAAGAAGA 2220
 TCGTAAGAAA CCAGCTAGTG ATTATGTAGC ATCAGTTACA AATGTCAATC TCCAATCTTA 2280
 TGCTAAGCGA CGCAAGCGTT CAGTGGATTC CATCGAGCAA TTGCTGGCTT CTATAAAAAA 2340
 TGCTGCTGTT TTTTCTGGCA ATACGATTGT AAATGGGCC CCTGCAATTA ATGCAAGTCT 2400
 AAACATTGCT AAAAGTGAGA CAAAAGTTA TACAGGTGAA GGTGTAGATT CGGTATATCG 2460
 TGTTCCAATT TACTATAAAT TGAAAGTGAC AAATGATGGT TCAAAATGA CCTTTACCTA 2520
 TACGGTTACG TATGTGAATC CTAAAACAAA TGATCTTGGT AATATATCAA GTATGCGTCC 2580
 TGGATATCT ATCTATAATT CAGGTACTTC AACACAAACA ATGTTAACCC TTGGCAGTGA 2640
 TCTTGGTAAA CCTTCAGGTG TAAAGAACTA CATTACTGAC AAAAATGGTA GACAGGTCTT 2700

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ATCCTATAAT ACATCTACAA TGACGACGCA GGGTAGTGGG TATACTTGGG GAAATGGTGC	2760
CCAAATGAAT GGTTTCTTTG CTAAGAAAGG ATATGGATTA ACATCATCTT GGACTGTACC	2820
AATTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGTAGTTGAA TCTAGCACGA CCAGTCAGTC	2940
ACTTTCACAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTGCG TCGGCTTCAG CATCAACCAG TGCCCTCGGCT TCAGCGTCAA CCAGTGCCTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAGTGCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCGTCAA CCAGTGCCTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACG AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGGTTCAG CATCAACGAG TACGTCAGCT TCAGCGTCAA CCAGTGCCTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	3480
ACGAGTGCCT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTCT	3540
GAATCGGCC CAACCAGTGC GTCACCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTGCCTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG	3660
CATCAACCAG TGCGTCAGCC TCAGCAAGTA CTAGTGATC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCGTCAAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG GCCTTGAGTA ATCTCAATTT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGGTCAT AATGGGGCTG GAAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTCGTATTT TGGTAGACGG TCAGGAGTTA TCGGAAAATC GCTTGGCTAT	180
TAAACGAAAG ATTGGCTACG TAGCAGACTC GCCTGACTTA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

1292

TCTAGCTAGG CTATTGAACG TTTTGTGATTT TGCTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCTTTCTCAC GGAATGCGTC AGAAAGTCTT TGTCATCGGA GCACTCTTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG TTTGGATCCC CAGGCTGCCT TTGATTTGAA	480
ACAGATGATG AAGGAACATG CACAAAAGG GAAGACAGTC TTGTTTTCAA CTCATGTCTT	540
AGAGGTGGCA GAGCAAGTCT GTGATCGGAT TGCCATTTTG AAAAAGGGGC ATTTGATTTA	600
TTGTGGTAGT GTAGAGGACT TGAGAAAAGA TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT TGCGGATGCG TCTCAAGGTC ATTAATAAAT	720
TAGTTGATAT CAATATCCTT TATTCATCTC AAGAAGCTAA TCTGGCTAAT CTACGAAAGA	780
AGCAGGCTAA GAATC	795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTAATGTG CTTGGCAGCw TCCTTGACAC TGCTACTACC ATTTCCCATATA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT TATCTGAGTC ACCAAAAGCC ATGACTTGGT	120
TGAGGTCAAA GCCATATTCT TTCCCAACTC GGCGAATGCC TTCTAATTTA GAATTTCCCT	180
GATTGATGAC ATCCGATGCA AAAGGATTGC TACGTGTCAA TTTCAAGTCT TCAAAATCAG	240
CTGCCGCCTT CTCAGATTCT TCTGGTGTCA TCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCCTTTT GGGGAACAAC CTTGCTGACC ATGCGATTAA	360
AAGACTGACT CACCGTCCGA GTTAAAACAG AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCAG ACCAAAGGAC ATGATTTTAG AACCCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC TAATTAGATG GCGCAAATGT AACTTGGAAA	540
TAGGGCTCGT GAACAAGACT CTGTCTTTAC TAAAGATATA CTGGCCATTA TAGGTTACCG	600
CAAAATCCAG ATCCAATCG TCCATCAATT CCTTAACAAA AAAAGTCTCT CGCCCTGTCG	660
CTACGCCAAC TAGTACCCCT TGTTCTTTGA CAATCTTAAT CGCATCCTTA GTGGATTTCA	720
AAACTCTTT GCGATTGTTG ACCAAGGTTT CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCCTATC CCAATCTCCC CTTTTGTGAT ACAATGATTA TACCACATTT CAGAAAGAGT	840
GAGTAAATCA TGCCTAAGAA AATCCTTGTT TTACATACGG GTGGAACATAT TTCCATGCAG	900

1293

GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC 960
 CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTA ACCTTCCAAG TCCCATATC 1020
 AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAG AGGAAGCAGA TAACTACGAT 1080
 GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC 1140
 ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TCGGTACTCC AATGAGCTCG 1200
 GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG 1260
 CTGACAAAGG AGTTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA 1320
 AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTGGTCTCA 1380
 TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCGC TTTGACCTTG 1440
 ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA 1500
 TTGATATGCT GGATTTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA 1560
 ATATTCCCAA AGAAACGGCT CAAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCCAGTCG 1620
 CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG 1680
 GCGTACAGTT GCAAAAAGCA GCGTTTTCT TTGTAAAGA ACTCAACGCC CAAAAGCTC 1740
 GCTTGAAACT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA 1800
 TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTGCGCT TACCGTATGT 1860
 ATGGtACTGA CTTCGTCAGT TTCATCTACA ACCTCAAAA CATGTTTTGA GCTGACTTCG 1920
 TCAGTTCAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGT TCTATCTACA 1980
 ACCTCAAAA CATGTTTTGA GCTGACTTCG TCAGTTCAT CTACAACCTC AAAAACATGT 2040
 TTTGAGCTGA CTTCGTCAGT TCTATCTACA ACCTCAAAA CATGTTTTGA GCTGACTTCG 2100
 TCAGTTCAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGk TCTATCTACA 2160
 ACCTCAAAA CATGTTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAAACATGT 2220
 TTTGAGCTGA C 2231

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

GAGTCAAAGG CTCCGAGGTT GACTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG 60
 TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA 120
 GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAT 180
 CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGA CAAGTCCTTT 240
 TCAGGAACGG GCACCATTTC CTTTTATCAG ACGCACAAGG AGGTTTCATGT CTCACGGCAT 300
 TACCAATCCC TCCTAAAAGA AAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG 360
 CATTGGTAT TGTTTTATTG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGGAA 420
 TTCCTTCTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT 480
 CCATTGAGTC CATCCTTAGA CGTCATCTCA CTTCGGCAGT TTTTACAGGT TTAGTGGCGC 540
 TCATCATTCG AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCT CTTATTTGGG 600
 CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG 660
 AAAAAAATG GTGGTACAAT GGGAAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG 720
 GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT 780
 TTGGGGATGC TAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA 840
 ATATGGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTC ACAACACTGG CGTGTAGATT 900
 TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA 960
 AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTTAAAT 1020
 AAAAAATCT TCACCTCAAC CATCAAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT 1080
 GCTCTGATTT CAGTTCATG GTTGTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAAGT 1140
 TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT 1200
 GATGTAGTGT CAAATGCCTT TAAAAACCG ATGATATTGG ACAGTTTTTT TGCCTTTAAT 1260
 TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGGAGAATG 1310

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5922 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT 60
 ATGTTGAGTC TGCTGCTGTT ATCGGTGCAG GTGACGTAC TGTTTGACA GCCTTGTTG 120

TAGCTATCTG	TTTTGCGATT	TCAAGCTTCT	TTAGCCCACT	TCTAGCGATC	GTACCAACAG	180
CGGCTACAGC	TCCAATCTTG	ATTATCGTTG	GGATTATGAT	GCTTGGTAGC	TTGAAAAATA	240
TCCATTGGGA	TGATATGTCT	GAAGCAGTTC	CTGCCTTCTT	CACATCTATC	TTTATGGGAT	300
TCAGCTACTC	TATCACTCAA	GGGATGTCAG	TTGGTTCTT	GACTTACACT	TTGACTAAGC	360
TTGTTAAAGG	TCAAGTTAAA	GATGTTTCATG	TCATGATTTG	GATTTTGGAT	GCCTTGTTTA	420
TCCTTAACTA	CATCAGCATG	GCCTTATAAT	AGAATGACCC	AGGGGGATTT	CCCCCTTTT	480
TTAATACAaG	GAGATAGGTG	ATGAAAGAGA	AAAATATGTG	GAAAGAATTG	TTGAATCGTG	540
CAGGCTGGAT	TTTGGTCTTT	TTACTTGCCG	TCCTTTTATA	TCAGGTFCCC	CTAGTGGTTA	600
CCTCTATTTT	GACTTTAAAA	GAAGTAGCCC	TGCTACAGTC	AGGGCTGATA	GTGCTGGCC	660
TTTCAATTGT	GGTTCGGCT	CTATTTATTA	TGGGAGCTCG	TAAAACCAAG	TTAGCTAGTT	720
TTAATTTTTC	TTTTTTTAGA	GCTAAAGATT	TGGCACGTTT	GGGCTTGAGT	TATCTAGTTA	780
TTGTCGGGTC	AAATATACTT	GGTTCATT	TATTGCAACT	GTCAAATGAG	ACGACAACAG	840
CTAACCACTG	TCAGATTAAT	GATATGGTTC	AAAATAGTTC	GTTGATTTCC	AGTTTCTTCT	900
TGCTAGCCTT	GCTTGCTCCG	ATTTGTGAGG	AAATCTTGTC	TCGTGGGATT	GTTCCATAAAA	960
AGATTTTCCG	AGGCAAGGAG	AACTTGGGAT	TTGTAGTCGG	TACGATTGTG	TTTGCTTTAT	1020
TGCATCAACC	AAGTAATTTA	CCTTCTTTAT	TGATTTATGG	AGGTATGTCG	ACAGTTCTAT	1080
CTTGACAGC	CTACAAGACC	CAACGTTTGG	AAATGTCGAT	CTTGCTTCAC	ATGATTGTTA	1140
ATGGGATTGC	TTTCTGTTTG	TTGGCTCTTG	TGGTGATTAT	GAGTCGGACA	TTAGGAATTT	1200
CTGTTTAAAA	GTTTTTATGT	AGGAACCGAC	CTCTTCTAC	CAGGGAAGA	TGAATGCAAT	1260
CGTGTCATC	TTTTTCTTTT	TATGGTAAAA	TAGAAAAATA	ATATGATGAA	AATCCTTGAG	1320
GGAGTGACCG	ATATGTCAAG	TAAAGCCAAT	CATGCAAAGA	CAGTTATTTG	CGGAATTATC	1380
AATGTAACCC	CAGACTCCTT	TTCGGACGGT	GGTCAATTTT	TTGCTCTTGA	GCAGGCGCTC	1440
CAGCAGGCTC	GTAATTTGAT	AGCAGAAGGA	GCCAGTATGC	TAGATATCGG	CGGAGAATCG	1500
ACTCGGCCGG	GAAGTAGCTA	TGTTGAGATA	GAAGAGGAAA	TCCAGCGTGT	TGTTCCAGTG	1560
ATCAAAGCGA	TTCGCAAGGA	AAGTGATGTC	CTCATCTCTA	TTGATACTTG	GAAGAGTCAA	1620
GTAGCAGAGG	CTGCTTTGGC	TGCTGGTGCC	GATCTAGTCA	ATGATATCAC	TGGTCTTATG	1680
GGTGATGAGA	AAATGGCTTA	TGTGGTAGCT	GAAGCGAGAg	CGAAAGTGGT	CATCATGTTT	1740
AACCCAGTTA	TGGCTCGACC	TCAGCATCCT	AGTTCGCTTA	TCTTCCCTCA	TTTTGGTTTT	1800
GGTCAAACCT	TTACAGAAAA	AGAGTFAGCT	GACTTTGAAA	CATTGCCAAT	CGAAGACTTG	1860

1296

ATGGTGGCTT	TCTTTGAACG	AGCACTAGCG	AGAGCGGCAG	AAGCTGGTAT	TGCACCAGAA	1920
AATATCCTGT	TGGATCCAGG	AATTGGCTTT	GGTCTGACCA	AGAAAGAAAA	TCTGCTTCTT	1980
TTACGGGACC	TGGATAAACT	ACATCAGAAG	GGCTATCCAA	TCTTTCTCGG	AGTGTGCGGC	2040
AAGCgATTTG	TCATCAATAT	CCTAGAGGAG	AATGGTTTTG	AAGTCAATCC	TGAGACAGAG	2100
CTTGGTTTCC	GAAATCGGGA	CACGGCTTCG	GCTCATGTAA	CTAGTATCGC	TGCGAGACAG	2160
GGTGTAGAAG	TGGTGC GCGT	GCATGACGTA	GCTAGTCACA	GGATGGCAGT	TGAAATTGCC	2220
TCTGCCATTC	GCTCGGCTGA	TGAAGCGGAA	AATTTAGATT	TAAAACAATA	TAAATAAGAT	2280
GAAAGAAATT	GAAAACAATC	AGTGGATTGC	TAAC TACCGG	ACGGATCAAC	CGCATTTTGG	2340
CTTGGAACGA	ATGGTGGAAC	TGTTAGCTTT	CGGTGGCAAT	CCCCATCTCA	AACTCAAGGT	2400
CCTCCATATC	GGAGGGACTA	ACGGCAAGGG	CTCGACTATT	GCTTTTTTGA	AAAAGATGCT	2460
AGAAAAGCTA	GGGTTGAGAG	TTGGCGTGT	TAGCTCGCCC	TATCTCATTC	ATTACACAGA	2520
CCAGATTAGC	ATCAATGGGG	AATCGATCTC	AGAAGCGAGG	CTAGAAGCTC	TCATGGCAGA	2580
CTATCAGTCT	TTGCTGGAGG	GAGAAGCGGT	CGCCAATTTA	CAGGGCACAA	CCGAGTTTGA	2640
GATTATCACA	GCCCTGGCCT	ATGACTACTT	TGCCTCAGAG	CAAGTAGATG	TGGCCATCAT	2700
GGAAAGTTGG	ATGGGTGGAC	TTTTGGATAG	TACCAATGTC	TGTCAGCCCA	TTTTGACAGG	2760
AATTACAAC T	ATTGGCTTGG	ATCATGTGGC	TCTACTTGGT	GACACCTTGG	AGGTCATAGC	2820
AGAGCAGAAG	GCAGGTATTA	TCAAACAAGG	GATGCCCTTG	GTAACAGGGC	GTATTGCTCC	2880
AGAAGCCTTG	GCTGTGATTG	ACCGCATTGC	GGAAGGGAAA	GATGCGCCGA	GACTTGCCCTA	2940
CGGGACAGAT	TATCAGGTTC	GTCATCAAGA	AAGTGTGGTG	ACAGGGGAAG	TCTTTGACTA	3000
TACAAGTGCT	GTCAGACAAG	GTCGCTTCCA	GACTAGCCTG	CTTGGTTTGT	ACCAAATAGA	3060
GAATGCTGGG	ATGGCCATAG	CTTTACTTGA	TACTTTTTGT	CAAGAAGATG	GTCGAGAGCT	3120
AGCAAGCAAT	GATTTTCTTG	GTCAAGCCTT	GGAAGAAACA	AGTTGGCCAG	GGCGTTTGG A	3180
AATCGTG TCA	AGAGATCCCT	TGATGATTTT	GGATGGAGCC	CACAATCCCC	ATGCTATCAA	3240
GGCCTTGTTG	GTAACCTTGC	AAGAACGTTT	TGCGGATTAT	CATAAGGAAA	TCCTCTT CAC	3300
TTGTATCAAA	ACCAAGCCTT	TGGAGGATAT	GTTGGACTTG	CTGGGAGCCA	TGCCAGTTAC	3360
CGAGCTTACT	CTAACACATT	TTGCGGATAG	TCGGGCGACG	GATGAAAACG	TGCTGAAAGA	3420
GGCAGCTAAG	TCTAGAAAATC	TCAGCTACCA	AGATTGGCAT	GATTTTCTAG	AGCAGAATTT	3480
GACAGATAAA	AAAGAAGAGA	AACAAACAGT	TAGGATGTGC	ACAGGTT CCT	TGTATTTCTT	3540
GAGCCAAGTG	AGGGCCTATC	TGATGGAGAG	GAAGAACGAG	AATGGATACA	CAAAAGATTG	3600
AAGCGGCTGT	AAAAATGATT	ATCGAGGCTG	TAGGAGAGGA	CGCTAATCGC	GAGGGCTTGC	3660

AGGAAACACC	TGCTCGTGTA	GCCCGTATGT	ATCAAGAGAT	TTTTTCAGGT	CTTGGTCAAA	3720
CAGCAGAGGA	ACATTTGTCA	AAATCCTTTG	AAATTATTGA	CGATAATATG	GTGGTAGAAA	3780
AGGATATCTT	TTTCCATACC	ATGTGTGAAC	ACCACTTCTT	GCCATTTTAT	GGTAGAGCGC	3840
ACATTGCCTA	CATTCCAGAT	GGTCGTGTGG	CAGGCTTGTC	TAAGCTAGCC	CGTACGGTTG	3900
AAGTTTATTC	GAAAAACCA	CAAATTC AAG	AACGTTTGAA	TATCGAAGTG	GCCGATGCCT	3960
TGATGGACTA	TCTAGGTGCT	AAAGGAGCCT	TTGTTGTCAT	TGAGGCGGAA	CATATGTGTA	4020
TGAGTATGCG	TGGTGTTAGA	AAACCAGGCA	CTGCAACCTT	GACGACAGTA	GCTCGTGGTC	4080
TATTTGAAAC	AGATAAGGAT	CTCCGTGACC	AAGCTTATCG	TTTAATGGGG	CTATAAAAAG	4140
AATCCGCTTC	AAGCGGATTT	TTCTAGAAAAG	GAATCATTAT	GGATCAACTG	CAGATTAAGG	4200
ATTTGGAAAT	GTTTGCCTAT	CATGGTCTTT	TTCTTAGTGA	GAAAGAATTG	GGGCAGAAAT	4260
TTGTCGTTTC	AGCCATCCTA	TCCTATGATA	TGACCAAGGC	AGCTACAGAC	TTGGATTTAA	4320
CAGCCTCTGT	CCATTACGGA	GAATTGTGTC	AGCAGTGGAC	GACTTGGTTT	CAGGAAACGA	4380
GTGAAGATTT	GATTGAAAACG	GTAGCCTATA	AACTGGTGGA	ACGTACCTTT	GAGTTTTATC	4440
CTCTTGTC CA	AGAAATGAAG	TTGGA ACTGA	AAAAACCTTG	GGCACCGGTG	CATTTGTCAC	4500
TAGATACTTG	CTCGGTAACC	ATT CATCGCC	GCAAGCAACG	AGCCTTTATC	GCCCTAGGAA	4560
GCAATATGGG	AGATAAAACAA	GCAA ACTTGA	AGCAAGCCAT	TGACAAACTG	CGAGCTCGTG	4620
GCATCCATAT	TCTCAAAGAG	TCCAGTGTCT	TAGCGACGGA	GCCTTGGGGT	GGAGTGGAGC	4680
AGGATAGCTT	TGCCAATCAA	GTGGTTGAGG	TGGA AACCTG	GCTACCAGCA	CAAGACTTGT	4740
TAGAAACCTT	GTTAGCCATT	GAGTCAGAGC	TGGGACGGGT	GAGAGAAGTG	CATTGGGGAC	4800
CTCGTTTGAT	TGATTTGGAC	TTGCTCTTTG	TGGAGGACCA	GATCCTTTAT	ACAGACGACC	4860
TCATATTGCC	TCATCCTTAC	ATAGCGGAAC	GCCTTTTGTG	CCTTGAGTCT	TACAGGAAAT	4920
TGCGCCTCAT	TTTATCCATC	CGATATPAAA	ACAACCGATC	CGCAACTTGT	ATGATGCTTT	4980
GAAAAAATAG	AAAAACTCTA	GTTTTCAGTT	ACTTGCAACT	GAAGGCTAGA	GTTTTTATAC	5040
TCTTCGAAAA	TCTCTCAAAA	CCACGTCAGC	GTCGCCTTAC	CGTACTCAAG	TACAGCTTGC	5100
GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAAAATAGGT	CATTTTCTTC	5160
TGGGAGGAGG	ATAGTTTCTC	TACCGTCCAT	GTCTAAAACC	AGTACTCTTG	GGGGATAACG	5220
AGGGTCGAAA	GGATGGTTAA	AGTCAAAATC	AATGGCTGTA	GGGAGGTGTT	GA CTGAAAA	5280
GTGGAAGGTA	ATCTTFCCTT	GGTTATTAAG	CAATTGAAAC	TCGAGTCTCT	CTTCCAATTC	5340
AAAGACATTT	TTTAAGAAAT	GGTCGATGAT	ATACCAAAAA	GAGTCAATGA	TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC	5460
TCTGTCCCCT TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG	5520
ATTTTTTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAAATCCT AAAAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA	5640
AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTA AAAATTT GGTATGATAG	5700
TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCAGAAC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA	5820
AACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTTGGACGTC TTTCTGCAGT AGTTGCTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAACATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTTCCCAA GAGGCATAGG	60
GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATCCCGTTC	120
CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT	300
AATGCCCAT TCCCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTCCGATG GATTGACCAG	360
CAGGTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTTCTA GGGTAAAGCA	420
AATCCTGCTT GCTTAACCCC AATTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTAAAC CCCTTAGCC ATAACCATCA TTTCAGGCGA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTAGT TCCTTGGTCA AGCTTGATTT CTTGACCAG CGCTTGCGAT	600
TGTTTTCATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTTAGTGTG ATAGTTTGAG GAGCTTTTCC	720
AAGTAGAGAG GCAATTTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTGTCAAAT GTTTGGCTTT TGTAGTATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTCTT ATGCCTACAA	900

1299

GAGCTTTCAT TATTTCCATT TTCTTTTGGG TTCTACTCTA TTCTGAAAAA CTTGTGTATA	960
TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG	1020
GGGAATCTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA	1080
CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA	1140
TATTGTCCTC AATATCGTCT AGAAAGACAC AATTTCTAGG TTATAACTGG TATTTATCGA	1200
TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT	1260
ACCTCCATAC TCACCTTACA GATTCCTTTG GTAATAATAT CTTTGCCTAA TGTAGAGACA	1320
GTCTTGCAA GAAAAAATT CCTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA	1380
CTGGTAAGTA TTGACAAAGG CAAAACAACA ATTTCGATTC TTAGCTTAC TTTCTGCCTG	1440
TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTCC TCTTTTACAA ACAAATACTC	1500
GATTTCTAGC CAATTTCCAA AAGTCTCTGC TATCAAACCT GCCAGGAGAT TGCCCTTTTC	1560
ATCTTCGACA TAAAGATTA GTGGCTCACT TTCAGCCTCT TCTCTTTTTC AACGGTTATA	1620
AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA	1680
GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAAG GAATTTAATC TAATTTCTAA	1740
CAATGTCTTA GAAATCAAAG TGACTATTT TAACTTCAAT GCACTATACA TCTAATACTC	1800
AATAAAAATC AAAGAGCAA CTAGGAAACT AGCCGAGGT TGCTCAAAAC ACTGTTTGA	1860
GGTTGTAGAT AGAAcTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTTG TAGATGAAAC	1920
TGACGAAGTC GGCTCAAAAC ATGGTTTTGA GGTGTAGAT GAAACTGACG AAGTCAGCTC	1980
AAAACAGG	1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATTT GTTTTATGTA ATTTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG	60
TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAAACAA AAAGGGAAT TAGTTGTGGC	120
AACCAGTCCT GACTATGCAC CCTTTGAATT TCAATCATG GTTGATGGAA AGAACCAGGT	180
AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGG TTAAGTTGGA	240

1300

AATCTCAAGC ATGAGTTTTG ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAATTAGTG CTA CTACTGACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAGATTA GTTCTTGGT TCGTAAGGCT GATGTGGAAA AATACAAGGA	420
TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCAAAAA GGGACTGTTC CAGAATCAAT	480
GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATGG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACGG	660
CGACGCCAAT GCCGyTGCTC TTAGAAaATA GTGATGATTT GAAAGAAGT	709

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAAACCTGAT	120
TGTGATGGGG CTATTCCTAGC TTTAGAAACC TTCAAAAATT AAAATTTAAG GCAATCAATT	180
ACTTGGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCCT AGGTCTAGAA TTACATATAT	240
ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTC TATTCTGAAA GATTTGAGCT	300
GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATFGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTTTCAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAATTTCTA CTCTTCGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGG AGTTGCGGAT ATTCAGGCTT ATAAAGATTA	540
TTACGTTTCCT ATGAACAAGG CTCTCTGGAA AGACTTGAG CTGAAGAAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCAG CAGGGACAAA CACTATCGGG	720
CGCTCATGAT CTCTTGACA GCCTCATTGA GCGTGATTAT AACTTGTATG CTGCGACAAA	780
TGGCATTACT GCCATTCAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960

1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA 1020
 TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT 1080
 GCTGGATTGT TTAGATAAAA ATATCTTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA 1140
 TGACTACAAA AAAGCTAATA TTACTATTGA AGAGTACATT GAAATGTCTG AAGTGTATTT 1200
 TAATGAAGCT GTTAATTATG AATTTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA 1260
 TCAATCTCTT TTTAAGTTTT TTGATAAGAA AAATTTCTCT GCGGATTTAA TTTTACTTGT 1320
 GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA 1380
 TAATCTTAGA GTAATAGGAA ATATATTTCC GAATTATCTT ACTAATCGAA AATATAGCCT 1440
 CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT 1500
 AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC 1560
 TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCATTGTAT TTTCGATTTT TTTCTAATTT 1620
 TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAACTCC 1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG 60
 CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATAGT TCTAATTTCT 120
 CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA 180
 TTTCTACCAG ACCGTTTGGC GTGagCTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT 240
 CTGATTGGGA AATTTGGATA AAATTGGTTG GCAAGAGTTT AAGAACCTGA TAGAGTCGCA 300
 AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCCGATTC TCGATATAGA 360
 AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTTT CCTTTGATTT 420
 TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT 480
 GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT 540
 TCATAGTTTT CTCTCCTTTT CAGTTATACA AGGTTGTGAT CACTTCCTGT ATATCCGG 598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

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CCAGCAAATC AATAACTGCA ATGCTATAA AATGGATTCT ATAGAGTTT TTCATGACAA      60
GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCTAAAAGA ATGGGAGTTA CAACTAAAAT      120
GATAAAAATA GCAGAAGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC      180
TTCTATTATC TAACTTCTTC ATCATTCAG ACAATAAAG CTCCGATTGC ATTGAGGATA      240
TAAAAGATGT ATTTACCGAT ATFGCGAAG TTTCCTTGAA TACCAGCTTT TGCAGCTGA      300
ACGAAATGT AAATCAACCA AAAGCCCCAC TGAGTTGTTA GTTTTAATGC ATCAAAGCA      360
TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTACGT AGGCAAGGAG ATTCATCTTG      420
CCCCATATC CGATATAGTT GGTACAAAAG GCAAAGAGGA AGCGATGAT GAAATGATG      480
ATGGCCGCCA ATTTTACCTG TTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT      540
TCCCCTTCT TTATAGCAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC      600
GCCTTATTC CAAGGATATA ATCAATAGCA CCGGACAAA TGGTATTAAC AATACCAAAG      660
TAATTTCCCA ATTTGCTTAA TTTCCCGTG AAACGAGTGG ACAACATGA AATCCCAACG      720
TTGGTTACGG AAATCAATCC AAAGGTACA AGAGCTGTCC ATGATCCCA GTCTACAAAT      780
TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCAACGAC CAAAGCAACC      840
CCGAGAGGTT CAACTATTT AGATGTAGCA AAAATTTTGA GTGATTTTTT CATAGGTAA      900
ACTACCTTTC TTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAAATAA AATGATAGAA      960
ATAAAACCCT GAAAATAAAG GTTCTATAAT ATTTGTAGTG GGTAAATCCA CTATAGATAT     1020
TATGGAGCCT ATTTTATTGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA     1080
AACAACTCAT TAGAAAGAT
                                                                                   1099

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(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

CTGGGATTCA	CGTGAAAAGG	AAGCCCAGAG	AGTAGCCAGG	TGTACTGCTA	GAACAGTGAG	60
TGAAATTGAA	TATTACCATA	GAGAGTCAAC	CCAGATAGCT	CAGGCTTTAG	TTGAAAATCA	120
AGCTCGTATC	GAGGGAATCT	ATAAATACTT	TAGCCTTAGC	ATGCCAGACT	ATTTTACTG	180
GCAATTAGAG	CGGAAAGCTT	CGCCTTATAT	ATCAGTCTCT	CTGTATGAAA	ATGTTGATGA	240
CCTCTATGTT	CGAAATGATT	TTGTAAC TGG	GGTGGCCATT	GCTTTTCAAG	ATTACAAGGA	300
AGTCTATGTT	TCTACTAAAG	ACAAACGTAG	GkKAGAAAAA	ATCAGGGCTG	AGGATTTCAA	360
ACCAGCAGGA	AATAGTTTGG	CCATTCCAGT	GTCAGATCCA	GTGTCAGATC	AAGACTTAGG	420
AGTGATTTAC	ATCTCCTTGG	ATCCTGCTGT	TTTATACCAT	GCCATTGATA	ATACTAGAGG	480
TCATACTCCG	ATGGCAGTAA	CAGTGACCTC	ACCTTTTGAT	ACGGAGATTT	TTCATATGGG	540
TGAGACAGTT	GATAAGGAGA	GTGAAAATTG	GCTAGTTGGC	TTAACTTCTC	ATGGATATCA	600
GGTTCAGGTG	GCAGTTCTTA	AAAAC TTTGT	TTTACAAGGA	ACAGTGACTA	GCTCTGCTTT	660
GATTGTGGGT	TFGAGCCTTC	TCTTTATGT	CATTCTTTAT	CTGACTTTGA	GGCAGACTTT	720
TGCTAATTAC	CAAAAGCAGG	TAGTGGATTT	AGTAGAATCC	ATTCAAGTCA	TTGCTCAAGG	780
CGAAGAGGGG	CGTCGGATTG	ACATTTCCGA	GAAAGATCAG	GAATTACTCC	TAATCGCGGA	840
GACGACCAAT	GATATGTTGG	ATCGATTGGA	AAAGAATATC	CATGATATTT	ACCAGTTAGA	900
GCTTAGTCAA	AAAGATGCCA	ATATGCGAGC	CTTGCAGGCG	CAAATCAATC	CTCATTTTAT	960
GTATAATACG	CTGGAGTTCT	TGCGCATGTA	TGCAGTTATG	CAGAGTCAAG	ATGAGTTGGC	1020
AGATATCATT	TATGAATTCA	GTAGTCTCTT	GCGTAACAAT	ATTTCCGACG	AAAGAGAGAC	1080
CCTCCTCAAA	CAGGAATTAG	AATTTTGCCG	TAAATACAGC	TATCTCTGCA	TGGTTCGCTA	1140
TCCCAAGTCC	ATTGCCTATG	GTTTCAAGAT	AGATCCAGAG	TTAGAGAATA	TGAAGATTCC	1200
CAAGTTTACC	TTGCAACCGC	TGGTAGAAAA	CTATTTGCGG	CATGGTGTG	ACCACAGGCG	1260
GACAGATAAT	GTGATTAGCA	TCAAGGCTCT	TAAACAGGAT	GGTTTTGTGG	AAATTTTGGT	1320
GGTCGATAAT	GGTAGAGGAA	TGTCGGCTGA	AAAGTTGGCA	AATATCCGAG	AAAAATTAAG	1380
TCAGAGATAT	TTTGAACACC	AAGCCAGCTA	CAGTGATCAA	AGGCAGTCTA	TCGGGATTGT	1440
CAATGTACAC	GAGCGTTTTG	TGCTCTATTT	TGGAGACCGC	TATGCCATTA	CTATAGAGTC	1500
TGCAGAGCAA	GCCGGTGTTC	AGTATCGTAT	TACAAITCAA	GATGAGTAGA	AAGGGAGAAA	1560
ATGTATAAAG	TATTATTAGT	AGATGATGAG	TACATGGTGA	CAGAAGGTCT	GAAGCGTTTG	1620
ATTCCCTTTG	ATAAGTGGGA	TATGGAGGTC	GTCGCAACAG	CCAGTCATGC	CGATGAAGCT	1680
CTAGAATATG	TTCAGGAAAA	TCCTGTCGAT	GTCATCATTT	CCGATGTCAA	TATGCCAGAC	1740

1304

AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC 1800
 CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG 1860
 GACTATTTGG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA 1920
 GGTCACTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT 1980
 GGATTTGTTA GTTATTTAGG GGATAAGGAG AATTGGTGGG TAGGTCTATC CAAGGAAAAA 2040
 CAAGGTTCCCT TCACCATTC CTAATATGTC TTGGGTCAAG ACTGGCAGAT TTCATTCT 2100
 GGCCACCCCT TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT 2160
 GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG 2220
 TCTGAGAGTC TCTTTGCCTA TTACGAACCG ATTTATAGGG TTATCATTCA GGGAAATCTC 2280
 AATCAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT 2340
 GTTTCGATTA CTAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTTCCA TTTATTTGAA 2400
 CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC 2460
 GATGAATTGG TTTCTTATAT CAAGGAAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG 2520
 AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC 2580
 CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG 2640
 CGTGAAACCG ATTCGACCTT TGCAGAGTTA CTAACAAAAC AACGTATTAA GGCTGCCCAG 2700
 CAGCTCTTGC TTTCAACTAG TGA 2723

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 836 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGCAGTTTT TTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT 60
 TGCAAACTTT TTAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA 120
 CCTTGCTTAA CAACCTGTTC FCCGGCGATA TAAACATCAT CTACATCACT AGATTTAACT 180
 GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTTGTTGGT 240
 TGAATGACCA GAAAATCTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT 300
 CCAAGGACCT TAGCCCCTTC GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAACCTGG 360
 CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAAACATA 420

1305

TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTGGAGC AATTCCTGAT GCCAGTTTGA GGTTACTGAT AGGATTGTGG	540
GCGATAGCnA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG	600
TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT	660
TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTGG TCTCCGCCAC ATGGACATGG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTC AACTCGCTT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTTG GATTTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTATTTT ACTTTT TAGG TGGTCTGGGG CTATTCCTTAT ATAGCnTCAA GACCATGGGA	60
GACGGTTTAC AACAAAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT	120
AATCCTTTGT TFGGAGTTCT GGTTGGTATT GGGATGACTG CTCTAATCA GTCTAGTTCT	180
GGTGTAACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTTAACCTT ACGTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTTG GTGTCGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTCGGTAC TGGCTTGACC	540
TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT	600
CTAATGATC TACAGGGAGC TTTGCCAGTT CTATTTGGTG ACAATATCGG GACAACCATT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTTGCCTTCA ACGTTATCGG AACAGTTGTC TGCCTATTTT TTCTAGTTCC TTTTACTGTC	780
CTGATTCATT GGTTGAAGC TACGCTAAAT CTAGCACCGG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTC CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTTG TCAAATACGA ACCCTTATAT	960

1306

CTTGATGAAC ATTTCATCAA ACAGGCCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG	1020
CTCTTGCACT TAGGAAACTA CGCTGCTAAA GCCTTTGACC TTTCTTATAA GTACATCATT	1080
GACTTGGATG AAAAAAGTGC TGAAAAAGGG CATAAAACCG AAGAAGCAAT TAACACCATC	1140
GATGAGCAAT TAACACGTTA TCTCATTGCC CTTTCAAGCG AAGCTCTCAG CCAAAAAGAA	1200
AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCCTGATT TGGAACGGAT TGGAGACCAC	1260
ACGGAGGCTC TACTCAATCT GACTGACTAT CTTC AACGGA AAAATGTTGA ATTTTCTGAT	1320
GCCGCCTTGA AAGAATTAGA GGAAGTTTAC CGCCAAACTA GTGACTTTAT CAAAGATGCT	1380
CTGGATAGTG TGGAAAACAA TGATATTGAA AAAGCACGCA GTCTTGTAGA ACGTCATGAA	1440
GCAATCAATA AGATAGAACG TGTTCCTCAGA AAAACCCACA TCAAACGCCT CAACAAAGGC	1500
GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTGTA	1560
TCAGACCACG CTATGAACCT TGCTGAAAAG GTTTTTGCAG AACAAATCTA AGAACCAAGA	1620
AGCTATCCAT CATAATTGGA TGGCTTTTTA CTTTTTCCTA AGCAAGACTA GGATGAATGA	1680
AACTGAAAGA GTATTCTGCA GATATATAGT CCCCAATTAT TCACCCCAA TCTAAAAACC	1740
ATCCAGAATC CTTGCCTTAG CTTAGATCCT GGATGGTTTC TTTTTTCACC CAATGGGTGT	1800
TTTTTACTAG ACAAAAAAGA GTTCCCTT TATGGTATAA GTGTAGAAA AAACACAAAA	1860
AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTTAC	1920
CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA	1980
CTTTTTTCCC AGTTGAAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA	2040
CGCCGCTACT GTCGTTATTC GGATTCAGAT ATCCTTGTC AGTTCCTCTT TCAACTGTTA	2100
ACAGGTTATG GAACGGACTA TGCTTGTAAG GAATTGTCAG CTGATGCCTA CTTTCCAAAA	2160
TTGTTGGAAG GAGGGCAGCT TGCTTCACAG CCAACCTTAT CCCGTTTTCT TTCCAGAACT	2220
GACGAGGAAA CAGTCCATAG TTTGCGATGC CTC AACCTTG AATgGkCGAA TTCTTTTTAc	2280
AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTC TACCCATTTC ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACT GTTGTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCTATTAG	60
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1307

TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA	120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT	180
GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA	240
AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA	300
GAAGCTGTAG CACTTGCAAA AGAACTAAC TTTGCAAAAT TTGATGCAAC TGTAGAAGTT	360
GCTTACAAC TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA	420
TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGT TTTCGCACGTGG TGCAAAAGCT	480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC	540
AACGACGGTT GGTGGACTT CGACGTAGCT ATCGCTACAC CTGATATGAT GGCTCTTGT	600
GGACGTCTTG GACGTGTCTT TGGACCACGT AACTTGATGC CAAACCCTAA AACTGGTACT	660
GTAACAATGG ATGTTGGCAA AGCGGTTGAA GAGTCTAAAG GTGGTAAAAAT CACTTACCGT	720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT	752

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GTCAACATG ATTCAAGGC TGTTGCTTT CTATCTCCC TTTTCATAA TGTATAATA	60
AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAA TCGATTTCTA ACAATGTTTT	120
AGAAGTAGAG GTGTAATAT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC	180
CATTTGAACG ATTTCAAATC CTTCTTTTTG GTAAAGATTC TGAGCTCTTT GATTTGCCTC	240
GAAGACATTT AGAGAAATAC TGCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT	300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTTCTGG GGGTTGATAA AAAATCTCCC	360
GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCCACAA ACTCTTGTTT	420
ATCAAAGATT GAAAAGACTC CTTCCAAGGC TTGAAGTGTC AGTAGAAAAG GAATCCTTGG	480
TCCCATCCAT TGTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG	540
AGCGTTTTCT GTGCTCACCT TTTCTTCAA ACGAATTGTC ATCTTTTCTT CACCACCTTA	600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTCTTACG AATAGATAAG TATGATTGAT	660

1308

TTTTATTTT	TTCTCGTCGG	GAGCATTCTA	GCTTCCTTTC	TTGGTTTGGT	CATFGACCGT	720
TTTCCAGAGC	AATCCATTAT	CAGTTCAGCC	AGTCACTGCG	ATTCCTGTCA	GACTCCCTTG	780
CGTCCCTTAG	ATTTGATTCC	GATTCTCTCA	CAGGTCTTCA	ATCGCTTTCG	CTGTGCGTAC	840
TGCAAAGTTC	GCTATCCTGT	CTGGTATGCC	CTCTTTGAAT	TAAGCTTAGG	ACTCCTCTTT	900
CTGCTTTACT	CTTGGGGATG	GCTCTCCTTG	GGGCAAGTCG	TCCTAATCAC	CGTGGTTTG	960
ACCTTGGGTA	TCTACGACTT	TCACCATCAG	GAATATCCCT	TACTGGTCTG	GATGACTTTC	1020
CAGCTAATCC	TAATAGCTTC	CTCTGGCTGG	AATCTGGTCA	TGGTCTCCTT	CCTCATACTT	1080
GGAATTTTGG	CTCATTTTAT	CGATATCCGC	ATGGGTGCAG	GGGATTTCCCT	CTTTTATAGCT	1140
TCTTGTGCTC	TCGTCTTTAG	CGTAACGGAG	TFACTGATCT	TGATTCACTT	CGCTTCTGCG	1200
ACGGGTATCC	TGGCCTTTCT	CCTGCAAAAAG	AAAAAGGAAA	GACTTCCTTT	CGTGCCTTTC	1260
CTCTTACTTG	CTACTTGTTC	GATTATTTTT	GGTAAGCTAC	TGCTTGTCTG	ATAAAATCCA	1320
ATTTCTGCCA	TATATCCTTC	ATGAAATTAT	TTCACAGTTA	AATTATAAAT	TATTTCTTTT	1380
GTACAAAGGG	ATGATGTTAT	CAAATCGATC	TGTTCTTCTA	TCTTCTTGAT	ACTGATCAAA	1440
AAATTTCAAT	TCGACTGAAA	ATATTTGCTT	TATAAACTGT	AAACGAATAC	TTTGTTTAGA	1500
CATTATAGTC	GCTAGACTGA	CTAGATGATT	ACTCAAAACG	ACGTCCAGAA	TACTCTTTAC	1560
TTTGCTTGGT	TTTTTAACAA	AAATTTGATC	ATCCAAGGGT	TCAATCATTT	TGTAACCTTT	1620
TTGCGCAATT	TGACGATAAA	AGTAAGAATG	TTGCTTTGGA	GTCAATAATC	CTAACTTAAA	1680
AGCTCGATAC	TCTAAAGCCT	GTATCGAAAC	ATTCAAATCC	GACTTCAATA	AAATATAACT	1740
ATCAGGATTG	CTGACACGCT	TGCCAACCCCT	CTCTTCAAAT	TTGACTAAAA	ACTCTTCTTT	1800
TGGCAATAAA	AAACATGATG	CAAATAAATT	TGCTTCTTGC	TCCAAACGAT	CGCCATCTTC	1860
ATTCATATCT	TTATATTTAT	GTAAAAGAAT	ATGTCCTAGC	TCATGAGCTA	AGTCAAAATT	1920
TCGACGTACA	GATGATTTAT	TCGTTCCCTAA	CACAATATAA	GGTCTTCCCA	ATTTTGACCA	1980
TGCGCTATAA	GCATCAGCTT	GGCCATTAAT	TAATCGTTCC	ACGATATAGA	TGCCTGAACG	2040
TTCTAATTTA	TAAAGCAAAT	CATGATTATC	TTTTGAAATA	CCTAATTTTT	CCCTGGCATA	2100
AAGAGCCAAT	TCCTCAATGG	ATTCTCCCTT	ATGATAAGAT	TCACTCACTA	CATTACTTAG	2160
GTCATGAATT	ATAATATTAG	GTATAATTAC	AAAAC'TTCA	AAATAATCAA	TCAAAC'TATC	2220
TACCTTATGT	AAATACATAG	TTTGAATATC	TATTGTTTTC	CGTGTGCTA	GGTCTGCATT	2280
TCTAAAGGCA	ATTACAGAAG	AATCAAATCG	AATGCTCTCT	TCTTCTGTT	CAAAAATAAGT	2340
TAAATCAACA	TGAAATTGGT	TGGCCAAATG	CATTTTGGTT	GATAATTTAG	GTTTCGTTTC	2400
GTTGGACTCA	AACTGCCAAA	TGGCTTGTTT	CGTTAAATTA	ATTCTCTGAG	CTAATCTGTC	2460

1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAA ACATTTACAT 2520
 ACTCCTTACT ACTTTTGACC TTCTTGTTTT TCTATTCTTG GAATAATTC AAAATCTTCT 2580
 GTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC 2640
 GGG 2643

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAGTGG CAAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG 60
 GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG 120
 TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAAACTGG CAAGCTGGAG AGTCAGAGTA 180
 TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAaAGGAG TTGCTCAAAC 240
 CTCTTTAGAG GGCTTGATTG AAGGTTTTGA TTATCTTGAT TTTCGCTCAG ATACGCATGC 300
 TGAAAACAAG GTTATGCAAC ATATTTTTGA AAAACTTGGT TTAAACAAG TCGTAAGAT 360
 GCCAGTAGAT GCGAACGCT TGGCCTATCA AAAATTAAG AAATAATGCA AAAGAAGTAT 420
 GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT 480
 TTGTATGGAA TTTGGGTTC AAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG 540
 ATAGAAGAAG TTGTWAGTCA TCCTATTTTA GACCCAGTTA TT 582

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AACTTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTTTA 60
 ATTCATGAT GAATTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT 120
 CCCTAGTAT AACAAGTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA 180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCCAAAG CCCCTGATA GTCAAAGCCG GTCACCTTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTCTT TTGATAAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGGTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTGTTGTTG GCTAAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC	120
CTTTAAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATTCT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGTA TCAGCTGAGA AAGCGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAAC TGCT CAACACTATC CAGCCTTGAA ACTTTTTGAT GGGCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGCGGAACA AGATTATCTT GAAAATCATG	360
TTTTCAATAC CTCGGCTTTG TACGGTGTG TTCCAGTCTT GTCACCCATG GCTCCTCACC	420
GTTTGGATTT TTTGATGAAA TTAAGTCTG CTGGTAAGAC TTTGAAGAGC CATTGGAAGG	480
CAGCCTATGA TGAACCTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAA TTCATGGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCGC GGGCCTTTC	660
TAACAGCTTT AATAGAAAAT CAAGTACAAA CTGTGGGGGg AGCACGTCGC TTGAACTTTG	720
CTGGATTTGT TTACCAGAGAA GATTTGTCAC AACCCAGGG GGATGG	766

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 901 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CCGGCCACGG TTCCATCCAA CTTCACAGGT GTGCACCTGA TTGTGTATGT AATTGTCACT	60
AACGGTAGAA TTTCACCTAT CCCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG	120
AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTTGCAAA	180
TAGATTTTAA AATTTTGGC TAATTGTCTG AATCAGGGTC GGAAGTTGA CGACCTTGTC	240
ATTGCCAGT TTTTCGCGTG CAATTTGAG AATGGCACCT GAGTCTTTG AAGCAAAGAG	300
GAATTTCCCT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCCTC CAGTGACATT	360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTTGA CATTGACATC	420
TGGGTAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTC CCAACTTCC CAGCGATAGA	480
GAGGTAGGAA GTGCCTGTCG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT	540
TAGTCTTCCCT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTAATATGC TGCTTTCTCT	600
TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG	660
ATGTTGATTT TGTTTTCAGA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC	720
TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTCGATTTT TGCATGATCT	780
ACTTTAGCCT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG	840
CGAGAACGGA GAATGATAGA AAGAWCGTCG ATACCTGTTG GCATATGTTT CCAACCGATG	900
T	901

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG	60
CTGCATTCGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATCTTTC	120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG	180
TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC TTACCTGGTT AGCTAATAAC	240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTCCA ACTCTTCCCC	300

1312

ATTTCTGGGA GTTGGGGTAA AAATGTTTAC TGGACGTTCC AACTCTTCCC CATTTCTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCCATTCGT CTTCTGAGTC TTCTGGGATT GGTTCGAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTCA ACTTGTCCGT CTTCTGCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTTACCA AATTCTTCTT TTCCATCAAT	600
TGTCAAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC	660
ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAATAATT	720
TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTTCTTGCG	780
CTTATGCGA CTGATATCTG CTTGTTC AAT CAACATGCGC TCAGCAGCCA CTGTTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTTATGT TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CCTTGTAAGT ATCAACCAAT TCCTTAACGC GGTCAAACC AAATTGGCCT	1020
TGTTCTTCAT TTATCTGGAT GATTTC AAGC CCTTGAGCTG TAAAACCAAG CGGATCGCTA	1080
ATCGCCACCC CTACCGTTTT TGAACCGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA	1140
TCGACTCCTT GTCCTTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTT ATCACGCTCA	1200
TACTTACGGA TTTGATTTTC TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATACGTAAC CTACGATTTG GTTAATTGGG TTGTAaCCCT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTTCTTTT TTATTGGAAT CGTCCAATTT AAAACGFACT	1380
GTTTCTTCAG TAAATCCCAT TCTAACACCC TCTTTCCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTTCTGTGC	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA	1560
AACCAATATT CTTCAGATGT TCCAACGGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAACTAGT CGTTGTTTGA AGTTCCGTTG CGCTCAATAG TTTTGTTC AAGTTTGAAC	1680
CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTTG	1765

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT	60
TGCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGGT	120
ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCCTATC TGAAAAATGG TATCGAGTCT GGACGATTTT CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGACTTTCAC TGACGCAAGG ACACCATTCA ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTCC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAAATA CCTCTTCAAC	480
TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTCACAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTTCTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTCAAAT ATCCTTTTCT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT	720
GAACGAGGCA TTGATGGGAT TGACTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG	840
CAAGACAAAC GATCTATCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCGTGTCA TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA	1020
GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTGTTT	1140
GAAAAAATC GTTTGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AACACCTTG TCCCCTCCT CATTATCCC TACACGATGG yTTATTGCTA	1260
GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC	1320
TTTGAAGAGG CCTATTTAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC	60
ATATTTAGAA AACTCCCCCA AAGAATTAAT TTTAAGAAAG ATTTTCTAG AATTTGGCC	120
CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG	180
TGGATTGACA AGAATGGAAA TATTTTTTCC TCTCTAGTAT TTTATTAGA AGATTTAATC	240
TATCCTTGGG TTGTAAACC TTTGGTTTTA GAGATAAATT CATTCGCTGA AAAAGGTTTA	300
CTTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTAA TAACAAATAT CCCGTTTTAC TGAGGCAAAT ATCGGAGTCT	420
TGTCTTCGGT TCTATACTTA TTTTATAGAA ATTTATCAA ATTTAGAAAA TGATTTAGT	480
GTGCTAGAAG AAGAATTAGG GCTAAGGGGG AAATPAAATG ATATAAAATT TGGAAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTTG ATACTCTTCT TTGATGACGC GAAAATTGTT	600
TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA	660
AAGGTTGATG AAAAAATTAG GATAAGAATA CCTCGAACTA TTGCTTATTC GGATCACAGC	720
TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAGA AAAATTTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTTAA TTTCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTTTATCA	60
GCAGATTATT GGTTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTT TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATCAAGC ACAAGAGGGT GGAGAAGTAA GGAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA	240
GCACCTGACG GATTTACAGA TTCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC	300
CCTTFACTTA GAGGACTTGG AGGGAATGG CATTGAACCT TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTTGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT	480

1315

GGGGCATATT CATCTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAACGGT 540
 GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA 600
 CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT 660
 CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT 720
 TGCCCAACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATTGGA 780
 AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA 840
 TGAAGGTAGA GCATCAATTG TA 862

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC 60
 GCGCTACCTC AATCATAGAT AGTTCACCTT TTTCTTGCCC AGCAAATACT TCTAATCCA 120
 AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA 180
 TCATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG 240
 TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCTT TTTCTGTTGC TCCATTTTCC 300
 ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG 360
 ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCOA TCAAAGCACT TAGAATCTTT 420
 TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA 480
 GATAGTGTA TATCCCAAT TGGAAACCAT TCTCCCTTCT CCTTGACTTC AATCCAAAAA 540
 AGCTCACCAT GCCGATyCar ATAGGAATAC ATGGCTTCCA AGGTCGcTtG ACTGTAAGGA 600
 AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC 650

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACTTC CATTCTCATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC	180
GCTCCACATC AAAATTTCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACTTTG	240
TAAAATTTTC TFGCAAATTA GTTAGATFGA TTTGGGAAAT GGACTCCTCA CTTCCTCACTA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTGCTGAAT AATATCCTGC TCTGTCAGAA	420
TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAACTACT AGAATCTTCT CTCTCAAATA	600
ATTTATGTTT AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAAT GTACAGTGAC ACTCCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCCAAAAGA GCAACTGTCA ATCCGTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTTCTT CAAAAACAAC CTTTGTCTATT CTATTCCTTC	840
CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC	900
AATTTGTCA AGCTTTGCAA TCCAACTTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTTGATA GCACGTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AAAGTCTGTA AAAAAACCTT TTTTAAATC	1080
AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTCGC GGGGACATGA CGAATTCCCC GTTCATCACG AAGGCCGCCG AGGAGTGGGG	60
GGTGCCGTCC AAGTCAAAAG CGGCCCCACA TCGATTCACT TCCCCGACGA ACAGCCCTTT	120
CCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA	180
GGCAGACGGA CTCCAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCG	240

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCTCCTC 300
 AAAAGTGGC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA 360
 GGGTCGCAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCATTT 420
 CACAGTCCCG CTCAACGCTA GCCCAGATCCC TTTTGGCAT GGTGACTCAA GCGTCCTTTC 480
 AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC 540

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1949 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTCG ACCAATTCAA GGTGAGGCA TCGCAAATA TGGACTGTTC CCCCCTCAGT 60
 TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT 120
 TGAAAAGTAG GCATCAGCTG ACAATTCCTT ACAAGCATAG TCCGTTCCAT AACCTGTTAA 180
 CAGTTGAAAG AGGAACTGGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG 240
 GTCATTCGTT ACTAAATACT TAGAAATCCG CTCCTTTTGT TCAACTGGG AAAAAAGTTC 300
 CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA 360
 AAAAGACTTG TTTTGGAAAGT GATGATTTGG TAACTGTTC ATGTGAGTTT CCTTCTTTTT 420
 TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAACTCT TTTTGTCTA GTAAAAACA 480
 CCCATTGGGT GAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT 540
 TTTTAGATTT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG 600
 ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC 660
 ACAAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCGAAA GTTTATTTAA AAAAAATCC 720
 TGCCAAAGAA TTTTGGCAG GAAACCAAT CAATTTATCA GTTCTATCA ATCGCTTATC 780
 GCTCTCAAAG ACTGGTAAAT AGGGATTCCG CAATCAAAT GCGATACTCT ATTATTTAAG 840
 AGTAACTGAA GCTCCAGCTT CTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC 900
 AACGCCTTCT TTAACAAGTG CTGGTGCACC GTCAACAAGT TCTTTAGCTT CTTAAGACC 960
 AAGACCAGTG ATTTACGTA CAACTTTGAT AACGCCAAT TTTTGTGCG CTGCAGATGT 1020
 CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC 1080

1318

AGCTACAGGA GCAGCTGCAG TTACACCAA	TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTT	AGCAATAATG TTTTCAATGT TCAATGCCAT	1200
TGTTATTTCC TCCAAATAAG TTTTAAATTT	TATAATAGTT TTTTTCGTAG CTAGksTACG	1260
CTGTGTAGCT TAAGATTAAG CCGCGTCTT	TTTGTCTTCT GCAACCGCTT TGA CTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTTGAAGTAC	AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG	1380
GTTTGGAAGA GTTGCAAGTG CAAGAATCTC	TTCTTTAGAT GCGACAGCGC CTTCGATTGC	1440
ACCACCTTTA ATTTCAAGTG CTTCAGCGTT	TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCTTCATTAG AAAATGCTAC	TGCAGATGGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTT CAGCTGCACG	ACGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTTCCACGAA GCTCACGACG	AAGAACTGTA TCTTGCTCAA CTGTCAAACC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC	AGCTTTCATT TTTTCAGCTA tACGTCAACT	1740
AGTTCGCTT TTTTAGCAAT AATTGCTTCA	CTCATTAGTG TGTTCACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTTTCAA AAAGAAAAC	GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTTGTCCT	CGGTAGGATA TTTATGAGTC GAGCTCCCCT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG		1949

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1023 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGCTGCTT	GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAGCTTGT GTCAATTCAT	TTTTTGAAAC ATAGCGGTTA CGTGGGTGAA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT	ACTTGTCTTC ATTTTCTTCT GATGTCAAGA	180
TACGACGGTT ACAGAATGGA TTTCCACAGT	TGACATAACG TTCACATGGT GTTCCATCAA	240
ACCAGTCTTT CCCTACGATA GTTGGGTTGA	CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTPCCCA TCCCAAAGCT	CACCTTGAAC TTCTGGGTCT TTACCGTAAG	360
TTGCGATTCC TCCGTGCAAT TGGCCGACAT	CTTTGTAGCC TTCACGGACC ATCCAGCCTG	420
AGAATTTCTC ACAGCGAACG CCACCTGTAC	AGTAAACCAC GACACGCTTG TCCATGAATT	480
TTTCCTTGTT ATCACGGACC CATTGTGGTA	ACTCACGGAA GTTGCGAATA TCTGGGCGAA	540

1319

TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG 600
 TATCTTTTATC AAGAAGCGCT TCTTTGAACT CTTTGGGAGA CAAGTAAGCA CCTGTTGTTT 660
 CAAGTGGGTT GATGTCATG TCAAAGTCGT TGTCTCCAA ACCAAGGTGG ACAATTTCTT 720
 TCTTG TAGCG AACAAACATC TTCTTGAAGG CTTGTTTCAAT TTCTTCGTCA ATCTTGAACC 780
 AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAGTCCAT GTATTTTGA GTTGTTCAT 840
 AGTCACCTGA AACTGTTCCG TTAATCCCT CGTCAGCGAC TAGGATACGG CCTTAAAGGn 900
 CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATG CTCTGCATTT TCAATTGGAG 960
 TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTgkCaw AAGATTTGTA TCTCTTATC 1020
 TAT 1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTTAAAT AGTTTAAAGC 60
 ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTAT CGAGAATATG 120
 GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA 180
 TTTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAATCGC TCCAATGACT TACGAAGAGA 240
 CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATTT TCTCTTACCA ACATTAACA 300
 CACCATCGGT TATTATTATG GATAATGTAA GATTCATAG AATGGGGAAG CTAGAACTTT 360
 TATGCGAAGA GTTTGGGCAT AAACTTTAC CTCTCCTCC CTACTCGCCT GAGTACAATC 420
 CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA 480
 ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGCGAG 540
 ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAAGATC TAGAAAGGAC 600
 AAATTCGTC CTTTCTTTT TGAAGTTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT 660
 GATAAGTTG ATGAGATTAT TGGTGGCTTC CAGTTGGCG TTGGAATAAG GTAATTGAAG 720
 GCGCTTGACG ATTTTCTCTT TATCTTTGAG GAAGGTTTA AACAAAGTCT GAAACAGAGG 780
 TGAAAAAGCA AGAGCTGATA GAGATTATAG TGGTGTAA AGTCTTCGGA ATAGCTCAAA 840

1320

AGTTTATCTA GAATTTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAAATCGT 900
 TTATCACTCA GTTCTGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG 960
 TATTCATGGG ATTTCCGATG ATGGCTTGTG TTCTGCTCTC AAGAACAGTT ATGATATTGA 1020
 GTTTATCAAA GTCCTGAGCA ATAAAGCTCA TCTCCATCTC CCGATGAAA CAGTCACTCC 1080
 CCGGACTGTT TCAACsTCCF AGGACATAAT CTCAGGAAGA CGCGAAAAAT CATGCTCAAA 1140
 GTGAAAATCA TTGTTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACF GATGATCAAT 1200
 GTCGGTCATA GAAGTCTTTT TAATTAGCTT CTGAGCAATC TTTTGGTTGA TGATACAAGG 1260
 AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTTTG AGCAATGATA 1320
 GCACTTAAAA CGGCCTTTTC TAAGAAGAAT TCTAGTTTGA ATTTTATTAT ACTAGAAAAF 1380
 CAGAACCATA ATACCTATAT AAAAATATTA TAGTCTAAT AGGATTTACC CAAAAGTTTT 1440
 AAGGCGGTCT TTTTAGAAGT TTAATTGTTT GAAATTTAGG TAGCAAATTT GTTCTATTT 1500
 TGCAACTTT TCCTATTTTT ATCTTGTTGA GGCTGGTATT TTAACAATTC AGGAATTGAT 1560
 AGTGAATGTG TAAAAATTTT TGTTAGAATA AGTTTATAAA AAAGAAAAGG AGTATTTGAT 1620
 TATGTTACAA AAAATTTATG AGCAGATGGC TAATTTCTAT GATAGTATTG AAGAAGAGTA 1680
 TGGTCTACA TTTGGTGATA ATTTGACTG GGAACATGTT CATTTTAAAT TTTTAATTTA 1740
 TTATTTAGTG AGATATGGCA TTGGTTGTCG TAAGGATTTT ATTGTTTACC ATTATCGTGT 1800
 TGCTTATCGT TTGTATCTTG AAAAATTGGT AATGAATCGG GGTTTTATTT CTTGTTGAGG 1860
 TAATTTTAGT AAATTTCCGA ACTAATTTAC TCTTTTATGG AAAGATGATA GTAAATAGCT 1920
 AGTAATTTTT CTAAATCATT TTTAATAGT TGGAAATAGC AAATCTTTCT ATTGTTTCTT 1980
 CTTGATAAAA AGGCGATTTT TTATTATAAT AAATTGTAAG ATATAATTGC AGGTGAGAGT 2040
 CCTGCCATGT ATGTGAGAAA GGAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT 2100
 GTTGTGTAG GTACCCAATG GGGTGATGAA GGTAAAGGGA AGATTACAGA CTTCTTTTCA 2160
 GCGAATGCAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGGTCA CACGATTGTG 2220
 ATTGACGGTA AGAAATTTAA GTTGCCTTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA 2280
 ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCCTAAAT CTCTGTAAA AGAGTTGAGC 2340
 TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCGTA TTTCTGATCG TGCGCATGTT 2400
 ATTTTGCCCTT ATCATATCGA GTTGGATCGC TTGCAAGAAG AAGCTAAGGG CGACAATAAG 2460
 ATTTGGTACGA CAATTAAGGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTGGGA 2520
 ATTCGTATTG CAGATCTTTT AGATAAAGAT ATTTTCCGTG AGCGTTTAGA ACCTAACCTT 2580
 GCTGAAAAGA ATCGTCTTTT TGAAAAATTG TATGACAGTA AAGCGATTGT TTTGATGAT 2640

1321

ATTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT 2700
 GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTGAAGG TGCACAAGGT 2760
 GTTATGCTAG ATATCGACCA AGGTACTTAT CCATTTGTTA CGTCATCAAA CCCTGTAGCT 2820
 GGTGGTGTGA CAATTGGTTC TGGTGTCCGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA 2880
 TGTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCCTTTCC CAACTGAGTT GTTTGATGAA 2940
 GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACTGG TCGTCCACGT 3000
 CGTGTAGGTT GGTTCGACTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT 3060
 AACCTTCTT TGAACCTCTAT TGATGTTTTG AGCGGTTTGG ATACTGTGAA AATCTGTGTG 3120
 GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA 3180
 CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTGGTCAG AAGATATTAC CGGAGTCCGC 3240
 AATTGGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTT GTCGTGTGAG TGAATTGGTT 3300
 GCGGTTGTA TTTCTACTTT CTCAGTAGGT CCTGGTCGTG AACAAACAAA TATTTTAGAA 3360
 AGTGTGTTGGT CCTAAGAGAT TTTTAAGATT TGTTAAGAT AGGTCGGGTA TACTATAGAC 3420
 GGTACAAGA AGACCTCCTA ACTTGTGTA ACAAATATCC TAACTTTTC TTTTCATAA 3480
 TAATCTCCCT ATAGAGTCAC CGCATTCGGT GGCTTTTTTT GTGTGGGAT TCATGATATA 3540
 ATAATAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG 3600
 AAGTCTTTAT GAGGGAGGCT TTGAGAGAGG CTGAGATTGC TCTTGAACAC GATGAAATTC 3660
 CAATTGGTTG TGTGATTGTC AAAGATGGG AAATCATTGG TCGTGGGCAT AATGCGCGTG 3720
 AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT GCGAACTTGA 3780
 GTGAGGAGAG TGCCTTGCT GGATGCACA CTTTTGTGA CCATTGAACC G 3831

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CCGCTGTTCC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCG 60
 TGAAAAGGCG GATGACTTAA CCCCTTGACC AACGGACCTG AGTTGTTAT TTCAACTCTT 120
 ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTGT TTTATTTTTT 180

1322

CAACTTATAG TAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAAACTTAGA	240
AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCACAAGCA CCGCAAGGCA TGGCTGAACT TCCACCATAA GGTGGTTTGT CTCGAAAGGC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATGGTAC ATATTGAAGA GGGCCGCCCG	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT	660
ATCCTCTTFA TTTAGAGATT TCTTTTAGCA TGTTTTCGAT ATGTGAAATP GATTTTTCAC	720
GTCCAAGCAA GAAAATTGTA TCTGGTAATT CTGGCCCATG CATTTCCGCT GAAACTGCCA	780
TACGAATAGG CATGAAAAGA TTTTCCCTT TAATACCTGT TTCTTTTGG ACTGCTTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAAT CATCATCTGT CATCGCTTCA AGTTTGTCTT	900
TGAATGCTTC AAGAACTGT GAACTGTTT CACCCGTCAT GACTTCGCGC TCTGCTTCTG	960
TCAATTCTGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAA CCGCCTGCTT	1080
CCTCTAAGAA TGGTTTTGCC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT	1140
CATTGCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGACTTG CTGAGGCGGT	1200
TTTCATCAA AAGTTTAAATG AATCTTTCAC GAGAGAAAAT CTCATCCCA CCACCTGGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCGGT	1320
AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGGTA	1440
T	1441

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA	120

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCG	180
ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCATT TCGTTTCTC AAGGCCAGTC ATCAAATTGA CCAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATATT GCGGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG	360
AATCTAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGA TGAAATTGAA AAACAATTAG	480
AAAATATCCA ATCTGAATTT TCACAATTTG TAACCTTGA TTCATCGGGT GACCCGTGG	540
AAGCCGAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATTGTGG	600
ATCGTGTCC AGCCTTGGTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTGAA ACGGATATTG	720
AAGCGGTTTT CCACTTGCTT TATGAAGCAT TCAAGAAAA CCAAGAGAAT ATTCGTGAGT	780
TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAAATCTA CTTGCAACTC	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCCTGAGA CAGCTGCAAG CCATGTTCGT CGTATTCAGA	1020
CAGAATTAGA GAGTTTGGAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA	1080
CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACCTCAA CTAAAAGATA	1140
TTGAAGATGA GCAAATTTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACGTCA AAAGGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGA GTTATTCTTT ACGGCAAGCA	1320
ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAAT GATTAACATT GAATCTGTTA	1380
CCCGAGTTCT TGAAATTGCA ACGAATGATA TGGAAGCTTT AGAAACGGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCGC TATCGCTCAT	1500
TTGATGAACG CATTCAAGAA GCATTTAACG AaGCTTAGA TATTTTGA AAAGAATTTG	1560
ATTATCACGC TTCATTTGAC AAGATTTCTC AAGCATTGGA AGTGGCAGAG CCTGGTGTA	1620
CCAATCGCTT TGTTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAGA	1680
AAAAGATTTT ATTTGTGAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCGAT TTATCCACTA CCTCAAACA	1800
GTGTTTTATA CTCTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCTTA CCGTACTCAA	1860

1324

GTACAGCCTG	AGGCTAGCTT	CTTAGTTTGC	TTTTTTGATTT	TCATTTAGTA	TTAAAGTGAT	1920
TTCGCCAGTC	TTATCTGCAG	CTTCAAATCT	GTACTTTGAG	TAACCTGGTA	ACCGTCCAAT	1980
AACGAAGTCT	ATTGAAAAAT	CTCCAGACTA	GAGAACTCAC	GGATAGTTCC	TAATCTGGAG	2040
ATTTCTTATT	TGCACTTTTC	TTGTACAAC	TTAGTCCACG	GTAAATAGAC	CTCTAAAACC	2100
TCTTTGTTTA	CGAGAGTTTC	CTCGTTTGG	AGACATTCTA	GAAGATAGGA	TAGATATTTTC	2160
TCGCTATTTA	TACTAGACTA	AAATCAAAAA	GCATTATATA	ATAGTGATAT	GAAATCAACT	2220
AAAGAAGAAA	TCCAAACCAT	CAAAACACTT	TTAAAAGACT	CTCGTACAGC	TAAATATCAT	2280
AAACGCCTTC	AAATCGTTCT	ATAGTAAAAT	GAAATAAGAA	CAGTACAAAT	CGATCAGGAC	2340
AGTCAAATTG	ATTTCTAACA	ATGTTTTAGA	AGTAGAGGTG	TACTATTCTA	GTTTCAATCT	2400
ATTATATTTT	GTCTGATGGG	CAAATCTTAT	AAAGAGATTA	TAGAACTTTT	ATAGTAGATT	2460
GAAATAAGAT	GTGAACAACT	CTATCAGGAA	AGTCAAATTA	ATTTATAGAA	ATATTTTAGC	2520
AGCCAAGGTG	TACTGTTATA	GATTCAATAC	ACTATAGACT	GTAATCAAAC	AACGATTTGG	2580
CGAAATGTAA	AAAAATATGA	GGAGTTCGGA	CTCGACTCTC	TCCTTCAAGA	AACACGTGGT	2640
GGTCGTAACC	ATGCATATAT	GACAGTTGAG	GAAAAGAAAG	TCTTTCTTGC	CGCCCATTTG	2700
AAGGTGCAG	AGGCAGGAGA	ATTTGTTACA	ATTGATGCCT	TATTTTCAGC	TTATAAAAAG	2760
GAGTTAGGTC	GTTCTTACAC	ACGTGATGCC	TTCTATCAAC	TGTTGAAGTG	CCATGGTTGG	2820
CGAAATATTA	TGCCACGTCC	AGAACATCCT	AAGAAAGCAG	ACGCTCAAAC	CATTGTCGCG	2880
TCTAAAAATA	AAATCTCAAT	TCAAGAAGAA	AAGAAAGCGC	TTTAAAACCA	GTAGACGTTT	2940
TCGTAAGGTT	CGCTTGATGT	ACCAAGATGA	GGCTGGTTTC	GGTAGAATCA	GTAAACTGGG	3000
ATCTTGTTGG	GCTCCAATAG	GAGTAGGTCC	ACATATCCAT	AGTCACTATA	TACGAGAATT	3060
TCGCTATTGT	TATGGAGCTG	TTGATGCCCA	TACAGGCGAA	TCATTTTCT	TAATAGCTGG	3120
TAGATGTAAT	ACTGAGTGGA	TGAACGCCTT	TTTAGAAGAG	CTTTCACAAG	CTTATCCAGA	3180
TGATTATCTT	TTACTCGTTA	TGGACAATGC	TATATGGCAT	AAATCAAGTA	CCTTAAAGAT	3240
TCCGACTAAT	ATTGGTTTTA	CCTTTATTCC	TCCATACACA	CCAGAGATGA	ACCCCATGTA	3300
ACAAGTGTGG	AAAGAGATTC	GTAACGTGG	ATTTAAGAAT	AAAGCCTTTC	AACTTTGGA	3360
AGATGTCATG	AATCAACTCC	AAGATGTTAT	ACAAGGATTG	GAGAAGGAGG	TGATAAAGTC	3420
CATCGTTAAT	CGGAGATGGA	CTAGAATGCT	TTTTGAAAAC	AGATGAGTAT	AAAAAGAAAG	3480
TCCTCATTTT	AATAGAAATC	ACGACTTTCT	GATGGATTTA	TAGTAAAATG	AAATAAGAAC	3540
AGGACAAATC	GATCAGGACA	GTCAAATCGA	TTTCTAACAA	TGTTTTAGAA	GCAGAGGTGT	3600
ACTATTCTAG	TTTCAATCTA	CTATATTTTT	GGAGTGATAG	AAAAGCCCTT	CATAAGCTAG	3660

1325

TCTACTTGTT CAGGTGCGAG AGCTTTGACA TCTTTTCTG TACTTAGCCA AGTCAGTTTT 3720
 CCGTTCTCAA AGCGTTTATA TAGTAGCCAA AATCCTTGAC CATCCCAGTA AAGGGCTTTA 3780
 AAGCGGTCTT TACGTCCACC ACAAAGAGA AAGACTTGAC CGGAGAAAGA ATCCAATTCA 3840
 AAGTGGGTTT TAACTACATA GGCTAATGAG TCTATTCCCT GCCTCATATC TGTCTTGCCA 3900
 CAAACAAGGT GAACCTGACC TAAATCACTT AGTTGAATTA TCATAGTACA ATACCTTTCC 3960
 TCCGATAATT ATTTTTTATC TAGTATACTG GAAGTTGGGG AATTAGGATA GATACCTTGT 4020
 TATGACGCGC TTACGTAACT TGTAAC TAGCCTAGTTT GATCTTTGCT TCTTCATTGA 4080
 TTAGCAGTAG ATTTCAAAT GATAAAAACG CATAGTATCA GGTATTGAAA TGTACTGCC 4140
 CAAAAGTTAG ACAGAAAAA TCTAACTTTT GGGGTGTTTT TGTATGAAA TTAAGTTATG 4200
 ATGATAAAGT TCAGATCTAT GAACTTAGAA AACAAGGATA TAGCTTAGAG AAGCTTTCAA 4260
 ATAAATTTGG GATAAATAAT TCTAATCTTA GGTATATGAT TAAATTGATT GATCGTTACG 4320
 GAATAGAGTT CGTCAAAAAA GGAAAAATC GTTACTATTT TCCTGATTTA AAACAAGAAA 4380
 TGATTAATAA AGTCTTAC 4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTTAG ACTTTGTCTT TAATCGTTC TTTTAGGGA TGATTGCGAC ACCTTCTTTT 60
 GGCTATTAAC TTTAGCAGGA GGGATTATCC TTGGTCTAGC GCCGGCTAGT GCCACCTTGA 120
 TGAGCTTATA TGCAGAACAT GGTTATAGCT TTCGGGAATA CAGTTTGAAG GAGGCTTGGT 180
 CTCTTTACAA GCAAATTTT GTCTCAAGCA ACCTGATTTT CTATAGCTTT TTAGGTGTGG 240
 GTCTAGTTT GACCTATGGT TTGTATCTCT TGGTGCAATT GCCTCATCAG ACCATTGTTC 300
 ATTTGATTC GACCCTTTG AATGTCCTAG TAGTTGCCCT GATCTTTTG GCTTATACAG 360
 TATCTTTAAA ATTACAAGTT TATTTGCCT TGTCCTATCG AAATAGTCTC AAATTATCCT 420
 TGATTGGCAT CTTTATGAGT CTAGCAGCTG TGGCTAAGGT TCTCCTTGGG ACTGTGCTAC 480
 TTGTAGCAAT TGTTATTAT ATGCCTGCC TGCTATTTT TG TAGGAATT GGGATGTGGC 540
 ATTTCTTAT CAGTGATATG TTGGAACCTG TCTATGAAAT CATCCATGAA AAATTGCGT 600

1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG 660
 ATCATATATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG 718

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAATTA TTTAACAGAT 60
 TTAGTCTAG TTTTCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAG 120
 GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT 180
 GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAAA AAATGCAATT 240
 AAAAATGGTG CCGTTGCTGT AATTCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA 300
 ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC 360
 AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAAAT TTTATAATCT GCCTAGGTCT 420
 TCTTATTACA ATATTTTGT CATTAAAGCT TGGAACAAAA GAAATTAATA TCAGAGATTT 480
 TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAAATCAA TTATATATAA 540
 rAGAATACCT AGAACTATTT TTGCAATTTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT 600
 ATTGATGCAA TCAGTTACTA GAAACCCAAT AGCTGATCCA GGTATACTCG GTATAAACAC 660
 AGGAGCAAGT CTTAGTGTAG TAATGGTCC TTctTTTTAG GGAATTCATC AAGCATAA 718

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAACTAATCA TTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG 60
 TTTTCTTGG CATAATGACT TTTCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA 120
 CCAAGTCCAC sCTTAAGTTA GATAATAAAT CTAACCTAAG GAAGCTAGAA GGATGAGAAT 180
 CCAGGTGGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT 240

1327

GAAGGCAAGG CCACGTTCCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCAGCTGA	300
TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCAATC TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGGAT AGGGTGGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AAATGAGGAA TGTTTGTGTG CATGAGGTGC CCTATCAGTG TGACTIONAAC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGCAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTTG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTTGTCTTT GAACCTTGCT GAGGAGTGGT GGTGGTCAA TAGTCAAGGA	840
TGAGTTTGT CTTCCCTTAC TATAGTGACT GTAACAGGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTTCG TTAACAGGC CTTGAAAGAC AATGCCTGAG CTACTIONGTTA TCAAATTAGC	1020
CCCTCCTGAA GCTCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGT TGTCCGCTTT	1080
TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGCCATA GTAGTGAAAA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAATCATG TAGAGGGCGT TAGGGTGGGT	1200
GCGTGTGCGG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCCTTAG TTGTTGCAAC	1260
GTTATAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGTTGGCC AAAAATGAAG	1320
AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTTGCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTTGGGA AAGAACGTAA GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCGTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC	180

1328

AAGGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC	240
TTGGTGGACG AGATGTGGAA GGTGCCCCAA CGTGAAGTGG CTACAGGATT TTTACTATGGT	300
ACACCATCTG AAAATGAGCA GTTGTTTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT	360
GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCG TCAACGAAAT	420
GTCATTAACG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTTCCTGCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG	540
GAACTATTGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAAGATGCA	720
TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT	780
ATGCTTGTTA TCGGTGTCAT GATTCATTAG AACATCACCC TTTTGAGCCG TATCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAAACTACTA ACATATAAGC	900
AATATAAAGA AAGCTTAAGT TGCCCCTTTT GTTTTTCTCG CTTTAATCCA GGTGCCCCAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAA TCATCTAGTT TTGAAGTAGG AGAAAACCTCA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAC GCATAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTCCTTTAT CTGGTATTTT	1140
GACTACTTGT TAAACTGGG TTAATTTTCG ACTGTTAAT AGTTATTATG CAAAGCTAA	1200
AAGGTTAGAA TTGTCAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTTGGGA AAGAACGTAA	1320
GAGTTTGCG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGGCGGCTG TGGATGCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA	1560
GGTTGCCCAA CGTGAAGTGG CTACAGGATT TTTACTATGGT ACACCATCTG AAAATGAGCA	1620
GTTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA	1680
TGATGATGCG GCGGTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1022 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA	60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTTCGATG TTCGCAGGTG	120
CATTTTTAAC CTTCAGTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATTTG	180
CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG	240
TTTTTTTTGAA TGCCGAGTTG GTCACTTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT	300
TAAAAAAAAT CTCTGGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTC AAC	360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA	420
CACACGATAG TTTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG	480
TCTTGCTTGA GCGGATTTG GCAAATATTT TTGTAAATAT TCGGATTC TG TCATTTATTT	540
TGGTCAAAGA TGGTGGTGCC AAACCTTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT	600
TCCTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CCGGATTGTG AAATTCAGTG	660
TTGCTGCGGA TTCAATTGCC AACTTCGGTG TTGAAATAT GCTTCGCCAC TGGGGTGTGA	720
CTTTCATCGG AAACCTTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA	780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT	840
CATTTTCAAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT	900
ArACTATAAC TCAAGGTGCT ACAATATCCT TAATAAAATA ATATGGAGGT CACCTTATGA	960
CTGTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA	1020
CT	1022

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 663 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGAATATCG ATATAATGGC	60
TCATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAAAC	120
CATTAATAAAA GTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAATTTAGA	180

1330

AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTCA GTTCCCCAAA AAGTAGCTTC ACTGCGTGGA GGAGTTTTTC CTATTCTGAA	300
GTTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTTCAT ATATAGGATA	360
AGAGGTGTGT TCGTCTTTGT TCCCATAATA AGAGTTATCA TCTCCTTGGG AAACAATAGA	420
AATGTCCAAA TCTTTCPTTT TAATCTTGCC TTCTTCAAAG AGTTTTGT TTTCTGCTCG	480
TATTTTTCAGTA AGTAAACTT CGACTGATTC ATCATTGGG TCTTGTCAA CTAATTTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATCTT TATCTAGCTG	600
TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAATTAAA CTAACAAAC TAAAATTATG TGATACTTCA	60
CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG	180
TTCGTCGACC AGAAGTGGTA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTCGAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAAACA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTAGCT GGTGCAGATG CCTTGTAGG TAAGGTTTCA AATGAAAGCC	480
CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG	540
TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAC AGCCTAAAA CAGAAAAAGG	600
AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTCCATT TTGCTACTCT TCGAAAATCT	660
CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTCGTCAGT TTCATCTACA ACCTCAAAC	780
TATGTTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAC TATGTTTTGA G	881

1331

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 949 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

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CCTTTTTTAA TACAAGTTAT TTTGATTTAA CCGGCTTGTC TTGAGCTGTC TGCAAAGCTG      60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA      120
AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT      180
CTGTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT      240
CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCCTCATA AGGAGTCACC AAAATCATAT      300
GGTGTCCTT AGGAAGATTT TTCACGATAC TGTCCAGTC ATCCTTGTA TTTCTCAGGAT      360
TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA      420
GCATGATTTC ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG      480
GAAGAGCTGT CTGTAGTGCT GTATTTGCC TTAAGCCAC TGAGTCACCA ATTAACATAG      540
TGCCATCAGC AATFCCCAA CTGTTTGCAT CTGCCCGTTC TGCCATCACC TTGGTCTGGC      600
CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA      660
CTTGTGGTGC CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG      720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAAGGTTT GACAATAGGT GTGTTCTTGC      780
CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA      840
GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAAATGATA TAGAAAGGCC      900
AATGAAAAG ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT      949

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(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

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AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GGAATTAAG      60

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1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA 120
 AACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC 180
 TTTGTAAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA 240
 AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT 300
 TACAACCTCT TAAACAGACT CTTGAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA 360
 AGTTAGATTT AATTCTCTGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC 420
 TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA 480
 AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTATAG AATAAAATAG GAGTTATGAA 540
 ATGAAAATG TTACTTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTA ACTGCCAGGT 600
 ATGACATTC TATTTGTCTC AG 622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1929 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAAACTCAA 60
 TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA 120
 ACGTAATTC TAAATCAGGT ACAACAACCTG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG 180
 AACTCTTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACGTATCTAT GCAACAACCTG 240
 ACCGCCAAAA GGGTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG 300
 TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG 360
 CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAGGTGC GAATGCAGCT CGCAAAGACT 420
 AACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC 480
 TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAAACTA TGAGCCATCA CTTCAATACT 540
 TCTCAGAATG GTGAAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT 600
 ACCCAACTTC AGCCAACCTC TCAACTGACT TGCACTCACT TGGTCAATTT ATCCAAGAAG 660
 GAACTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA 720
 TTCTACTTT GGAAGAAGAC CTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT 780
 TTGTAACAAA AAAAGCAACT GACGGTGTTT TCTTGCCCA CACAGATGGT GATGTACCAA 840

1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT	900
TCGAATTGGC AATTGCCCTT TCAGGTACT TGAATGCTAT CAACCCATT GACCAACCAG	960
GTGTTGAAGC TTATAACGT AACATGTTG CCCTTCTTGG AAAACCAGGA TTGAAGAAT	1020
TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAA AGATATCCGC GTACGTACG	1200
CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATG TTTAATTACT	1260
TGTATGCGCG CCATCATGGT GGAACATTC TCATCCGTAT CGAAGATACT GACCGTAAAC	1320
GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTT GACTTGTATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG	1680
ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGGTTATCC	1740
AAAAGAAAAGA CGGTTACCCA ACTTACAAC TTGCCGTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTTATCCGT GGAGATGACC ATATTGCTAA TACACAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAGTA TTATTTATCG TCGGATCACT	60
ACGTCAAGGT TCTTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATTCAGC CCTTCTCTC TTCAGCCAAG ATTTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240

1334

GATTTTCTCT CCAGTCTACA ACTTCTCTAT CCCTGGTACA GTGAAAAACT TGCTTGACTG 300
 GCTATCTCGT GCCCTTGACT TGTCTGATAC ACGTGGCGTT TCTGCCCTTC AAGACAAGTT 360
 TGTACAGTA TCATCTGTAG CCAATGCAGG GCACGATCAA CTTTTCGCTA TCTACAAAGA 420
 CCTCTTGCCA TTTATCCGTA CACAAGGCGT TGGTGATTTT ACTGCTGCAC GTGTAAATGA 480
 CTCTGCCTGG GCAsACGGAA AATTGGTTCT TGAAGAAACA GTCCTAAACT CACTTGAAAA 540
 ACAAGCTCAA GACTTGGTCG AAGCTATCAA GTAAC TAACA CTCAATAAAA ATCAAAAAGC 600
 AAACTAkGAA GCTArCCGCA AGCTACTCaA gCACTGCTTT GAGGTTGTAG ATAGAAGTGA 660
 CGAGTGnnA ACATATATAC GGTAAGGCGA CACTGACGTG GCTTGAAn 708

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CTCTTTTCT TGGAAATAGG TGTATAATAC GTTTATTAAA TTTTGAGGA GTTGTCTATG 60
 AAGAAAAGTT TTATCCATCA ACAAGAAGAA ATTCCTTTG TCAAAAACAC TTTTACCCAG 120
 TATTTGAAAG ATAAGCTAGA AGTTGTCGAA GTTCAAGGTC CTATCTTGAG TAAGGTCGGT 180
 GACGGAATGC AGGACAACCT GTCTGGTGTG GAAAATCCAG TATCGGTCAA GGTCTCCAA 240
 ATCCCTGATG CTACTIONTGA AGTGGTGCAC TCACTIONGCTA AATGGAAACG CCACACCTTG 300
 GCTCGTTTTG GCTTTGGTGA AGGAGAGGGT CTCTTTGTCC ACATGAAAGC CCTTCGTCCA 360
 GATGAGGATT CCTTGGATGC AACCCACTCT GTTTATGTTG ACCAGTGGGA CTGGGAGAAG 420
 GTTATCCCAA ATGGTAAGCG TAACATCGTT TATCTAAAAG AAACAGTTGA GAAGATTTAT 480
 AAGGCTATTC GCCTGACTGA GCTAGCTGTT GAAGCCCCT ATGACATCGA GTCTATCTTG 540
 CCAAACAAA TTACCTTTAT CCATACAGAA GAATTGGTAG AACGCTACCC AGACTTGACA 600
 CCGAAAGAAC GTGAAAATGC GATTTGTAAA GAATTGGAG CCGTCTTTT GATTGGTATC 660
 GGTGGCGAGT TGCCAGATGG TAAACCGCAC GATGGACGTG CACCAGACTA TGATGACTGG 720
 ACAAGCGAGT CTGAGAATGG CTACAAGGGT CTAAATGGTG ATATTCTTGT CTGGAATGAG 780
 T 781

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:

1335

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

CCCGCATCTT GTAGGGTTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC	60
GCTTCTAGGG CTGTTTGGA GTTGTTTTTC GCGTCCGAT GCGCCTTTG TTCTTCTTCG	120
CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC	180
TTCTTATCAA TACCTCCAAT GTCTCCACA TTACCATCGC GGTCAATGGT ACCTGTACCG	240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA	300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG	360
CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAATTC CATTTTTGCC ATTTTCCAAG	420
GTGATGATTT TTCCTTCTGC AGACTTGTTT TGCCCATCCT CTCATAGGT GACCTTGACG	480
GAATCCCCTA ATTTTTGAGA ACTGACGTAA TCAATCAAGT CTTTGGAAC ATCAAAGTC	540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTGAATTA	600
TCCGTACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT	660
TTTAGTCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGTAGAATG ATGATTTCG	720
ATAAATCAA CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA	780
GGTGTCAACC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG	840
AATTGT	846

(2) INFORMATION FOR SEQ ID NO: 307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 829 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC	60
CATATAAAGT CCACCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG	120
TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT	180
GACTAGGGTC AGCAAACCTGA TTAAAATGGT TCGCTTCAAA ATCACCTTGC GCTTGACACC	240

1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCATAAC TGTGGAAGAG GCGATGGTA GGTAGTTGCA AACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTGCGG TTGCGGAACA TGGCCTGAAG	420
CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAACTG CAAAGACAAA	480
TAAGCCCAGA GCCAACTAT CTGGCTTACC ATAGAAGACC GTATAAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCTTG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTTCCGTCA AAAGTGGCAA	660
ACCAACTC CCAATCGAAA CCCCTACAGA AATCAAATC ATCGTGATTT TATTAGGATT	720
GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATG CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCCCCGCGTG TGCATCATTT	120
GCTCATCTAG TAACGTATGA GGTTCGCTT CGCTGTGCGAT AAACCGATAT TCAATCGCAC	180
CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA	240
GATCACGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGTTT GATCGGCGTT CGGTTGCTGA CTAATAACTC	360
GGTGCACGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTTGTCTTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GGCGCACGCA GGCC	464

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 982 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGTCTATAA TGGTAATAGA TTTTATTTGG AGGTTTTTAT GTCATTTCTA TCAAAAAATG	60
GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGGATTCT	120
TCCCTGTGGT TGGCGCGCCC GTTTTGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC	180
TCTCGTCCTA TAAACAAC TGATGCTGGT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT	240
ATGCCGTTGT CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT	300
CTTCACTCCC TGTATCCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC	360
AGCGTTTCTT TGCCTGGAT ACAAACCTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT	420
GTGGGGGTTC TGCCATTGCA GCGACAGGCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC	480
CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCT	540
CGGCACCTGG CTTTATCTAT CCAATGAAGG CTTGCCCCC TTGCAGGGA CTGCGGTCAA	600
CGACACTTCC TCTGTAACGG CTGCCGCCAG CGTTGGGAC AGTCTTTACC AAAGCAATAC	660
CCTCGAGTCT GCAACCATTG TTAACCTCAC ACGTACTTTG GCCATTATCC CTATCACGCT	720
CTTTCTATCC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA	780
AGTCTTCCCA CTTTTTATCC TTTACTTTAT CCTTGCCTCT CTCCTACTA CACTACTCAC	840
CTCTCTAGGT GTGTCCAGTA GTTCTTTTAC TCCTCTCAA GAACTCTCTA AATTCCTTAT	900
TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG	960
TGGAAAATCC ATTCATCATG GA	982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT	60
CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA	120
GGCTGTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC	180
TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT	240
TGCCAGCATG AGCTGGATCA CTTGGAAGGA CGAATCATTT AGGAGGAAA CAAATGAAAC	300
GAATAGTCTT TGAACCTATT TTTATCGCAA CGACCTGGTA TATCTTTTTA CCGCCCCTTA	360

1338

ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG	480
CGGAAGCTGC CTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTAG	540
CTTCGATTGG AGGAATCTT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT	600
TCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTC	660
CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG	720
ACCGCTACTT GGGTTCCTTA ACCGATAAGG TGTCGCAATA CGTAGCGGCA GATACCTATA	780
CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA	840
TCAAATGGTT TAACAATCAA GCCAAGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGAAAATGC GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTCAGAC TCGGAGTATT	960
TTAACCGTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAAATC	1020
CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAAGC	1080
AATTTGGACT TGCTGTTCCT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTT CAGAATGGGT GGACAGGATC TATCCAGCAG	1200
AGGAAACCAT TGAGCAAATC AACTACAACG GCAAGTACAA GGACGGTTT TGAATGCCA	1260
TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT	1380
TCATCCTTGA AAATATGCGA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGACAG	1440
AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTCAGGA GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATTGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAAAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTTGGTA TCGAAAGATA TCTGCGGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAAATTTC TGACAATTTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCACTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTTTT	360
TAATTTAGTA ATCTTCAGC AGTTTTAAAG ATTTCTTTGA TAGTATAGCC TTTTTTAGTT	420
CCTAAGTTAA AGATTTGAGA AGAACTGTCT TCTTGAAATA GGTAGTTCAI TCCTTTAACA	480
TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA	540
TCTGATGCAT CTCCAAATAT TTTTAAGCTA TCATTTTGTC CCAATGCGGT CTTGTTGATA	600
TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTAGCC	660
CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG	720
TAAATCATTC GTTCGCCCAT CAGTTTTGTC TCTGCATAAG GGTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG	840
AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTTGTTT CATACCAGCA	900
ACGTTGG	907

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTGGGCATC CAAGAAAAGC AATTGGGCAA	60
TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTTCATAAATACAG	180
GAATCATTCA TTTCTCCTTT TGAGTTTFAA TTTTGTGTTGTT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA	TCTTGGTCAA	AAAAGGTCAA	ATTTTGGCTC	TGCTTTCATT	AGACAGAAAC	300
AAAAACCCAA	CCTCCTTTCG	TGACTGGAAA	TACTTTTCCA	AGTCATTCTT	CTTTTCGATC	360
TTATTTTGTA	CCGAACAAGC	GGTCTCCAGC	ATCTCCAAGA	CCTGGAACGA	TATAACCGTG	420
TTCGTTCAAA	CGTTCATCCA	AGGCTGCTGT	AAAGATTTCT	ACATCTGGAT	GAGCTTCTTG	480
AAGGGCTTTT	ACACCCTCTG	GAGCAGATAC	AAGGCAGACA	AATTTGATAT	TTGATGCGCC	540
ACGTTTTTTA	AGAGAATCAA	CAGCCAAGAT	TGCTGAGCCA	CCTGTGCCA	ACATTGGGTC	600
TACTACAAAA	ATTTGACGTT	GGTCAATGTC	CTCAGGCAAT	TTCACCAAGT	ATTCAACTGG	660
TTGAAGTGTT	TCTTCATCAC	GGTACATACC	GATGTGGCCA	ACTTTAGCAG	CTGGAACCAA	720
GTTCAGAGA	CCATCAACCA	TCCCGATACC	TGCACGCAAG	ATTGGGACGA	TGGCCAATTT	780
CTTACCTGCC	AATTGTTTTT	GAACTGTTTT	TGTAATTTGT	GTTTCGATTT	CCACATCTTC	840
TAGTGGAAGA	TCACGAAGTA	CTTCATACCC	CATCAACATT	GCAATCTCAT	CTACTAGCTC	900
ACGAAAAGCT	TTTGTAGAAG	TATCTGTACG	ACGCAAGATT	GACAATTTGT	GTTGAATCAG	960
TGGGTGATTA	ATAACTTCAA	TTTTTCCCAT	TTTTGGAATT	CCTTCTTCA	ATTTATTTCTT	1020
CTTATTATAC	CAAAAACCG	TTTAAAAATC	TTTCTAAACC	ATTTATTTTT	GATAATTTTT	1080
ACATTAGATC	AGCCTCTTTA	AGAGCTGTCT	GTAAGTGTCT	AAGTGGTAAA	TGGGTCAATT	1140
CTGTCCCTTT	TTCTTGATAA	AGGTATTGGG	CGTAGTCGTC	CATTCGGTAC	TGGTTGATAT	1200
AAACCACGCG	CTTGCAGCCG	ACCTGAAGCA	ATTGTTTTGT	ACAGTTGAGA	CAAGGAAAT	1260
GGGTACATA	GGCTGTAAAG	CCTTTGGGAA	CACCACGCTC	AGCACCTTGA	AGGATAGCAT	1320
TGACCTCAGC	GTGAAGGGTG	CGAACGCAGT	GGCCTTCAAT	GACCAAACAT	TCGTGATCAA	1380
TACAATGCTC	AGTCCCTGAC	ACCGAACCAT	TGTAACCAGT	GGAAATAACC	TTATTATCTT	1440
TTACCAGAAAT	CGCGCCCACT	TTAGCACGTT	TACAAGTGGA	ACGATTCGCA	ATTAGTAGAG	1500
CTTGGGCTGC	AAAATACTCA	TCCCAGGCCA	GTCTTTTTTC	AGTCATCTCT	TTTCTCCTTT	1560
TTCTCTATTT	TTTAAAAAAT	GGTAAACCTA	AATCTGCAAT	CTTTTCAGCT	GGTACCTTCA	1620
TGCCATCCTT	GATCCATTTT	AGAAGGACAG	AGACGATGGC	TGAGCTCCAG	AAGGAATGAA	1680
GATAAGAGCT	GACACCTTTT	GATTTCCCAT	GGTATTTTTC	TAGAAATTCC	TGCATGGCTT	1740
GGACAAAGAT	TTTTTCCAGA	TGGTAATCCA	AGGCCAATTG	AATTACTCTA	GCTTCCTTTC	1800
TGGCCTCCCG	GAAAAGGTGA	ACCCAAACCA	AATAAAGGTC	TGTCTTTAAA	TCGTAATGAT	1860
GCAGCTGTTT	CATAATATTG	TGGACAGTTC	GTTTAAAGAC	GCTCTCTAAA	ATTTCTCTTT	1920
TGGAGTCATA	ATTGCGATAA	AAGGCCGCAC	GCGAAACACC	TGCACGTTTG	ACCAATTCAG	1980
AAATACTAAT	CTTGGTCAGT	TCCTTTTTTT	CCAAGAGTTG	CAAGAGGGCT	GTTTCAATGG	2040

1341

CTTCTCTGGT TAATAAATG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT 2100
 CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG 2160
 CTTTGTGTTTC 2170

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG 60
 AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGGAA ACAAGCTCGT CGTCTTGGCC 120
 TTCACTTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACAGC 180
 GACCAAACAA CCGTTCATAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAAC 240
 TTCGTTTAC TTAGCGTGTA GGTGAAAAAC AATTCGGTAA CTTGTTTCGTA CAAGCTACAA 300
 AAATCAAAGG CGGAATCCTA GGTTCACACT TTATGCTTCT TTTGGAACGT CGTTTGATA 360
 ACGTTGTTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC 420
 ACGGTCACAT CCTGTGAGC GGGAAACGCG TTGATATCCC ATCATrCCGC GTAACCTCCAG 480
 GTCAAGTGAT CTCAGTTCGT GAAArATCAT TGAAGTTC AGCAATCCTT GAAGCAGTA 539

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 667 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTGC TCCTTCTCTA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT 60
 CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTCT GCCGTCGTAT 120
 AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATTCTCT TTCAAGTTTC TTAGGTCTAA 180
 CAGGACCTGG ACCTGGTCTT GATCCACTTT CTCCGCTGG AGAAGAAGGT ACATCTTGAC 240
 TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA 300

1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTTCATT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTTACTTT TTCTAAATCT CTCAGAATCT	480
GCTCTTTAAA GCGTAATTC TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT	540
TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATAACCAT GTTCCCCTG CAAAGGTTGA	660
CTGGGAA	667

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTTACTAGT TCTTCACCGA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGAATCG	120
TTCTGCTGAA ATGATTGCCT CTAATCAAC CACTAATGGT TTAGATAAATT CGTTAAGTGT	180
TAATAGTATC AGCTCTAATG GACTATTCG TTCCAATTCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT	360
AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT	480
TTTTTTAAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATGGTAT	540
AAATATTAAG AATCACCCCT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATCTTCAGG	720
TGCATTTGCT ATTGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AAATTGCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CAAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG	900
CATTGAGATT GAACCATTA CTAGAAAAGG TTTTCCTTAT GCCTTGAATG ATGATGGGAA	960
AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT 1080
 TAAAATTCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT 1140
 CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGATACA 1200
 TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAACA CTAAAGACCT 1260
 ATTAGATTTA AATAAACAGG TGGTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA 1320
 AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAAaTwT TTAGGAAAAG TATCAGATAT 1380
 TACTGTAACA AAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGAACAAC CAAATATTGA 1440
 ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT 1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTATAAAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG 60
 ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAACTCATTT TTGAAAAGAC 120
 GTTAAAATCA TCTAAATTCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC 180
 TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG 240
 CAACTTTTTT TCTTCAATTT GAGTTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA 300
 AATATTATTT CTATTATCAA TAAGTATATT ATTAAATGAT AAATCTCTAT AGGAAAGATT 360
 ATATTTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC 420
 ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA 480
 CGAATTC'TTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC 540
 TACTAATATT TCTCTTTCAT TTATTAAACG ATTCACAGAA TCTCTATTTG TAAAATCAAC 600
 CAACGATAAA TCACTAGCTT CTTTAAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC 660
 TTTATAAACT CCACCTTTGG CATTTTLAGA AATCACTTCC AAAATAATAT ATTGATCAGG 720
 AATAGTGTTA TATCTTGAA TATAGTAATC CCTTATTGGA ACATTCACAT TTGAAGGGAT 780
 TTTCTTATCT CTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCCAT ATCTGTAATA 840
 TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT 900

1344

ATACAATATT TCTAATTGT GTAACAAACG TTGAAACTCT TTATTATCTT TTGGATAAAT	960
TGTAATGAAT TTCCCGACTT GTGAATAACC ATTAAGCCCT GTATTTTGCA AAGAAAGTTC	1020
TTTAATGCTA ACCAAAATTT TGAAATTTAT CTCTCTCTCT CTAGAAAATA TAAAATCAAA	1080
GAATTTTTTA GCAACCAAAT TAGCATTTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG ACGGCAAATT ATATAACCAA TGTTTCATCAC TAAAATTATC	1200
ACTAATTTTA TATTCTAATA ATAAATATAG GTATGCGTCT TCTATTTTCAG TTTCATAGTC	1260
CAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTCTCCATA AATTTTTAGA	1320
CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAACT	1380
TTCAGTCCCTC TATTTGTAA TTCCTCACC AATAATTTTA TGCTATATCT ATTTTCTCGA	1440
GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT	1500
CCAGTTTCAG AATAATTTTT TAGAAAAATA TCTAGTGATT CTGATAATTC ATCCGGAATA	1560
ATTCTTTTAA CATCGTATTT ATTTTTCATA TCGGCCACTC TTCCTTAAAA AGCTCACAAT	1620
AAAATTTTAA ATTTCTATAC AACAAATCCGA GAGTAGTCTC ACAATTTGAA CATTTCACAT	1680
CACTCTTAAT ATATAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACTTCT ATATCATAGT AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTTAT	1800
GTTTTATATA TTAACAATTA TGCGGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCC CAGAAGCGA TGCAACGCTA TTTTGAATTG AAAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTTC CGACAATTCC AAATTTTCTA	1980
ATTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACCT CCATATTTC TTGAAGTTCA	2040
TTCAAGAAAG CTTTCATTTG ACTACTCATT ATATAGCTCC TTTTCTATTA CTTTATTTGG	2100
AATCAAACT TACTTGTAACA TTGGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG	2160
ACACTTTC AAATCAAATG CTAAAAATA TTTTTAAAG CTTAATTTAG ATTTAATTAC	2220
ATATATCTCA AAAAATGTT TTGAAATTAG TAAATAAAA TAGGTTCTG TACTTATAGG	2280
AACTAGTTAT AAAAATTCG CCCATCATAA AATATCTATT TAAGTAAAAC AAAAATTTTA	2340
TAATTTTTTG ATTTTAAAGT GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT CTTATGAACT TGAGTTCCTC CAGACAGTCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT	60
TCCAGCAgTA CTCAAAAACCT TTACTTATCA CCAGTTTTAG ATGGCTTTAA CAGCGAAAT	120
ATTGCTTTTA ATCTTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTTCT TTGGCATT	360
TTT GAAATCGGAG	
ATGTTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAACCT TACTATATTC ACAATGTTAT CCAGTGT	660
TTTT TTCTCTAATA TTTAAGGAGT	
GTTCTGTTTC TCGAATAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTCATCAG TTAATTAGT AGTATAACTT TTATCGGCTA	780
ATTTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTGGCCCG TCCGATTTTC	900
TAATTGCCCG ATAAACATTT CCTTTATTTG ATCTCTTAAT AATTTTTTCC ATTTTGTATT	960
TATTTATGTC AGAGTCCTTA CTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTTCTGA AAATAAATCC ATTTTCCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGGTTATTT ATTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAA TTATGCTGAT AAATACAAA	120
TGAATCCTAA AGTAATTTAC CCTCATCTT TTAGGCATTT ATTTGCTAAG AATTTTTTAG	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA 240
 CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACAAACAAA TATTGTAGAT AAAATFGTTA 300
 ATTGGTAAAA AATAACAGGT GGTCAAAC TG ACTACCTGCT ATTTTTGTGA TTATGGCTCT 360
 TATTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTCAATA 420
 AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTA ATAATAAAGG TGTTAGAATT 480
 ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTAACACTT 540
 GATACACAAT TCATCTCCTC TGAGCAAGTT TATTTAAAAC ATAATCAGCT AATAACACCT 600
 GTATCAACCT CTTTAGAACA TATTGGAAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT 660
 GTTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTTC AAAGTGCAGA GATGATGTCA 720
 AAATGTCTAT TATGTAAC TTGCTCTCCG TTATTTTATA AACAAATTGAA AGCAAT 776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA 60
 ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTGATC AGGATGATCT 120
 GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTCG CCAGGCTCAA GGC GCGCATG 180
 CCCGACGGCG AGGATCTCGT CGTGACCCAT GCGGATGCCT GCTTGCCGAA TATCATGGTG 240
 GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT 300
 CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC 360
 CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTCGC AGCGCATCGC CTTCTATCC 420
 CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TGTCGACAGC CCGCCTAATG 480
 AGCGGGCTTT TTTTTCCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGC AGTGCAAATC 540
 CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA 600
 GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC 658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1475 base pairs
 - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

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CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA      60
AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG      120
CTCATTCTAC AATTGACTCG AGGATTATTC ACTTCAAATF AGAATTTGCA AATGAATTTT      180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA      240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACCTTATAT GAGTACCGAT GTTATTCCAG      300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT      360
TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC      420
ATTACTTGCA GTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAAGT GCTTATTTGG      480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA      540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAATGTG AAAATGAAGC CAATCTTTTA      600
CAGACTCTAG TTTAAGAAAA ATTTAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG      660
GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGATCCA TCATGTTGAA      720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATG TTCACCTGAT CTACTTCTTA      780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCTTACA CTGACGAGAA GTTTTTGAGT      840
CTTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA      900
ATTGCTAGAA ATGAATTTCA ATCTCCAAT TTATTTGTTC ATATCTTCTT TTAATATATT      960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTT CATTACGAAT     1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA     1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA     1140
TAATATTTCT TTTGATACTT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC     1200
AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA     1260
TATTGTTAGA AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTTAC     1320
TATATCTCAA ATTGAGTATG ACGAAGTGCG TCCTCATGTC CTGGGAACGC ACTTCTTCA     1380
TATTTTTCAT ATTCCTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA     1440
CTAATCATTT TTACAGGATG AGATTTACAG CAGAG                                     1475

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(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATAACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTTT GGTGCGGGTT	240
TGAATTTAAA AAATTTGTTA TGTAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGTAAA AGCTCTCTTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT	420
TTTCTAAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAA r ACTCT GGGGTTGGGA AAGGAAGATA AGAA a CGTAT	540
TTAGCCCATATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCGGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TGCGTGTCCG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG	240
TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TCCGGCGACT GGAGGAATGG CGCCTTTTTC CGGTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GGCGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA	480
TTCAGGTCGA GCCTTTTTC TGCCTGGCCT TGCCTGGGTA GGCAGCCGAG AAGA a CTTT	540

1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG 600
 GCATTTAGAC GGTCAAACGG AACGAGCACG TAGGGTACTG TGC 643

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TGCGAGTTGA 60
 AGTCAAGAAG AGGAAAAAAA CAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC 120
 AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAAACTCG TCGCTGGAAAT CCTAAGATGG 180
 CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAAACTGTAA 240
 AATACGCTGA CCAAGCATA CACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT 300
 TGTTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTTCA 360
 GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACCTCT TACAAACTGG GGAACAATCC 420
 AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTCGAAG 480
 TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAAACAACG TCGCGCTCTT GAAAAATPCT 540
 TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTATTG ACCCACATAA 600
 AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA 660
 CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720
 TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 624 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAC 60
 AGGTGTGCGAA TTGGAACAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC 120

1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT	240
GACTACTTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTT	300
GATTCAAGAG ACGATGGCGA AAGATTTGCT ACAAATTCTT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATCACAG ATTTAAAATC AGGACAAGTG GATGCCGTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGGATTTG TGGAAAATAA TCCTGATTTA GCAATCGCAG ACCTCAATTT	480
TGAAAAAGAG CAAGATGATT CCTACGCGGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAAGTACTT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATGATGC GAGTACAGAG	180
GAGGCAGACT TGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC	240
AGTCCTGCGA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCCCTG	300
ATCCCGGTAG GTCAATTTTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTAATCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTTCATA TCGGACACTA ACCGAGCGG ATATGGTTAA AAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTCCGG AAGGAAACAC TCGGACGGTA	540
ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTG ATATTGATAA TACACCATTT	600
CAGCAACATF CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAAA GATTTTACAG	660
CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAAATCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTTATAATC CTAATACTGA	780
GTAAACATTG AATTTTAGGA AAAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTTGG CTCTTTGTCA ATGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTTCCGGC CTTTCCTTTT TGATGTTTCAG AGCGATAAAA ATCCGGTTTT TTGAAGTTTT 960
 CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT 1020
 CCAGTTTGGC ATTAGAATAG TGTAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA 1080
 GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA 1140
 GTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC 1200
 GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAG 1237

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA 60
 AGTGCATTTT CTTTGTAGTCA AAAATTGAAA AAGCTAACCT TTTCCTCAAG TTCAAAATTA 120
 GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAACT AACATTACCA 180
 AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTA CTAGCTT AAAACATGTT 240
 GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTGT TTTCAAAGAT 300
 AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAATGACG AAAGTTATAA AACGCCTAAG 360
 GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAAT CTTACTTGAA AAAACTCGAA 420
 TTGAATGAAG GTTTAGAAAA AATCGGTACT TTTGCATTTG C 461

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTTAAACAAT 60
 ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTTCATAGA TTGGATCAAT 120
 AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTCAAAA GTTTTATTTT GATTATTTT 180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTA	AACAATTTGT TCACTAGTAA CATCTATTTG	240
ATTAATAATA GCATGGTCTA AAAATCTCTC	ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCTGA TTTTTTGTA	AATAATTTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CTTTTTCCC	TTTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTTCC ATTTTCGTTA CTAACATGAC	GCAGTCACCT AGCATCATAT ACTCCAACTT	480
TTTTTCTGAA AGTTTAGCAA ATATTGGTAA	GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTGTTAGA	AATCGATTTG ACTGTCCTGA TTGATTTGTC	600
CTATTATTAT TTCATTTTAC TATACTCTGT	TAATTTATAT GAGTTTAAAC CGATTTCATC	660
TTTAACTCG AGTAAAGCAG TTTCAAATAT	TTGTTTAAGA GTTTTTGATT CTTTACAATT	720
AACCACAAA CTTTCTGATA AAATATGTAC	AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTGAATTA TATAAATCTG TAGCTCCACC	AATAATCCAA AAATACTGAT TTTGTGAACC	840
TACAATATCC TCATTTTCTA CGGAACTTCC	TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAACTACT CAACCCTTTT AGTGTCAAAA	GTAACCAAT TCCTGTCACT GTTAAGAATA	960
GTTCCATAAT CTTATTCGAA CCAGTCTTTG	GTAATTTTTG TTTKACATCT ACTATyTCTT	1020
TAGATTTATT AATATGATTT TCAGTTTCTC	TGCCATCTCC AACTATTTTA TAGTTFACTT	1080
CTTCTGTCTT ATTATCTTGT TTATTGTGCA	TCTTGTCAAT CATTGTGCTA TTATCTTTAC	1140
TTGAGTTAAA CTCTCCGTTT TTCTGGTTAC	TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCTCTTT GTTTTTTCT TTTTCGTTTT	TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCAT CTCCGTTACA ATATGAAAT	TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTTGC ATTAGATTTG ATGAATGATA	TATACTTACC GGATAAATTA TAAAATTGGT	1380
TATTTAAAAC GGTATTTTA CCCTTGAAT	CCTCAATAAC AATTCCTTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA	ATCTCAAATG GTTCGTCAAT GGTTCCTGAT	60
ACGTATTTTC CGTCTTTCTT CCGTTGCTTG	ACACACTCTG TGAGGAGATA TTCGATTTGC	120
CCATGACTG AACGAAAGTC GTCTTCTGCC	CATGATGCCA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTTA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG 240
 TGTTGACAAT TGGTTGTGCA TCATGATGTC CACAAAGAAC GACAAGGAGA TTTGAAACCA 300
 TGGCAGCTTT TCGTTCCTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTCTAGTG 360
 CCATTTCAAC CATTCCTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG 420
 ATGCTTGTTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA 480
 TACGTGCTTC AAGGATTTC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCTTCACGAA 540
 TACGGGTAGC AACAATTCG CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC 600
 CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC 646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTCAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTTGAG 60
 GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTTGCCT 120
 AAAATTGCCG AGATTCGTGC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT 180
 ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTTGTTAA GGTGGTATT 240
 GGACCAGGTT CTATCTGTAC TACTCGTGTG APTGCTGGTG TTGGTGTTC GCAAGTAACA 300
 GCTATCTACG ATGCTGCAGC TGTTGCGCGC GAATATGGTA AAACGATTAT TGCTGACGGT 360
 GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTATG 420
 CTTGGATCTA TGTTTGCTGG AACTGATGAA GCTCCAGGCG AAACGAAAT CTTCCAAGGA 480
 CGTAAATTC AACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAAGC 540
 GACCGTTATT TCCAAGGTTG TGTCAATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA 600
 GGTTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT 660
 CGCTCTGGTA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA 720
 TTTATTGAAA TGTCTGGTGC TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTA 780
 AATGAGGCAC CAAATTATTC TATGTAAAA ACAATGAAAA GAACTCCAGT GAAAACAGGA 840
 GTTCTTTTAC AATGTTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG 900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TGTTTGTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTAACTGTC TAGTGTGTC AAGTTCACCTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTTGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT	1260
TGTTTGTGAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATTT TTTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCAATCG AAGGTGCTCC TTTAATTAGT TGTAATCTT CAGGAGCAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTTTGT AGTTTAAAAT TACTCCCAT CTTCTTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAA ATACTAGATT CTATTTTTTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTGTAGTCC CAGTCCCAGT ACCGGAGAAA	180
TATTGTTTTA ATATAATATC TCTTTTGTG TTCTAAGCTC TTAAAAGCAA AAGAACAAGT	240
AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTATATCC ATTTTCAA TCAAATTTAT TCAGACTATA	420
TATGCACATA TACACTTAAA TTCATATAAA AACATGGCTT GTAAAAAATT ACTTTAATCA	480
CAATAATCGC ATTTAAAATT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGAAGT	540
TTCCCTTGT ATCTTTTATA ATAGATAGAA AATTGCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTATAGG TAGTTCAGTG TTTAAAAGAA GAGTTCAGC TACATTCATT	660

1355

CTTTTCTTT GAGTGTACTC TGTAATGCTT TGACAATATT TTTCCTTAAA TAAATTTTTT 720
 AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTAC ATTCGTTGCA 780
 AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT 840
 TTATATTTTT TTCTATTTAA GTATGTGTC AATTACTATAC TTATCCATTC ATTTGCCTTT 900
 GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC 960
 ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAAA 1020
 GATTCTGGAT TAATGTTAAT AGATGCTAAA TGTTTTTCTA TTAGCTCTTT TTTAAAACcm 1080
 ATGGAACACG CAAGATAACA ACAATTCTCG TGAATAAAAA AAACAAAATT ATCTTTTATA 1140
 TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATPAAACTTT 1200
 TCTCCGTTG CACTGACAAT GTAACCTGAA TAAATTGAAA CATAGTCTGA CATACTATAA 1260
 GTGCTATTTT GAACTACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG 1320
 CCTCCTTCAT AAAACCGGTA 1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTG ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAAGTT 60
 GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GTTTGTATCC GGCCTTATTT 120
 GAAATGAGA AAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT 180
 TTTGCACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCTTCA ATTGGAATAT 240
 AGTGATTTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA 300
 GAATTTTATG CCAATGATCG AATAGATTTT TTTTCTTAG GTGATTTTAA TGAGGTTGAA 360
 ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTTCCAG 420
 TATTGTCAAC CTTATCTTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA 480
 TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC 540
 ATGGATGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC 600
 CGGGAAA 607

1356

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAATACC GAATTTTGTGTT TTGTCCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAAGATATAA CCAAAATAGT TGTCATTTGC TTTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATTG ATTTCCAAAA	180
GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC	240
TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATGTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTTCGCTT ATTCTCCAGC TTTTCTTTGT	420
AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTGATAAT TACCATTGCT TTTTTCATTG	480
ATTTTATCCT TAATTTTAAA CAGAAATGTT TACATTTTCGT CGTATGCAAG TAAATGTAAT	540
CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCCATCGC CTAACTACAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG	660
CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAWGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTCG CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT	780
CTCTACTTTC AAGAAAGGCG ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA	840
AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT	900

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTCTGGC ACACTGGTCT TGGAATACGG CAAAACCTCT GAAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA	120
TGCTTTTGAT CGCGGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC	180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATTG AGGAATTCGC TGGTGAGTTC 240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA 300
CTGCGCAGaA GcATTAACAG AAAGGAAGCC TATGACCTTT AAACTTCTCA GCCAAGAAGA 360
ATTCATCCAG CATACTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC 420
AGAGCTGCTG AGCAAGCGTG GCTFCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG 480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC 533

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACCT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG 60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC 120
TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG 180
AGGTTGCAGA TAGAACTGAC GAAGTCAnnA ACCACACCTA CGGCAAAGTG AATCTGAAGT 240
GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC 300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG 360
TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG 420
AGCAGATTAT AGACTATCAG GGAGCTTGA TTATGCCTGG TTGGTCAAT TGTCACACCC 480
ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA 540
ATGA 544

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTTCCCT TTTTGTATA TTTTCAAAT AACGCCTCTA 60

1358

CACTATTTGT AGCAAATFCA CCAACTACAG TTGTATCTTA GTTAAAATAA GTTAGAATAT	120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCATCT AAGGTATATT CAAAATACAA	180
AAGTTGACCA ACTAGATTTT TGAATATCCT TATATATCCA TTCTTAAAAT TGGTTTAAAT	240
AGCGTAGTCT TTTAAACTAG TTTTGAGAAT CCAAAAAATC TTCCTACATA TGTAAGAAGA	300
TTTTTTAGTT CAGAATGATT AGATTTAGCT AATGGATACC TATCCTACC	349

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC CACACCAGCA ATGGAAATAA TTCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAAATTG AATCAATTTC GTGATTTGTT TCTGACGCTA	120
AATTTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTTAGGAT AGTTGTTAAT CCACTTTTCG ATGAATGCGA CTTCTTTGGG AGTCATTTTC	240
TTGGTTCCT TAGGTAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTCCCAGG	300
ATCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC	360
GATGACTGGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT	420
CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTT	540
ACACCGCATA TGGTGCCTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTTT CACCGTCAATC	720
ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCTA TTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTCTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC	840
TATTTGTTTA TTTGTCTAAA TACATTCAA TATGTATCCG CTCGTGAGAA AATAAACCTG	900
ATAAATGCGT CAATAATATT GAAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTGCG	960
CCTTATACCC TTTTTGCGG CATGTTGCCT TCCTGTTTTT GCTCACCCAG AAAACGCTGG	1020
TGAAAGTTTA AGATGCTGAA AAATCATTTG GGTGCACAAC TGGGGTTACA TCCAACCTGA	1080
ATCTCCANCA GCAGTTAAGA TCCTCTGACA GTTGTACACG CCGCAAGAAC TATTCCCGAT	1140

1359

GAATGAGCAA CTTTAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTGTAG 1200
 GCCCCG 1206

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT 60
 GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTGCGCCTT ACCGTATGTC AAAAGATTTT 120
 TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAECTCA ACGGATCCCT TACTCATTTA 180
 CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG ACAAAAAATA TCTGCTAGAT 240
 ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300
 TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360
 TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC 420
 TTGCAGACTA GAGCCAGTGA CAAATATTC TTGGCAAAAAG AAATGAACGC CTTCTACCAG 480
 CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA 540
 GGTGTCAACA AGGCCTTTC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA 600
 GATTTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG 660
 GGTATGCCA TGAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC 720
 CTTACCAACG ACCAAGATGG GGTGCCAAA ACCCTACAAG ACTTATTCCT ATAACCTATA 780
 CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGGAGA TTGATGATGG 60

1360

ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAAC TTT TTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTTATGCT AACTTACCTT ATGCCCAAGC GCCAGGTATG GGA CTCAATG	300
CCTTCTTTAC CTTTACAGTT GTATTTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGATT ATTTTCATGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCCAAT GCTCTTCGCT CAGCTATTTT AGCTGGTATC GGTGTCTTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTGTG AGGAGAAGGG GCTGACAAAG CTCACGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGTCTGTGC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTT CACCAGTATC GATTATTTAA	240
TTATTTAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGCGGAG TTTAGTTGCT GCTTATGTCG	360
TTAATTTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTGCTT TGCAATGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTGCGAG ATTAGTCCGG	660
TGTTATCCTC TATTCGGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATTGTGC	720
CCTTAGTATT CATTCTACTT GGACTATACA TCATGTATGA AAATGGCACG ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT 840
 CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG 60
 GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120
 CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG 180
 AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240
 AGAGAACAGA GTTAGTAAAC CTAAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300
 ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360
 AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCTTGT AAAGCCTGAT AGATAATGCC 420
 ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAAATCATC TGACCAAATA AGATCAAAAA 480
 CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AAACCTGACTA GGAGACTTAG CATCTGATGG 540
 GAAATAAGTC CACGACTCTT TTCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA 600
 TTCATAGATT TTGAAAAACT CCATAACGCC GATAAACAG AAAAATCAA TAAACCTGTT 660
 GAAGGTTGCG TCAAGACTTC TCTGGCTATT TTTCCACAC CTTTCATAGAG GCTTGGGGGG 720
 CAGACGTCTT TCATAAAGCC CAAAATTTCT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 707 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGCACAAG AAGTCAGGAT 60
 TTTTATGCAG GTTGGGCGCT TCATCAGACA GGGAAGATTT ACAGCGACTA TTATGGAAGT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC 180
 TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG 240
 ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT 300
 CTTGCTTTTG GTGGAGGCTA TCGGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT 360
 AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTTGT ACGGATTGGG 420
 CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATGCTGTA 480
 GTGAGTTTAG GCTTGTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTTAT 540
 CAGTTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAACCTGC CTACTATAGT 600
 GCTGCAACAG GAAGTTTTGG GGATGCGwTT AGTGGTATTC GTTATCCTAT TGACAGTATT 660
 CGCTTTGATT TTACTTCTAA AATTTTAGAG AATATGTTTT TTTAAGG 707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTTGACGA CGTATATTCC AACATTTTC CTCAGTCAAA 60
 CGTTGGCCAT CAATTACAAT CTCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA 120
 ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC 180
 ACGTGAAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA 240
 GATTTTTTAC ATCAATTATT GATTTCAATT CGAACCAAAT GTCCCTTTAA ATACATAGGC 300
 ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG 360
 AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA 420
 AGTTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAGTTT CAACCAATAA 480
 AAGCCTTAAA CCTGTACAG CTAACCTACG ACAGATAATC ACTGCAACAA TCCAAGCCGG 540
 AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT 600
 AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC 660
 TAAATAGTCG GTAATACTGG CAACAGCAA GATAATAGCT GCAACTATAT GACTCTCTAT 720
 CGAATTTCTT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA 762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

CTTTTGATAC ACTTAAACTA TGAATACAAA TCTCAAGCCC AACTTCAGC GTTTGTCTTC      60
TGCGACTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT      120
CAAGTGCTGC AACCGTCATT CTTTGTACTT GCGGAAATTT GGCTATGTCA ATCTAGTCCC      180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT      240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA      300
AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTTCT GCAAACCTACA      360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT      420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCAGACT      480
TC                                                                              482
    
```

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```

TTTATTTTAA TAAAGTCAAT ACCTGTCTTT ACTTTTCTT AAAAAAGTT TATTATGTTC      60
TTTAAGGAGG TGTA AACAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAT      120
ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAA      180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTTACCAA ATAAAGAAAA CCTACTAAAA      240
ATTGCATCTA TTGAAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT      300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC      360
TCTTTACACG ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAATAC CATTTCTAAG      420
ATTGATATAC AAATTTTACA CGAAACGATC AAAAAATTA TTGATTTAGC TATCGAACAA      480
TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT                                520
    
```

1364

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1003 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```

GCATCAAATC GCCCATCAAA GAAGTTCCTCT GGATTTACCA AGACCAGTCA AATAGCTTAG      60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG      120
GAACCATTTG TGAGCGCTAT GGTGCCGTTG TTAAGAAACA CGACATTATC AATAAGCTTC      180
TCAAACAGTT GGAAACCAAT CCTTGGAACC GCCGCAATAT TATTTGCTC TGGGATTACC      240
AAGCTTTTCGA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTT      300
GGCGTGTGTA TGGGGAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC      360
TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC      420
ATTTTGGCTG GAAGGTTGGG AAGTTCCTCT ACTTCATCAA CAACCTCCAT ATCTATGATA      480
ATCAATTTGA ACAAGCTCAG GAATTGCTCC GTCGGGAGCC GTCAAACTGC CAACCACGCT      540
TGTTTAAATA TGTTCCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT      600
TGGTGGATTA TGACCTGTT AAGCCACAGT TGAAGTTGA CCTAGCTATT TAAAAGAATA      660
GAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTGTTC TTAACGTGAT ACGCGCGGAC      720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTTCGATTA      780
CTTCTTTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG      840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG      900
CCAGCCTCCT CAAGAGGTCA CATTTCCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA      960
CGAAAAAATG GGAATTTTTC AAGGAAAAAA GATGAGAACA AAA                          1003
    
```

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```

CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC      60
    
```

1365

TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATTT GCTGGTTGTG AGAGAACAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCCTAGCTC CTTTTTGTTT ACGATTATT TCTCTCTTA TGGCGTTCGT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCTGGAGCA TATTTTTCTT CCCAATTATC	300
TGGTTTTAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTCTT GGGTCCACCC CCATCAAGAC	420
AAAAC TGCCG TAGGTGAAGT AAAGCGTGC AATCAAGGCA TCCACTTGCC CTATCAAATC	480
TTGCTGAGCA GGTGTCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC	600
CAATTCTTCT ATTTTAAAAC CAGCCCTATG GTTTGACCCC TCTAAATCCC AAGCTCGAGG	660
TTCTTCTTGG GTTCGTTCAT CCATCATGTG GTGAAAGTC TTGACCTTAT TGAAATGATA	720
GTCACGGCTG ACAAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAC TGGGA TAATGACTTT GGTACGCAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCATTTTGT CTTGGATACC TACCGGATTT TCACCATAGT	360
TATTCAAAGC AACATCAAT TTAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT	420
GAGAACTGC ACCATGATAG ATGGTCCAC CTGGTGTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCAGT TCACCGCCTG TCTCATCAGC	540
ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA      60
GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA      120
ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCATTGTT GATATCGACT      180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA      240
CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTTCAACTT TTGCTTCTTT GATAGCTTTA      300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA      360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTCAG CCATACCACC GTCTACTGAG      420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCAA      480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC      540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG      600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTC      660
ACTTCTACAA GTG                                                    673
    
```

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

```

GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAACTA TGGAGTAGGT      60
TGGACAGGAA CTTTTGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT      120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAC CTGAGGCATG GGCTAGAGCT      180
TCCCTACCA AGATTCCG                                                    198
    
```

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 891 base pairs
 - (B) TYPE: nucleic acid

1367

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG	60
GACCAATCCA CTACTAATCC TAAGAACAAA ACACTCAAGA GAGCAGAAGA GAGAGGTTCA	120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG	180
AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA	240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA	300
ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAAGG TTGGGGCAAG	360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGGCGTC	420
ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC	480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG	540
AGGATAAAGA CAGGGCTAAT AAAGTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT	600
ACACAGAGAT AGAAAAATA CTGAACTGAA AAAATCCCA AAATAGCATA GGCTAAAAAG	660
GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA	720
GACCAAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA	780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG	840
CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A	891

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCGTTC AATAGAACAT TGCTTTPTTA TTTTATAGAGT AAGCTAAGCG CTTCAGCATC	60
TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC	120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT	180
AATAGACTTG GCATCCAAAA TGTTTTTAAT CCCCATGAA ATAGCTTGGG TTGGGACGTC	240
TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG	300

1368

ATGCGTTTGA CTGTCAAATG GAGTG

325

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TGCGAATTTA AAATACAAAT ATGGCAATCG	60
CAAGTTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCG	180
AGTCAGTAGA TCCGTTTACT GCGGAAATAA ATAAGAGGAA GTAACGTnAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGTT	344

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 692 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGFACTTTC TGCTGGACTC TATCTTCTTC TAGGTGCTAT CGGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGT	300
GTAAAGATTT TTCTTGCAA CCTCTTGGGT GATGCCCTTG TCTTTGTCCG CGGGATTCTC	360
AGCTTGCATT TCCTAGCTGG AATGGCATT GAAAAAGCTC TTGCTGTGGG GGTCTTCCC	420
TTTATCATT CAGACCTTGG CAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCCT TTTCTTTTAT TTTGAAACT TATACTCAAT GAAAATCAA GAGCAAATA	600
GGAAGCTAGC CGCAGGCTnG CAAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1005 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTTTT TCGATAATGT CGGACCTCTT	60
GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTCC ACTTGATGAA GGAAATGGGA	120
GTTAATTCCT TCCGCACTTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT	180
GAGCCTGATC CAAAAGGTAT TGCTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTTAC CAGTGGAACT TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTGC CAAGACTGCT	360
TTCACATGCT TTGGAGATAA GGTTCATTAC TGGACAACCT TCAATGAGCC AATGGTCATT	420
CCAGAAGCAG GGTACTTATA TGCTTCCAT TATCCAATC TAAAAGGAAA GGGAAAAGAG	480
GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATCA ACTATATCGC	540
TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA	600
AGTAATTCCT CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC	660
TTCTTGAATC CAGCTGTTAA AGGAACCTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT	780
GATTTCTTG GAGTAAACTA CTACCATCCA AAACGTGTTT AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA	1005

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 973 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTA AAAA GAGTAAACTA TTAAGTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAGAATG AAAATTAATA AAAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTTGTTC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAAGGCA GAAAACCTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTT CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATGCCG ATAATATTCC	540
GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAACCT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCCT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCG TCAAACCTCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGTAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA	240
TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCTTGAT GGTGTTGATG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGGG CATTTCAC ATGTGGCTA CCTGGAACAC CGATTCATT CGCTGCCATG 420
 ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA 480
 AGTGTTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGGAG TCAAGTCTTT TGCCAAGTCT 540
 TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCTATCT TGTTCCTGGAT ATCCACTTG 600
 GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA 660
 ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGAAAGA AGAAAGTTC 720
 ATAACAAGCG TGTCCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA 780
 TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTCCCGGGn TCCTCTAGAG 840
 TCG 843

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTTA TTTATTATTT TTGGCAAAA AAGACCAATT TGCTTTGGAG 60
 CATTGCTTCT GCATTAAATT GTCTATTTTT GTCGTGCTG TTACGCTCTT TGTATCATGT 120
 ATTAAGTAGC AAGTGCAACT TGCAAACACT TAGTAAGAGG AGAAAAACA AATGGTTATG 180
 ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA 240
 GACTTGAAG TACCTGCATC AAACATCAA AAAGGGATTG CTGAAATCCT TAAACGCGAA 300
 GGTTTTGTA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT 360
 CTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA 420
 GGACTTCGTG TCTACAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGAATT 480
 GCCATCCTTT CAACTTCTGA AGGTTTGTCT ACTGATAAAG AAGCACGCCA AAAGAATGTT 540
 GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA 600
 GCAAAATTAG GAAGTTGGAG AAGTTTGTTT ACAAACAGGC CAACTTATCT ATTTTGCACA 660
 GTTCTTAGAG CGTGTTCAGT TCAGCTCTTG AGCTAAGTAA GATCTGAAC CCCGTGAAAA 720
 CTGGCCGTGC TGGCATGTT CCGGTAACAGG AGAaATAAA CATGTCACGT ATTGGTAATA 780
 AGTTCAGCTA AGGCCTTCGT AAAAGTT 807

1372

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC	60
TTAACCATCT tTGAACAAAA TCCTCAGGCT CAGGTCAC TA TTTTCGGTGC CTTGGGTGGC	120
CGTATTGACC ATATGTTGGC CAATGTCTTT CTGCTAGCA ATCCTAAGTT GGCACCCTAT	180
ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC	240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC	300
CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTTAAAAAA GTGTACGCTT CTAACGAATA	360
TATAGATAGG GAAGTGTCGG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCATAGCAA	420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATTGCCAAT CTAGCTGGTC	480
TCTTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG	540
ATCAGGCAGA TCATTTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA	600
GCCAGTTAGA CAAAAAGAT TTGGAAGTGG TTGTCAGCGA CCGTTTGCAA GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 641 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCGAGCCAT CGTGTGCAAT	60
GACTCTTCCC GATGTAATCT TGTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG	120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGCGAGTT GACCAGTCAG GAAACAGATG	180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTTA CCTAAAACAA GCCTTCCAAG	240
AAAATAGCAA CCTCCTAGAG CAAGTGGTAG AACCTTGAC TATTATCACT GGTGGACACA	300
ACCACAAGGA CCAGTTGACC TATGCTTGGG AAACACTTTT GCAGAATGCG CCACATGATA	360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGCGAGAT GGAAACGCGT TTTGCCAAGG	420

1373

TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAG GGTA AAAATTG 480
 CTACGGATAA GGCTCAAAGT GACTATCTCT TTACTGTCAT TAACACAGGC TTGCATGATA 540
 AGGTCGATAC TGTCAGCACA GTGATGATG TGGCGACTTG TGATTTCAAG GAATTGCACC 600
 CAACAGAAGG CTACAAAAG ATGGCTGCTC TTATCTTGCC G 641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1958 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA 60
 TTTGCCATTC CAGCAAGTAC TCAAAGCTT TACTTATCAC CAGTTT TAGA TGGCTTTAAT 120
 AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCA ACT TAGAACAAGT ACAAACAATG 180
 TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC 240
 TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT 300
 ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTCTT TGGCATTFTA 360
 AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA 420
 GCCATTATAG ACTATATTGA TTACTACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA 480
 CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTTGG 540
 GGTCAGTACA AAACCTTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTCTT 600
 CTCAAATCGA GTTTTTACTC AATTTTCTTA CTTGATTGGG ATTGAAATTC CAATTAATTT 660
 CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT 720
 CAAGAAAAAT TCTTGAATGG TTTGATTTTC AGGCTCACGA ATAGCACGGT GTTTGTTTGA 780
 GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA 840
 ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCAGGTG 900
 TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTTCTCCG ATTTTCTAAT TCTATTATAG 960
 CACTTTTTGA ATAAAGTCGC TTGATTTATA CTCAATGAAA ATCAAAGAGC AAAC TAGGAA 1020
 GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT 1080
 TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG 1140

1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTTGTAC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTCGT CAGCTTGTCG GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCAATTTT TCCACATGGT AGGAACCAAG CACCATTGCG TTCTTGAACA	1440
AGAACAATTT GTTTTTGTTC AGGATTAGGG ATAACTGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACCTTTTT TCTCCGAAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTTTCCA AATCTCACGT AATACCATTT ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAAATA AATTTGGGAT AmACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATGTGT TAAGAATTAA TGA CTGAGT TTCGTTAGAT CTTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG	600

1375

TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG 660
 CTTGATGAAA GTACTCAATt TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA 720
 TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCOA GGCCAATTTG AAGGCTCTAA 780
 AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCAGTAA GTACTTAAAA 840
 GCTTTACTTA T 851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAAGTGTAAA AAGATTTTCGw 60
 CCAATTCAGG GTTGGAGCAT CGCAAATAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA 120
 AACGGGATAA GGTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTTT GGAAAGTAGG 180
 CATCAGCTGA CAATTCCTTA CAAGCATAGT CCGTTCATA ACCTGTTAAC AGTTGAAAGA 240
 GGAAGTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA 300
 CTAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAGA 360
 TAAGACCACC ATACTGGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT 420
 TTTGGAAGTG ATGATTTGGT AAAGTGTCA TGTGAGTTTC CTTTCTTTT GTGTTTTTTT 480
 CTACACTTAT ACCATAAAGG GGAAACTCTT TTTGTCTAG TAAAAACAC CCATTGGGTG 540
 AAAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG 600
 GGGTGAATAA TTGGGGTTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAATTAC 660
 TCATCAACCT TTAGTGGAAA TCCAACFACA TTTAACTATC TATTAGACTA TTACGCTGAT 720
 AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG 780
 GTAATACCTT TTTGAGGTGC TTTTGTGATAT GAGCCCATGT TTTCTCAATA GGATTGACT 840
 CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA 900
 ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTAATG 960
 TTGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GCTCGTCATC GTCTCTTCGT 1020
 AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT 1080

1376

ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC 1140
 GATAAAAATA AGTATCGAAT CCTGTTTC 1168

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CCGCTTCAGC 60
 GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC 120
 GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC 180
 TTCAGCAAGC ACAAGTGCCT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC 240
 GAGTGCCTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA 300
 ATCTGCATCA ACCAGTGCCT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC 360
 CAGTGCCTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC 420
 ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC 480
 ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGCCT CAGCTTCAGC 540
 AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC 600
 CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC 660
 AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCCTCA GCCTCAGCAA GTACTAGTGC 720
 ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC 780
 AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAGTGC 840
 GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGCCT CAGCCTCAGC 900
 AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCC GCTTCAGCAA GTACTAGCGC 960
 CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGCCT CTGAATCGGC 1020
 ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC 1080
 ATCGGCTTCA GCATCAACGA GTGCGTCCCG TTCAGCAAAGT ACTAGCGCCT CAGCCTCAGC 1140
 GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGCCTCT GAGTCAGCAT CAACGAGTGC 1200
 GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CAGCCTCAGC 1260
 ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCCTCA GCTCAGCGTC GACAAGTGCs 1320

1377

TCrGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC	1440
TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT	1500
AGTGTCATCAG CTTCAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCCTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAGTGC TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCGG CATCAACAAG TGCTCGGCT	1800
TCAGCAAGCA CCAGTGCCTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG	1860
AGTGCCTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC	1920
CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACCAGTG CCTCGGCTTC	2040
AGCAAGTACC AGTGCCTCAG cTTCAGCAAG CACAAGTGC TCAGCTTCAG CATCAACCAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCTTC AGCATCAGCA TCAACGAGTG CGTCACTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGATC CAGCCTCAGC AAGTATCTCA	2220
GCGTCTGAAT CGGCATCAAC GAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACCAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAGCTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACGAGTGATC CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCCTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA	2520
GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAGT	2580
GCGTTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACGAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCCTCT GAATCAGCAT CAACAAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGATC CGGCTTCAGC ATCGACAAGT	2820
GCGTCTGAAT CGGCATCAAC GAGTGCCTTC GCTTCAGCAT CAACGAGTGC GTCAGCCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC GTCACCAGT	2940
GCGTTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCG 3120
 GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA 3180
 GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT 3240
 GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG 3300
 GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT 3360
 GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA 3420
 ACCAGTGCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG 3480
 GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT 3540
 ACCAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG 3600
 GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT 3660
 ACCAGTGCGT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA 3720
 GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT 3780
 ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCCTCG 3840
 GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT 3900
 ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA 3960
 GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA 4020
 ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG 4080
 GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA 4140
 ACAAGTGCAT CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCCTCA 4200
 CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TCGGTCACTT CCGCATCAAC 4260
 AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC 4320
 TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCCTCGGCT TCAGCAAGTA 4380
 CCAGTGCGTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGGC 4440
 TTCGGCATCA ACAAGTGCTT CAGCATCAGC ATCAACGAGT GCG 4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC	GTCCTTCCGC	CTCAACCAGT	GCCTCCGCTT	CAGCAAGCAC	AAGTGCCTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCGGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACTT	CCGCCTCAAC	CAGTGCCTCG	GCTTCAGCAA	GCACAAGTGC	180
GTCAsCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	TGAGTCAGCA	240
TCAACGAGTA	CGTCAGCCTC	AGCAAGCACA	TCAGCTTCTG	AATCGGCATC	AACCAGTGCG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCTTC	AGCCTCAGCG	360
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	420
TCAGCAAGTA	CTAGTGATC	AGCTTCAGCA	TCAACGAGTG	CATCGGCTTC	AGCATCAACC	480
AGTGCCTCGG	CTTCAGCGTC	AACCAGTGCG	TCAGCTTCAG	CAAGTACCAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGACAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACAAGTGCG	TCGGCCTCAA	CCAGTGATC	TGAATCGGCA	660
TCAACCAGTG	CGTCAGCCTC	AGCAAGTACT	AGTGATCAG	CTTCAGCATC	AACGAGTGCA	720
TCGGCTTCGG	CGTCAACCAG	TGCATCAGAG	TCAGCAAGTA	CCAGTGCGTC	AGCTTCCGCA	780
TCAACAAGTG	CCTCGGCTTC	AGCAAGCACA	TCAGCATCTG	AATCAGCGTC	AACCAGTGCT	840
TCGGCTTCAG	CAAGTACCAG	TGCTTCAGCT	TCAGCATCAA	CCAGCGCCTC	GGCCTCAGCA	900
AGCACCTCAG	CTTCTGAATC	GGCCTCAACC	AGCGCCTCGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCTTC	GGCTTCAGCA	1020
AGCACAAAGG	CCTCGGTTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAGTGCT	1080
TCAGCCTCAG	CATCAACAAG	TGCGTCAGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACAAGTGCT	1200
TCAGCCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCATC	AGCGTCAACA	AGTGCTTCGG	CTTCAGCGTC	AACGAGTGCG	1320
TCTGAGTCAG	CATCAACGAG	TACGTCAGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	TACCAGTGCG	1440
TCAGCCTCAG	CAAGTACCAG	TGCTTCAGCC	TCAGCGTCGA	CAAGTGCGTC	GGCCTCAACC	1500
AGTGATCTG	AATCGGCATC	AACCAGTGCG	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGATCG	GCTTCGGCGT	CAACCAGTGC	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACT	TCCGCATCAA	CAAGTGCTTC	GGCTTCAGCA	AGCACATCAG	CATCTGAATC	1680
AGCGTCAACC	AGTGCTTCGG	CTTCAGCAAG	TACCAGTGCT	TCAGCTTCAG	CATCAACCAG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAAGTGGC TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGGC TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCCTCAG CTTAGCAAG	2280
TACCAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTAGCAAG	2400
TACCAGTGCG TCAGCCTCAG CGTCGACAAG TGCCTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GGCCTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAGTGCG TCAGTTCAG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TCGTTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAC	120
CTCAGCAAGT ACTAGTGAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAGTGC GTCAsCTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCGTCGG CTTAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCCTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCGTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAGTGGC TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600

1381

TCAGCAAGTA	CCAGTGCCTC	AgCCTCAGCA	AGTACCAGTG	CTTCAGCCTC	AGCGTCGACA	660
AGTGCGTCGG	CCTCAACCAG	TGCATCTGAA	TCGGCATCAA	CCAGTGCCTC	AGCCTCAGCA	720
AGTACTAGCG	CCTCAGCCTC	AGCATCAACG	AGTGCCTCCG	CTTCAGCAAG	TACTAGTGCA	780
TCAGCTTCAG	CAAGTACTAG	CGCCTCAGCC	TCAGCGTCGA	CAAGCGCCTC	AGCTTCAGCA	840
AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGCCTCCG	CTTCAGCAAG	TACCTCAGCG	900
TCTGAATCAG	CATCAACAAG	TGCGTCGGCT	TCAGCATCAA	CGAGTGCATC	AGCTTCAGCA	960
TCAACAAGTG	CTTCAGCTTC	AGCAAGTACC	AGTGCCTCCG	CTTCAGCATC	AACGAGTGCT	1020
TCAGTCTCAG	CGTCAACCAG	TGCCTCTGAA	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	1080
AGCACCAGTG	CTTCGGCTTC	AGCGTCAACG	AGTGCCTCTG	AGTCAGCATC	AACGAGTGCG	1140
TCAGCCTCAG	CAAGCACATC	AGCTTCTGAA	TCTGCATCAA	CCAGTGCCTC	AGCTTCCGCA	1200
TCAACAAGCG	CCTCGGCTTC	AGCAAGTACA	AGTGCCTCAG	CCTCAGCATC	AACCAGTGCA	1260
TCAGCTTCAG	CCTCAACAAG	TGCTTCAGCC	TCAGCGTCAA	CCAGTGCCTC	GGCTTCAGCA	1320
AGTACCAGTG	CGTCAGCTTC	AGCAAGCACA	AGTGCCTCAG	CTTCAGCATC	AACCAGTGCT	1380
TCGGCTTCGG	CATCAACAAG	TGCCTCAGCA	TCAGCATCAA	CGAGTGCCTC	AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA	CACCGTGCTG	ACCAGCACCC	GTTCCCTGCGA	TAATTTTCTT	TTTACCCATG	60
CGTWTGGCAA	GCCAAACTTG	TCCTAAGGCA	TTGTTAATCT	TGTGGGCTCC	TGTATGGTTA	120
AGGTCTTCCC	GTTTGAGATA	AATCTTGCTC	CGCCAATATG	CTGGGTCAAG	TTTTTTGCGT	180
AATAAAGAGG	AGTTTCACGT	CCTACGTA	GGCGAAAAG	CTGGTTAAT	TCCTCTTGGA	240
AACTTGGGTC	TGCCTGACTT	TCACGGTAGG	CCTTCTCCAA	CTCCAAAAC	GCTGTCATCA	300
ATGTTTCTGG	GACAAAACGT	CCGCCGAATT	TTCCGTAAAA	TCCATCTTTA	TTTGGTTTCT	360
GATATGCCAT	GCTTTACCCT	CTCTATAAAT	CTTCTAATCT	TTTCATGATC	TTTTTGTTCA	420
TCTGTCTCCA	CTCCGCTCGA	TACATCTACT	GCATAGGGAG	TAAAGTGTG	AATTGCTTTT	480
ACTACATTAT	CTTCATTAAG	GCCACCTGCG	ATAAAGAAGG	GCTGTGCTAG	TCCAGTCGTA	540

1382

TCCAGTTGAC	CCCAATCAAA	GGGCTGGCCA	CTTCCTGCCA	CAGGGGCATC	AAAGAGTAGA	600
TAATCTGCCT	GAGAATTGGG	GACATGCCCA	TTTCCATCTA	CCTGCACAGC	CTGAATACTG	660
GCACAAGGCA	AAT'TCTCAA	TAAATCATCT	GCCACCTGAC	CGTGAACTTG	AACCAAGTCC	720
AAGCCGGGGA	TCCTC					735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC	TCAGCCTCAG	CGTCAACAAG	TGCATCGGCT	TCAGCATCAA	CGAGTGCCTC	60
CGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCATCGG	CTTCAGCGTC	120
AACGAGTGGC	TCTGAGTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	180
TGAATCTGCA	TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	240
TACCAGTGGC	TCAGCCTCAG	CGTCGACAAG	TGCGTCCGCT	TCAGCAAGTA	CCAGTGCCTC	300
AGCCTCAGCA	AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGCCTCGG	CCTCAACCAG	360
TGCATCTGAA	TCGGCATCAA	CCAGTGCCTC	AGCCTCAGCA	AGTACTAGTG	CATCAGCTTC	420
AGCATCAACG	AGTGCATCGG	CTTCAGCATC	AACCAGTGCA	TCAGAGTCAG	CAAGTACCAG	480
TGCGTCAgCT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	540
AGCGTCAACA	AGTGCTTCAG	CTTCCGCGTC	AACCAGCGCC	TCGGCCTCAG	CAAGTATCTC	600
AGCGTCTGAA	TCGGCATCAA	CAAGTGCCTC	GGCTTCAGCA	TCAACGAGTG	CATCAGTCTC	660
AGCAAGCACC	AGTGCGTCCG	CCTCAGCAAG	CACCAGCGCG	TCTGAATCCG	CATCAACCAG	720
TGCCTCAGCT	TCAGCAAGTA	CCTCAGCATC	TGAATCAGCA	TCAACAAGTG	CATCGGCTTC	780
AGCAAGCACA	AGTGCTTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCCG	CATCAACGAG	840
TGCGTCCGCT	TCAGCAAGTA	CTAGCGCCTC	AGCATCAGCG	TCAACAAGTG	CTTCGGCTTC	900
AGCGTCAACG	AGTGCGTCTG	AGTCAGCATC	AACGAGTACG	TCAGCCTCAG	CAAGCACATC	960
AGCTTCTGAA	TCTGCATCAA	CCAGTGCCTC	AGCCTCAGCA	TCGACAAGCG	CCTCAGCTTC	1020
AGCAAGTACC	AGTGCGTTCAG	CCTCAGCAAG	TACCAGTGCT	TCAGCCTCAG	CGTCGACAAG	1080
TGCGTCGGCC	TCAACCAGTG	CATCTGAATC	GGCATCAACC	AGTGCCTCAG	CCTCAGCAAG	1140
TACTAGCGCC	TCAGCCTCAG	CATCAACGAG	TGCGTCCGCT	TCAGCAAGTA	CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCGTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG AGTGCTTCAG TCTCAGCGTC	1500
AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCGTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TCGTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 941 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACCTCAG CAAGCACAAG TCGGTCACTT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACCAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTCAGCAAG CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCGTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAAGTGC TCTGAATCAG CATCAACAAG TGCCTCGGCT 900
 TCAGCAAGCA CCAGTGCCTC GGCTTCAGCA AGTACTAGTG C 941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA 60
 GTGCATCAGA GTCAGCAAGT ACCAGTGCCT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT 120
 CAGCAAGCAC CAGTGCCTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA 180
 GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT 240
 CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA 300
 GTGCGTCTGA ATCGGCATCA ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT 360
 CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA 420
 GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CCGCTTCAGC GTCAACGAGT GCGTCTGAGT 480
 CAGCATCAAC GAGTGCCTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA 540
 GTGCGTTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT 600
 CAGCGTCGAC AAGTGCCTCG GCTTCAGCAA GTACCAGTGC CTCAGCCTCA GCAAGTACCA 660
 GTGCGTTCAGC CTCAGCGTCG ACAAGTGCCT CCGCCTCAAC CAGTGCATCT GAATCGGCAT 720
 CAACCAAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT 780
 CCGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCCTCA GCTTCAGCAT 840
 GCAACAAGTG CCTCGGCTTC AGCAAGTAC 869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA 60

1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA	180
TCAGTCTCAG CAAGCACCAG TCGGTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TCGGTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TCGGTCAGCC TCAGCGTCGA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCGGTA GCGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGCGACTT ATGAGAAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTTAACCAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCCAGCTA A'FCGAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGACTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTG GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGCAGTCA	900
TAAGCGTCCG ATTGGTTCCT TTATGTTTCCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAAGTGC GTCACATTCG GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAAGTGC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCCT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAAGTGC GTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCCTCCG CTTTCAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG ACAAGTGCCT	240
CGGCTTCAGC AAGTACCAGT GCGTCACTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG	300
ACAAGTGCCT CGGCCTCAAC CAGTGCATCT GAATCGGCAT CAACCAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAGTG	420
CATCAGAGTC AGCAAGTACC AGTGCCTCAG CTTCCTGCATC AACAAGTGCC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCCTC AGCTTCCGCG TCAACCAGCG	540
CCTCGGCCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCCTC GGCCTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTTCAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCCTC AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCCTCCG CTTTCAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAGTGCCT TCAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCCTC AGCCTCAGCA AGTACCAGTG	1020
CTTCAGCCTC AGCGTCGACA AGTGCCTCCG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACCAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAGCAAGC CCCAGTGCCT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCCTCT GAATCGGCAT CAACGAGTGC TTCGGCTTCA GCATCAACGA	180
GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCCGyTT	240

1388

CAGCGTCAAC CAGTGCCTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTCTGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTGCCT	360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCAAGTAT CTCAGCCTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCTGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCCTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTTGGGGC GCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA	240
AGTGGTGCGT GAAC TAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTTT	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGGTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTC	CATCGTACCG	CCGAAAATCC	CAGCGCCTCA	GCCATCAAAT	ATCCTATCAA	60
CGTTCTCAA	AAAAGTGACC	GCTCTCTCAT	CATGTTTCCA	AGTGGTAGCC	GCCACTCAA	120
CGATGTCAA	GGGGGCGCAC	ACTskATTGC	CAAAATGGCC	AAGGTCCGTA	TCATGCCGGT	180
TACCTACACC	GGTCCCATGA	CTTTGAAGGG	CTTGATTAGC	CGTGAACGTG	TCGATATGAA	240
CTTTGAAAT	CCAATCGATA	TCTCAGATAT	CAAGAAAATG	AATGATGAAG	GCATTGAAAC	300
AGTCGCCAAT	CGTATTCAAA	CAGAATTCCA	ACGTCTGGAC	GAAGAAACGA	AACAATGGCA	360
CAATGATAAA	AAACCAAATC	CACTCTGGTG	GTTTATCCGC	ATCCCTGCC	TCATCCTTGC	420
TATTATCCTC	GCTATCCTAA	CCATCATCTT	TAGCTTTATC	GCAAGCTTCA	TCTGGAACCC	480
AGATAAGAAA	AGAGAAGAAC	TTGCATAGAA	GAAATGAACC	TTGGCCAAAC	AGCTAAGGTT	540
TTTCAATTTATA	TAGTAGATTG	GwACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTTTGTAG	600
AAATCGATTT	GACTGTCCTG	ATCGATTTGT	CCTAATCTTA	TTTCAATT		648

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT	TTCAGCATCG	ACAAGTGCCT	CTGAATCGGC	ATCAACGAGT	GCTTCGGCTT	60
CAGCATCAAC	GAGTGCGTCA	GCTTCAGCAA	GCACATCAGC	TTCTGAATCT	GCATCAACCA	120
GTGCGTCCGC	TTCAGCGTCA	ACCAGTGCCT	CGGCTTCAGC	GTCGACAAGT	GCTTCGGCTT	180
CAGCATCAAC	GAGTGCGTCG	GCCTCAGCAA	GCGCAAGTAC	CTCAGCGTCA	GCTTCCGCCT	240
CAACCAGTGC	GTCCGCTTCA	GCAAGCACAA	GTGCGTCAGC	CTCAGCAAGT	ATCTCAGCGT	300
CTGAATCGGC	ATCAACGAGT	GCGTCGGCCT	CAGCAAGCGC	AAGTACCTCA	GCGTCAGCTT	360
CCGCCTCAAC	CAGTGCGTCG	GCTTCAGCAA	GCACAAGTGC	GTCAGCCTCA	GCAAGTATCT	420
CAGCGTCTGA	ATCGGCATCA	ACGAGTGCCT	CTGAGTCAGC	ATCAACGAGT	ACGTCAGCCT	480
CAGCAAGCAC	ATCAGCTTCT	GAATCGGCAT	CAACCAGTGC	GTCAGCCTCA	GCATCGACAA	540
GCGCCTCAGC	TTCAGCAAGT	ACCAGTGCTT	CAGCCTCAGC	GTCGACAAGT	GCGTCGGCCT	600
CAACCAGTGC	ATCTGAATCG	GCATCAACCA	GTGCGTCAGC	CTCAGCAAGT	ACTAGTGCAT	660

1390

CAGCTTCAGC ATCAACGAGT GCATCGGCTT

690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1003 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTT CAATATGTGC ACGTTGGAAT GTTAGTGCTT 60
 ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT 120
 CTTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT 180
 TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTTATA TACTAGTGGT GTTTTTGGGG 240
 CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATACT TACAGTTGTT CTGCTCCAAA 300
 GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG 360
 CACAGGATAA CCTGATGCAT TTTTTAGCG ACAATGCTTG CTAATCCTT CTGTCGAATT 420
 TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC 480
 TTAGCTTAGA TCCTGGATGG TTTCTTTTTT CACCCAATGG GTGTTTTTTA CTAGACAAAA 540
 AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAACAC AAAAAGAAAG GAAACTCACA 600
 TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGCTTTT TTACCAACTA TCTTTCGATG 660
 GAGGTCATTT AACCCAGTAT GGTGGTCTTA TCTTTTTTCA GGAACTTTTT TCCAGTTGA 720
 AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT 780
 ATTCCGATTC AGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG 840
 ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTCC AAAATTATTG GAAGGAGGGC 900
 AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTCCAG AACTGACGAG GAAACAGTCC 960
 ATAGTTTTCG ATGCCTCAAC CTGAATTGG TCGAATTCCT TTT 1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTC TGATTGGTTT GCTCTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT	60
TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT	120
ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG	180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT	240
TATCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCT CAGATATTCA	300
CCTTTTGTGG ATTGGTCTGA AGTTTCTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC	360
TAGGAAGCTA GCCGCackGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGc	420
GACTCAAAAC ACCGTTTTGA GGTGTAGAT ATAAGTACG AGcGACTCAA AACACCGTTT	480
TGAGGTGTG GATAGAACTG ACGAGcGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA	540
CTGACGAAGT CgCTCAAAAC ACCGTTTTGA GGTGTGGAT AGAACTGACG AatgctCAA	600
ACACCGTTTT GAGGTGTGG ATAGAACTGA CGAAGCgaaC ATATATACAG CAAGGCGACG	660
CTGACGTGTT TGAAGAGTA TTAAGTCTA TATTTTGGT AAAAATCAAC TTTTACTTGG	720
ATGAAGGTTT TTTTTTTT	738

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 695 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC	60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT	120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCCTCGTCT ATATCAATCT	180
TAACACCTGT TTCAGCGATA ATCTTGTCGA TGTTTTCTCC ACCCTTACCG ATGACAATCT	240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG	300
GACGAACTTC TGGAAATGGT GCTTCAATGA CATCAAGGAT TTCAAAACGC GCTTCTTTGG	360
CTTGAGCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT	420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT	480
CTTCAAAC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA	540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC	600

1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACCTCT GCTACTAGAC 660
 GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG 695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT 60
 TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT 120
 CAGAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC 180
 CAGAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCAA TGGGTGTTTT 240
 TTACTAGACA AAAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAA CACAAAAAGA 300
 AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA 360
 CTATCTTTCG ATGGAGGTCA TTTAACCCAG TATGGTGGTC TTATCTTTT TCAGGAACTT 420
 TTTTCCAGT TGAAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC 480
 CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTTCA ACTGTTAACA 540
 GGTATGGA CGGACTATGC TTGTAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG 600
 TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC 660
 GAGGAAACAG TCCATAGTTT GCGATGCCTC A 691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC 60
 CAAGTTATGC CTAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT 120
 CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT 180
 AATATGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCAT TGAACAAGTG 240

1393

TGAAAGAGA TTCGTAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTTGAAA ACAGATGAGT ATAAAAAGAA AGTCCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG	480
TTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCA GGTGCGAGAG CTTTGACATC CTTTTCTGTA	600
CTGGACCAAG TCAGTTTTCG GTTCTCAAAG CGTTTATATA ATATCCAAA TCCTTGACCA	660
TCCCAGTAAA GAACCTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCACT	60
ACTCGAGTCG CAGCTTCACG GGCCAATTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA	120
CTGTTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCTACT	180
TCTGCTTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATCTTTG	240
ACAGCTTCGT GCCCTTAAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGACT TGGGTGATG ATGATTTGGC CATCTACATA TCCCACCTGT	420
ACCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGCAAAC ATAGGACCAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATACATTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCAGTT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

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CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT      60
TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTTCA ATAGACTTCG TTATTGGGCG      120
GTTACTTTCG AAAC TTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATTC TTTT      180
GGGGTCAAAC TCAGTAACTT ATTGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC      240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATATCTG AATCATCTCC TTCTTGTTCT      300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT      360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT      420
TCGAGAAAC CATCATAAT GGAGTTTGA CGCCTTGGC TCTCAGCCGC TTACAAACTT      480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTTCGTTT      540
CTGCCAAAGC TAAGGCCTTC CGTCCATTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC      600
TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT      657

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(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

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CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG      60
CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGTA TCTCAGCGTC      120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC      180
ACCAGTGCGT CGGCTTCAGC ATCAACCAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT      240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGATCAGCA TCAGCATCAA      300
CGAGTGCATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGCGTCAC      360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC      420
CAGTGCCTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA      480

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1395

TCAGCATCAA CGAGTGCCTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC 540
 AGTGCCTCAG CTTCAGCATC AACGAGTGCG TCAGCTGCAG CAAGTA 586

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT TCAGCTTCAG 60
 CAAGTACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAGTG 120
 CCTCTGAATC CGCATCAACA AGTGCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG 180
 CGTCAACGAG TGCCTCTGAG TCAGCATCAA CGAGTGCCTC ACCTCAGCAA GCACATCAGC 240
 TTCTGAATCT GCATCAACCA GTGCGTCAGC TTCGCGATCA ACAAGCGCCT CGGCCTCAGC 300
 AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC 360
 TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAGCAAGT ACCAGTGCGT CAGTTcAGCA 420
 AGCACAAAGTG CGTCAATTTA GCATCAACCA G 451

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA 60
 CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120
 GGCTTCAGCA AGCACAAGTG CTTCAGCtCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA 180
 ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG 240
 GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTGAGC CTCAGCAAGC 300
 ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA 360
 GCTTCAGCAA GTACAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTGC 420

1396

ACAAG

425

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 572 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTT ATCATGTAGT	60
AGACAAACTC TTCATACTCC AACACTTGCC CATTATATGC GAATCTCATC TATTTTTTCT	120
TTTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTTG	180
AGCAAGTTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT	240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTCG	300
TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT	360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT	420
TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC kAGTkTGCTC	480
TTTGATTTwC ATTGAGTATC AGATTTAGGA AATTAAGTTC CTCGkCTCCA AAAAAkAGCT	540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT	572

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT	60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT	120
CAAcAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT	180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCGTCA GCCTCAGCAT	240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT	300
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAGTGC ATCTGAATCG GCATCAACCA	360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT	420

1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480
 GCGCCTCAGC TTCAGCAAGC ACCGG 505

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC 60
 AATACTGTAC TTTTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120
 AACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA 180
 GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA 240
 ATTTAAGTCA AAAAAATTA CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG 300
 ATTAGTACTC AATGAAAATC AAAGAGCAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC 360
 AGTGTTTTGA GGTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420
 GGATAGAACT GACGAAGTCG GTACCGA 447

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGTAAATAT TTTATTGAAT AAGATAGGCC 60
 TTGATATTAA GCACTTTGGG ACGTTCTCCC TTAGTGCTTT TTTGATTTCT CTTAGTATCC 120
 AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAAATGAA 180
 CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA 240
 AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCCA 300
 AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA 360
 CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT 420

1398
AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAATA CTATATAAGT 480
TCTATAATCT CTTTATAAGA TTTGCCCATC AGACAAAATA GAACGATTTG AAGGCGTTTA 540
TGATATTTAG CTGTACGAGA GTCTTTTAAA AG 572

MISSING UPON TIME OF PUBLICATION

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

- 25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.
- 30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.
- 35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:
- 45 a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;
- b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
- c) retrieval means for obtaining said homologous sequence(s) of step (b).
- 50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 55

60 7. A method for identifying an expression modulating fragment of
Streptococcus pneumoniae genome comprising the step of comparing a database
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a
representative fragment thereof, or a nucleotide sequence at least 95% identical to
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
65 nucleic acid molecule comprised of a complementary nucleotide sequence to said
target sequence, wherein said target sequence comprises sequences known to
regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*
pneumoniae genome, wherein said fragment consists of the nucleotide sequence of
any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a
degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a
degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,
wherein said fragment modulates the expression of an operably linked open reading
frame, wherein said fragment consists of the nucleotide sequence from about 10 to
200 bases in length which is 5' to any one of the open reading frames depicted in
Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome of claim 8.

12. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

130

20. A method for producing a polypeptide in a host cell comprising the steps of:

135

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

Figure 1

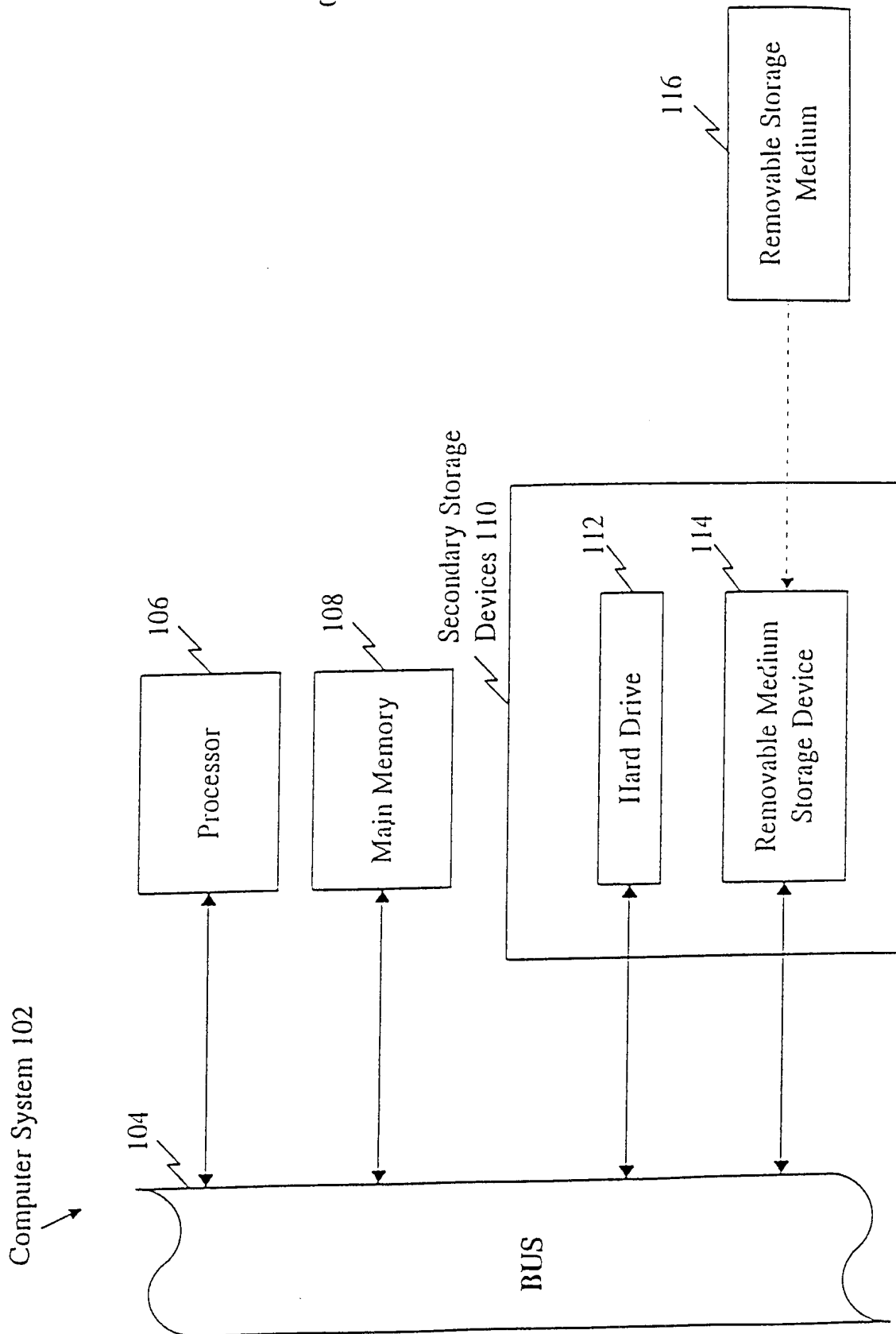
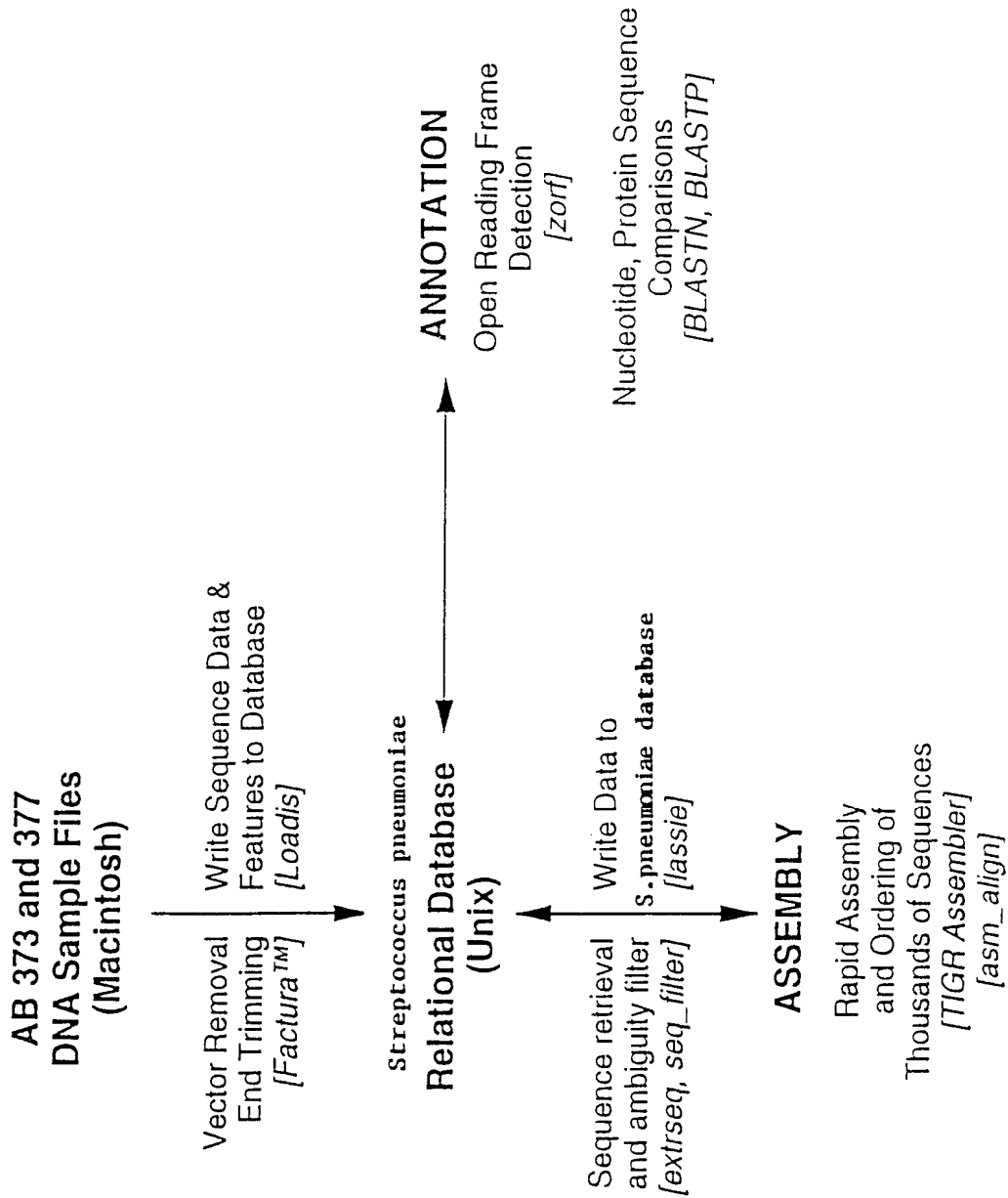


Figure 2

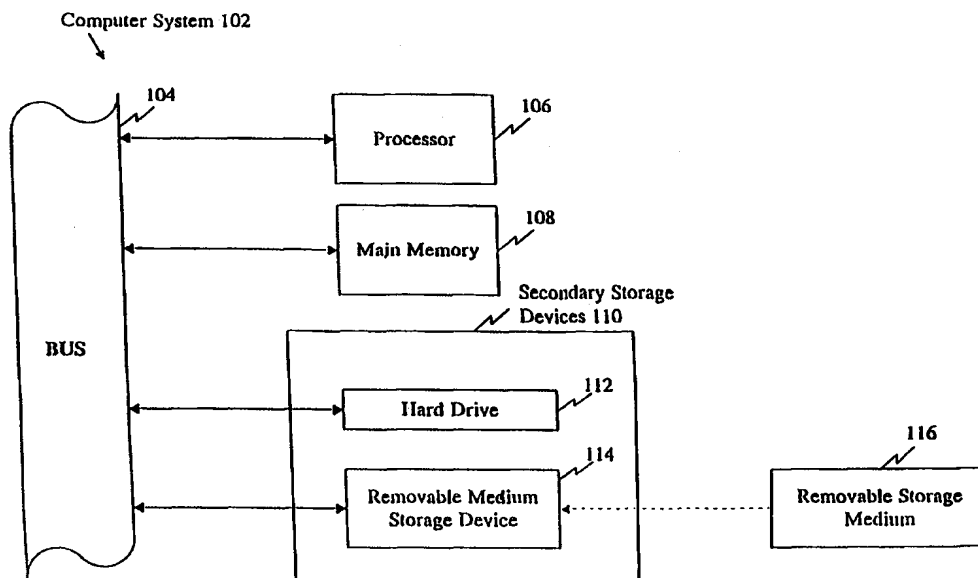




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<p>(21) International Application Number: PCT/US97/19588</p> <p>(22) International Filing Date: 30 October 1997 (30.10.97)</p> <p>(30) Priority Data: 60/029,960 31 October 1996 (31.10.96) US</p> <p>(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).</p>		<p>(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p> <p>(88) Date of publication of the international search report: 20 August 1998 (20.08.98)</p>

(54) Title: *STREPTOCOCCUS PNEUMONIAE* POLYNUCLEOTIDES AND SEQUENCES



(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/19588

<p>A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/31 C07K14/315 C07K16/12 C12Q1/68</p>		
<p>According to International Patent Classification (IPC) or to both national classification and IPC</p>		
<p>B. FIELDS SEARCHED</p>		
<p>Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N C07K C12Q</p>		
<p>Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched</p>		
<p>Electronic data base consulted during the international search (name of data base and, where practical, search terms used)</p>		
<p>C. DOCUMENTS CONSIDERED TO BE RELEVANT</p>		
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 see claims 1-7	1-7
A	<p>--- ALTSCHUL S F ET AL: "BASIL LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, vol. 215, 1990, pages 403-410, XP000604562 cited in the application see the whole document --- -/--</p>	1-7
<p><input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.</p>		
<p>° Special categories of cited documents :</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&" document member of the same patent family</p>		
<p>Date of the actual completion of the international search</p> <p>27 March 1998</p>		<p>Date of mailing of the international search report</p> <p>08.07.98</p>
<p>Name and mailing address of the ISA</p> <p>European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016</p>		<p>Authorized officer</p> <p>HORNIG H.</p>

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/19588

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	W.R. PEARSON AND D.J. LIPMAN: "Improved tools for biological sequence comparison" PROC. NATL. ACAD. SCI., vol. 85, April 1988, NATL. ACAD. SCI., WASHINGTON, DC, US;, pages 2444-2448, XP002060460 cited in the application see the whole document ---	1-7
A	WO 95 06732 A (UNIV ROCKEFELLER ;MASURE H ROBERT (US); PEARCE BARBARA J (US); TUO) 9 March 1995 see the whole document ---	1-7
A	WO 95 31548 A (UAB RESEARCH FOUNDATION ;YOTHER JANET (US); DILLARD JOSEPH P (US)) 23 November 1995 see the whole document ---	1-7
A	WO 95 14712 A (RES CORP TECHNOLOGIES INC) 1 June 1995 see the whole document ---	1-7
A	WO 96 05859 A (AMERICAN CYANAMID CO) 29 February 1996 see the whole document ---	1-7
A	WO 93 10238 A (US HEALTH) 27 May 1993 see the whole document ---	1-7
A	EP 0 687 688 A (UNIV OVIEDO ;UNIV LEICESTER (GB)) 20 December 1995 see the whole document ---	1-7
A	EP 0 622 081 A (UAB RESEARCH FOUNDATION) 2 November 1994 see the whole document -----	1-7

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 97/ 19588

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-4 could be, at least partially be considered as a mere presentation of information Rule 39.1(v), and claims 5-7 at least partially as a computer program, Rule 39.1(vi)PCT, the search has been carried out as far as possible in our systematic documentation.
2. Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-7

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID nos. 1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-391; a computer-based system for identifying fragments of the Streptococcus pneumoniae genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the Streptococcus pneumoniae genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the Streptococcus pneumoniae genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-20) partially

An isolated protein-encoded nucleic acid fragment of the Streptococcus pneumoniae genome, wherein said fragment consists of the nucleotide sequence of the fragment of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising the fragment of the Streptococcus pneumoniae genome SEQ ID no.1; an isolated fragment of the Streptococcus pneumoniae genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frame of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frame of SEQ ID no.1 and Tables 2 and 3 or a degenerate variant thereof; an isolated nucleic acid molecule encoding a homolog of SEQ ID no.1; an isolated polypeptide encoded by SEQ ID no.1 and depicted in Table 2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

molecule whose nucleotide sequence consists of SEQ ID no.1 and depicted in Table 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and b) isolating said protein;

3-392. Claims:(8-20) partially

Idem as subject 2 but limited to each of the sequences of SEQ ID no. 2 to 391;

For the sake of conciseness, the second subject matter is explicitly defined, the other subject matters are defined by analogy hereto.